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79 242.8 92.0 649 14 RSU41731
80 241.6 91.5 532 14 RSU41726
81 239.6 90.8 649 14 RSU41730
82 232 9130 6 AX359935
83 232 87.9 5130 6 AX382149
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88 230.4 87.3 9392 14 AF033808
89 230.4 87.3 9625 14 ALRCG
90 228.8 86.7 793 14 ALDRME
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92 228.4 86.5 1065 10 HAMBSPRI
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96 226.2 85.7 2960 14 REPPROT
97 224 84.8 3189 6 A30504
98 224 84.8 3277 6 A30505
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ALIGNMENTS

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RESULT 1
AX175190 AX175190 648 bp DNA linear PAT 03-JUL-2001
LOCUS Sequence 1 from Patent WO0142444.
DEFINITION
ACCESSION AX175190
VERSION AX175190.1 GI:14598581
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1 Rivera, V., Zoltick, P. and Wilson, J. M.
AUTHORS Methods for expression of genes in primates
TITLE Patent: WO 0142444-A 1 14-JUN-2001;
JOURNAL ARIAD GENE THERAPEUTICS, INC. (US) ; THE UNIVERSITY OF PENNSYLVANIA
(US)
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Matches 264; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AATGAGTCTTATGCAATACCTTTGTAGTCTTGCACATGTTAAACGATGAGTTAGCAACA 60
Db 349 AATGAGTCTTATGCAATACCTTTGTAGTCTTGCACATGTTAAACGATGAGTTAGCAACA 408
QY 61 TGCCTTACAGGAGAGAAAAGCACCCTGTCATCCGATTTGGTGAAGTGGTAGCA 120

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Db 409 TGCCTTACAGGAGAGAAAAGCACCCTGTCATCCGATTTGGTGAAGTGGTAGCA 468
QY 121 TCGTGCCCTTATTAGGAGGCAACAGCGGTCTGCATGTTGGAGCAACCACTAAATT 180
Db 469 TCGTGCCCTTATTAGGAGGCAACAGCGGTCTGCATGTTGGAGCAACCACTAAATT 528
QY 181 CGCATTTGCAGAGATTTGTTATTTAAGTGGCTAGCTCGATACATAAAGCCATTGGACC 240
Db 529 CGCATTTGCAGAGATTTGTTATTTAAGTGGCTAGCTCGATACATAAAGCCATTGGACC 588
QY 241 ATTCACCACATTTGGTGTGCACCTC 264
Db 589 ATTCACCACATTTGGTGTGCACCTC 612
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AX175195 AX175195 648 bp DNA linear PAT 03-JUL-2001
LOCUS Sequence 6 from Patent WO0142444.
DEFINITION
ACCESSION AX175195
VERSION AX175195.1 GI:14598586
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1 Rivera, V., Zoltick, P. and Wilson, J. M.
AUTHORS Methods for expression of genes in primates
TITLE Patent: WO 0142444-A 6 14-JUN-2001;
JOURNAL ARIAD GENE THERAPEUTICS, INC. (US) ; THE UNIVERSITY OF PENNSYLVANIA
(US)
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/notes="MluI/RSV promoter/BglI"
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Best Local Similarity 100.0%; Pred. No. 1.2e-65;
Matches 264; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AATGAGTCTTATGCAATACCTTTGTAGTCTTGCACATGTTAAACGATGAGTTAGCAACA 60
Db 349 AATGAGTCTTATGCAATACCTTTGTAGTCTTGCACATGTTAAACGATGAGTTAGCAACA 408
QY 61 TGCCTTACAGGAGAGAAAAGCACCCTGTCATCCGATTTGGTGAAGTGGTAGCA 120
Db 409 TGCCTTACAGGAGAGAAAAGCACCCTGTCATCCGATTTGGTGAAGTGGTAGCA 468
QY 121 TCGTGCCCTTATTAGGAGGCAACAGCGGTCTGCATGTTGGAGCAACCACTAAATT 180
Db 469 TCGTGCCCTTATTAGGAGGCAACAGCGGTCTGCATGTTGGAGCAACCACTAAATT 528
QY 181 CGCATTTGCAGAGATTTGTTATTTAAGTGGCTAGCTCGATACATAAAGCCATTGGACC 240
Db 529 CGCATTTGCAGAGATTTGTTATTTAAGTGGCTAGCTCGATACATAAAGCCATTGGACC 588
QY 241 ATTCACCACATTTGGTGTGCACCTC 264
Db 589 ATTCACCACATTTGGTGTGCACCTC 612
RESULT 3
AX743955 AX743955 7086 bp DNA linear PAT 14-MAY-2003
LOCUS Sequence 3 from Patent WO03031630.
DEFINITION
ACCESSION AX743955
VERSION AX743955.1 GI:30722652
KEYWORDS
SOURCE synthetic construct

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ORGANISM
synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Fazio,V., Rinaldi,M., Sonzogni,L., Tonon,G. and Orsini,G.
TITLE Multi-cistronic vectors for gene transfer protocols
JOURNAL Patent: WO 03031630-A 3 17-APR-2003;
Keryos Spa (IT)

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Best Local Similarity 99.6%; Pred. No. 2.6e-65;
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QY 1 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGGCAATGCTAAACGATGAGTTAGCAACA 60
DB 1796 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGGCAATGCTAAACGATGAGTTAGCAACA 1737
QY 61 TGCCTTACAGGAGAGAAAAGACCGTGCATGCGGATTCGTTGGAAGTAAGTGTGACGA 120
DB 1736 TGCCTTACAGGAGAGAAAAGACCGTGCATGCGGATTCGTTGGAAGTAAGTGTGACGA 1677
QY 121 TCGTGCCTTATTAGGAAGCAACAGACGGGTCTGACATGGATTGACGAAACCACTAAATT 180
DB 1676 TCGTGCCTTATTAGGAAGCAACAGACGGGTCTGACATGGATTGACGAAACCACTAAATT 1617
QY 181 CCGCATTCGAGAGATATTGATTATTAAGTGCCTAGCTGCATACATAAAGCCATTGACC 240
DB 1616 CCGCATTCGAGAGATATTGATTATTAAGTGCCTAGCTGCATACATAAAGCCATTGACC 1557
QY 241 ATTCACACAAATTGGTGCACCTC 264
DB 1556 ATTCACACAAATTGGTGCACCTC 1533

RESULT 4

BD268239 8238 bp DNA linear PAT 17-JUL-2003
LOCUS Adenovirus vector, packaging cell line, composition and method for
production and use.

ACCESSION BD268239
VERSION BD268239.1 GI:33078007
KEYWORDS JP 2002534130-A/43.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1 (bases 1 to 8238)
AUTHORS Nemerow,G.R., Seggern,D.J.V., Hallenbeck,P.L., Stevenson,S.C. and
Skripchenko,Y.

TITLE Adenovirus vector, packaging cell line, composition and method for
production and use.

JOURNAL Patent: JP 2002534130-A 43 15-OCT-2002;

NOVARTIS AG, THE SCRIPPS RESEARCH INSTITUTE

COMMENT OS Artificial Sequence

PN JP 2002534130-A/43

PD 15-OCT-2002

PF 14-JAN-2000 JP 2000593765

PR 14-JAN-1999 US 60/115920

PI GLEN ROBERT NEMEROW,DANIEL J VON SEGGERN,PAUL L HALLENBECK, PI
SUSAN C STEVENSON,YELENA SKRIPCHENKO

PC C12N15/09,A61K35/76,A61K48/00,A61P35/00,A61P43/00,A61P43/00,

PC C12N5/10,

PC C12N7/00,C12Q1/68,G01N33/53,G01N33/566,C12N15/00,C12N5/00 CC

Description of Artificial Sequence: plasmid

FH key Location/Qualifiers

FT source 1..8238

FEATURES
FT /organism='Artificial Sequence'.

Location/Qualifiers

1..8238

SOURCE

ORGANISM
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 99.4%; Score 262.4; DB 6; Length 8238;
Best Local Similarity 99.6%; Pred. No. 2.5e-65;
Matches 263; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGGCAATGCTAAACGATGAGTTAGCAACA 60
DB 541 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGGCAATGCTAAACGATGAGTTAGCAACA 600

QY 61 TGCCTTACAGGAGAGAAAAGACCGTGCATGCGGATTCGTTGGAAGTAAGTGTGACGA 120
DB 601 TGCCTTACAGGAGAGAAAAGACCGTGCATGCGGATTCGTTGGAAGTAAGTGTGACGA 660

QY 121 TCGTGCCTTATTAGGAAGCAACAGACGGGTCTGACATGGATTGACGAAACCACTAAATT 180
DB 661 TCGTGCCTTATTAGGAAGCAACAGACGGGTCTGACATGGATTGACGAAACCACTAAATT 720

QY 181 CCGCATTCGAGAGATATTGATTATTAAGTGCCTAGCTGCATACATAAAGCCATTGACC 240
DB 721 CCGCATTCGAGAGATATTGATTATTAAGTGCCTAGCTGCATACATAAAGCCATTGACC 780

QY 241 ATTCACACAAATTGGTGCACCTC 264

DB 781 ATTCACACAAATTGGTGCACCTC 804

RESULT 5

ALRSV40LTR 330 bp DNA linear VPL 30-NOV-1999
LOCUS Rous sarcoma virus-SV40 recombinant long terminal repeat DNA.
DEFINITION M27329
ACCESSION M27329.1 GI:341667
VERSION M27329.1
KEYWORDS LTR; long terminal repeat.

SOURCE Simian virus 40

ORGANISM Simian virus 40

REFERENCE 1 (bases 1 to 330)
VIRUSES; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.

AUTHORS Weber,F. and Schaffner,W.

TITLE Enhancer activity correlates with the oncogenic potential of avian
retroviruses

JOURNAL EMBO J. 4 (4), 949-956 (1985)

MEDLINE 85257513

PubMed 2990916

FEATURES Location/Qualifiers

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/organism="Simian virus 40"

/mol_type="genomic DNA"

/db_xref="taxon:10633"

/note="Recombinant sequence of SV40 and Rous sarcoma
virus; Unknown which part is from which virus."

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Query Match 99.0%; Score 261.4; DB 14; Length 330;
Best Local Similarity 99.6%; Pred. No. 7.5e-65;
Matches 262; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGGCAATGCTAAACGATGAGTTAGCAACA 60
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QY 61 TGCCTTACAGGAGAGAAAAGACCGTGCATGCGGATTCGTTGGAAGTAAGTGTGACGA 120
DB 61 TGCCTTACAGGAGAGAAAAGACCGTGCATGCGGATTCGTTGGAAGTAAGTGTGACGA 120

QY 121 TCGTGCCTTATTAGGAAGCAACAGACGGGTCTGACATGGATTGACGAAACCACTAAATT 180
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QY 181 CCGCATTCGAGAGATATTGATTATTAAGTGCCTAGCTGCATACATAAAGCCATTGACC 240

81	TGCCTTACAGGAGAGAAAAGCACCGTGCTATCGCCATGCTGGTGAAGATTAAGGTGGTGA	140	
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141	TCGTGCGCTTTATTAGGAAGGCAACAGACCGGCTTGA CATGGATTGGACGAACCACTGAATTT	200	
181	CCGCAATGTCAGAGATATTTGATTAAAGTGCGCTAGCTCGATACAATAAAGCCCAATTTGACC	240	
201	CCGCAATGTCAGAGATATTTGATTAAAGTGCGCTAGCTCGATACAATAAAGCCCAATTTGACC	260	
241	ATTCAACACATTTGGTGTGCACCT	263	
261	ATTCAACACATTTGGTGTGCACCT	283	
RESULT 7			
REASV4	700 bp	DNA linear	
LOCUS	Avian sarcoma virus	right and left ends (plus environment).	
DEFINITION	Avian sarcoma virus		
ACCESSION	V01168	N00022	
VERSION	V01168.1	GI:61497	
KEYWORDS	Avian sarcoma virus		
ORGANISM	Avian sarcoma virus		
REFERENCE	Viruses; Retroid viruses; Retroviridae; Avian type C retroviruses.		
AUTHORS	1 (bases 1 to 700)		
TITLE	Swanstrom, R., Delorbe, W.J., Bishop, J.M. and Varmus, H.E.		
	Nucleotide sequence of cloned unintegrated avian sarcoma virus DNA: viral DNA contains direct and inverted repeats similar to those in transposable elements		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A.	78 (1), 124-128 (1981)	
MEDLINE	81223697		
PUBMED	6264426		
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QY	61	TGCCTTACAAGGAGAGAAAAGCACCGTGCTATCGCCATGCTGGTGAAGTAAAGGTGGTGA 120	
Db	81	TGCCTTACAAGGAGAGAAAAGCACCGTGCTATCGCCATGCTGGTGAAGTAAAGGTGGTGA 140	
QY	121	TCGTGCGCTTTATTAGGAAGGCAACAGACCGGCTTGA CATGGATTGGACGAACCACTAAATTT 180	
Db	141	TCGTGCGCTTTATTAGGAAGGCAACAGACCGGCTTGA CATGGATTGGACGAACCACTGAATTT 200	
QY	181	CCGCAATGTCAGAGATATTTGATTAAAGTGCGCTAGCTCGATACAATAAAGCCCAATTTGACC 240	
Db	201	CCGCAATGTCAGAGATATTTGATTAAAGTGCGCTAGCTCGATACAATAAAGCCCAATTTGACC 260	
QY	241	ATTCAACACATTTGGTGTGCACCT	263
Db	261	ATTCAACACATTTGGTGTGCACCT	283
RESULT 8			
ALRDAI	1239 bp	DNA linear	
LOCUS	Rous sarcoma virus (Schmidt-Ruppin A), 5' LTR and gag gene.		
DEFINITION	Rous sarcoma virus		
ACCESSION	L29198	J02018 J02026 J02338 N00020	

VERSION L29198.1 GI:459671
 KEYWORDS gag protein; long terminal repeat (LTR); polyprotein.
 SEGMENT 1 of 2
 SOURCE Rous sarcoma virus
 ORGANISM Rous sarcoma virus
 REFERENCE 1 (sites)
 AUTHORS Viruses; Retroviral viruses; Retroviridae; Alpharetrovirus.
 TITLE Nucleotide sequence of cloned unintegrated avian sarcoma virus DNA: viral DNA contains direct and inverted repeats similar to those in transposable elements
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 78 (1), 124-128 (1981)
 MEDLINE 81223697
 PUBMED 6264426
 REFERENCE 2 (sites)
 AUTHORS Swanson, R., Varmus, H.E. and Bishop, J.M.
 TITLE Nucleotide sequence of the 5' noncoding region and part of the gag gene of Rous sarcoma virus
 JOURNAL J. Virol. 41 (2), 535-541 (1982)
 MEDLINE 82192582
 PUBMED 6281465
 REFERENCE 3 (sites)
 AUTHORS Misra, T.K., Grandgenett, D.P. and Parsons, J.T.
 TITLE Avian retrovirus pp32 DNA-binding protein. I. Recognition of specific sequences on retrovirus DNA terminal repeats
 JOURNAL J. Virol. 44 (1), 330-343 (1982)
 MEDLINE 83059884
 PUBMED 6292495
 REFERENCE 4 (sites)
 AUTHORS Petersen, R.B., Hensel, C.H. and Hackett, P.B.
 TITLE Identification of a ribosome-binding site for a leader peptide encoded by Rous sarcoma virus RNA
 JOURNAL J. Virol. 51 (3), 722-729 (1984)
 MEDLINE 84292449
 PUBMED 6088795
 REFERENCE 5 (sites)
 AUTHORS Hughes, S., Mellstrom, K., Kosik, E., Tamanoi, F. and Brugge, J.
 TITLE Mutation of a termination codon affects src initiation in reversible transformation of mammalian cells
 JOURNAL Mol. Cell. Biol. 4 (9), 1738-1746 (1984)
 MEDLINE 85016324
 PUBMED 6092936
 REFERENCE 6 (sites)
 AUTHORS Maroney, A.C., Qureshi, S.A., Foster, D.A. and Brugge, J.S.
 TITLE Cloning and characterization of a thermolabile v-src gene for use in reversible transformation of mammalian cells
 JOURNAL Oncogene 7 (6), 1207-1214 (1992)
 MEDLINE 92278773
 PUBMED 1375718
 COMMENT The following base pairs can be found in the references listed below:
 1-350 J. Virol. 44, 330-343 (1982)
 230-1239 J. Virol. 41, 535-541 (1982)
 1-330 Proc. Natl. Acad. Sci. U.S.A. 78, 124-128 (1981) 230-619 Mol. Cell. Biol. 4, 1738-1746 (1984)
 253-318 J. Virol. 51, 722-729 (1984)
 For a description of the life cycle and the RNA transcripts of Rous sarcoma virus, see the Rous sarcoma virus Prague C strain entry. Positions 331-348 are complementary to the 3' stem of host-encoded Trp-tRNA. Trp-tRNA binds to virion RNA at this site and serves as a primer for DNA synthesis by reverse transcription. The gag-Pr76, gag-pol-Pr180, and env-Pr95 reading frames all begin with the fourth 'atg' start codon of their respective mRNAs at position 601-603. [4] used anisomycin to stall ribosomes at the initiation codon and found that ribosomes were stalled at the initiation codon at position 270-272 indicating that this 'atg' start codon is actually used to produce a 7 amino acid leader peptide. [4] found a small peptide that comigrated with a synthetic 7 amino acid peptide identical to the peptide predicted from the sequence following this start codon.
 The src cds is the only coding region that does not utilize the 'atg' start codon at position 601-603. In the src mRNA this start codon is followed by an in-frame stop codon. [5] mutated this 'tga' stop codon to 'cga' and found that an src protein extended at

the N-terminal end was produced. [5] predicts that the 'atg' start codon at position 601-603 is utilized in the 21S src mRNA to produce a 9 amino acid leader peptide. Cells infected with the mutant RSV encoding the extended src-p63 exhibit a different morphology than those infected with wild-type RSV producing src-p60.
 The Prague strain subgroup C Rous sarcoma virus has been shown to encode a transcriptional activator protein from a reading frame that corresponds to positions 601-618 (exon 1) and 902- greater than 1239 (partial exon 2), (see Prague C entry).

FEATURES

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 /note="5' LTR"
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 /note="35S virion RNA"
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 /note="5' terminal repeat"
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 /bound_moiety="Trp-tRNA"
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 GRVSPPECIETKATSERIDKGEVETTVQORDAKWAPKATPKVTGTSYCHCGTA
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 DB 61 TGCCTTACAGGAGAGAAAACCGCTGCATGCCGATTCGTGGAAGTGTGTACGA 120
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 DB 121 TGTGTCCTTATTAGGAAGCAACAGACGGCTCTGACATGGATTGGACGACCACTAAAT 180
 QY 181 CCGCATTCGAGAGATATTGTATTTTAAGTGCCTAGCTGCATACATTAAGCCATTGACC 240
 DB 181 CCGCATTCGAGAGATATTGTATTTTAAGTGCCTAGCTGCATACATTAAGCCATTGACC 240
 QY 241 ATTACACCATTTGGTGTGCACT 263
 DB 241 ATTACACCATTTGGTGTGCACT 263

RESULT 9

ALR22

LOCUS ALRDA2 3256 bp DNA linear VRL 12-APR-1999
 DEFINITION Rous sarcoma virus (Schmidt-Ruppin A) env-src-3'LTR.
 ACCESSION L29199 J02038 J02026 J02352 K01194 K01195 N00021
 VERSION L29199.1 GI:459672
 KEYWORDS c-myc proto-oncogene; kinase; protein kinase; src oncogene.
 SEGMENT 2 of 2
 SOURCE Rous sarcoma virus
 ORGANISM Rous sarcoma virus
 REFERENCE 1 (sites)
 AUTHORS Viruses; Retrovirdae; Retroviridae; Alpharetrovirus.
 TITLE Czerlinskiy,A.P., DeLorbe,W., Swanson,R., Varmus,H.E., Bishop,J.M., Tischer,E. and Goodman,H.M.
 The nucleotide sequence of an untranslated but conserved domain at the 3' end of the avian sarcoma virus genome
 JOURNAL Nucleic Acids Res. 8 (13), 2967-2984 (1980)
 MEDLINE 81053726
 PUBMED 81053726
 REFERENCE 2 (sites)
 AUTHORS Czerlinskiy,A.P., Levinson,A.D., Varmus,H.E., Bishop,J.M., Tischer,E. and Goodman,H.M.
 Nucleotide sequence of an avian sarcoma virus oncogene (src) and proposed amino acid sequence for gene product
 JOURNAL Nature 287 (5779), 198-203 (1980)
 MEDLINE 81052295
 PUBMED 8253794
 REFERENCE 3 (sites)
 AUTHORS Swanson,R., DeLorbe,W.J., Bishop,J.M. and Varmus,H.E.
 Nucleotide sequence of cloned unintegrated avian sarcoma virus DNA: viral DNA contains direct and inverted repeats similar to those in transposable elements
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 78 (1), 124-128 (1981)
 MEDLINE 81223697
 PUBMED 6264426
 REFERENCE 4 (sites)
 AUTHORS Swanson,R., Varmus,H.E. and Bishop,J.M.
 Nucleotide sequence of the 5' noncoding region and part of the gag gene of Rous sarcoma virus
 JOURNAL J. Virol. 41 (2), 535-541 (1982)
 MEDLINE 82192582
 PUBMED 6281465
 REFERENCE 5 (sites)
 AUTHORS Hughes,S.H.
 Sequence of the long terminal repeat and adjacent segments of the endogenous avian virus Rous-associated virus 0
 JOURNAL J. Virol. 43 (1), 191-200 (1982)
 MEDLINE 82269131
 PUBMED 6286997
 REFERENCE 6 (sites)
 AUTHORS Misra,T.K., Grandgenett,D.P. and Parsons,J.T.
 Avian retrovirus pp32 DNA-binding protein. I. Recognition of specific sequences on retrovirus DNA terminal repeats
 JOURNAL J. Virol. 44 (1), 330-343 (1982)
 MEDLINE 83059884
 PUBMED 6292495
 REFERENCE 7 (sites)
 AUTHORS Czerlinskiy,A.P., Levinson,A.D., Varmus,H.E., Bishop,J.M., Tischer,E. and Goodman,H.
 Corrections to the nucleotide sequence of the src gene of Rous sarcoma virus
 JOURNAL Nature 301 (5902), 736-738 (1983)
 MEDLINE 83141780
 PUBMED 6298633
 REFERENCE 8 (sites)
 AUTHORS Sorge,J., Ricci,W. and Hughes,S.H.
 cis-Acting RNA packaging locus in the 115-nucleotide direct repeat of Rous sarcoma virus
 JOURNAL J. Virol. 48 (3), 667-675 (1983)
 MEDLINE 84036404
 PUBMED 6313966
 REFERENCE 9 (sites)
 AUTHORS Hughes,S. and Kosik,E.
 Matagenesis of the region between env and src of the SR-A strain of Rous sarcoma virus for the purpose of constructing

helper-independent vectors
 JOURNAL Virology 136 (1), 89-99 (1984)
 MEDLINE 84251740
 PUBMED 6330999
 REFERENCE 10 (sites)
 AUTHORS Petersen,R.B., Hensel,C.H. and Hackett,P.B.
 Identification of a ribosome-binding site for a leader peptide encoded by Rous sarcoma virus RNA
 JOURNAL J. Virol. 51 (3), 722-729 (1984)
 MEDLINE 84292449
 PUBMED 6088795
 REFERENCE 11 (sites)
 AUTHORS Hughes,S., Mellstrom,K., Kosik,E., Tamanoi,F. and Brugge,J.
 Mutation of a termination codon affects src initiation
 JOURNAL Mol. Cell. Biol. 4 (9), 1738-1746 (1984)
 MEDLINE 85036324
 PUBMED 6092936
 REFERENCE 12 (sites)
 AUTHORS Resnick,R., Omer,C.A. and Paras,A.J.
 Involvement of retrovirus reverse transcriptase-associated RNase H in the initiation of strong-stop (+) DNA synthesis and the generation of the long terminal repeat
 JOURNAL J. Virol. 51 (3), 813-821 (1984)
 MEDLINE 84292461
 PUBMED 6206236
 REFERENCE 13 (sites)
 AUTHORS Fellman,D., Garber,E.A., Cross,F.R. and Hanafusa,H.
 Fine structural mapping of a critical NH2-terminal region of p60src
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 82 (6), 1623-1627 (1985)
 MEDLINE 85166183
 PUBMED 2984663
 REFERENCE 14 (sites)
 AUTHORS Maroney,A.C., Qureshi,S.A., Foster,D.A. and Brugge,J.S.
 Cloning and characterization of a thermolabile v-src gene for use in reversible transformation of mammalian cells
 JOURNAL Oncogene 7 (6), 1207-1214 (1992)
 MEDLINE 92278773
 PUBMED 1375718
 COMMENT The bases as they are found in the references are listed below:
 1-3107 Nature 287, 198-203 (1980)
 2907-3256 Proc. Natl. Acad. Sci. U.S.A. 78, 124-128 (1981)
 2244-3176 Nucleic Acids Res. 8, 2967-2984 (1980)
 700-908 J. Virol. 43, 191-200 (1982)
 2927-3176 J. Virol. 44, 330-343 (1982)
 1-3107 Nature 301, 736-738 (1983)
 706-900 and 2791-2830 J. Virol. 48, 667-675 (1983)
 721-1140 Mol. Cell. Biol. 4, 1738-1746 (1984)
 2912-2938 J. Virol. 51, 813-821 (1984)
 873-882 and 930-1128 Virology 136, 89-99 (1984)
 1121-1173 Proc. Natl. Acad. Sci. U.S.A. 82, 1623-1627 (1985) [1]
 revised by [7].
 [7] revises [1].
 See comment in segment 1.
 The src gene is believed to have been obtained from avian DNA when an ALV-like virus recombined with host DNA. Homology to the c-src gene of chicken begins at position 1032. A direct repeat of about 100 bp is present near either end of exon 2 the 21S (src) mRNA. These repeats include positions 772-899 and 2703-2799. A polyadenylation signal is present at position 3149-3154. [7] contains a revision of the sequence in [1]. Individual revisions are not noted in sites.
 [9] mutated the 'tga' stop codon at position 1057-1059 to 'cga' and found that the mutant strain produced an src protein extended at the NH-terminal end.
 [10] created a synthetic Rous sarcoma virus lacking the direct repeat 5' of src-p60 and with Clai sites flanking src-p60 to create a vector capable of expressing genes inserted in place of src-p60 (see RSV vector in synthetic section).
 [11] used mutants with alterations in the N-terminal region of the src-p60 gene to determine the requirements for N-myristylation of residue at amino acid position 2 (position 1126-1128 of this sequence).

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    /db_xref="taxon:11886"
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Best Local Similarity 99.6%; Pred. No. 5.6e-65;
Matches 262; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  1  AATGAGCTTTATGCAATCTCTTGTAGTCTTGGCAACATGCTAACGATGATTAGCAACA 60
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Qy  61  TGCCTTACAGAGGAGAAAGACCGTCGATCGCGATTTGGTGAAGTAAAGTGTAGCA 120
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Qy  121 TCGTGCCTTTATTAGGAAGCAACAGACGGGTCTGACATGATTGGACCAACCAATAATT 180
Db  3047 TCGTGCCTTTATTAGGAAGCAACAGACGGGTCTGACATGATTGGACCAACCAATAATT 3106

Qy  181 CCGCAATTCAGAGATATTGTATTTAAGTCCTAGCTCGATACAAATAAAGCGCATTTGACC 240
Db  3107 CCGCAATTCAGAGATATTGTATTTAAGTCCTAGCTCGATACAAATAAAGCGCATTTGACC 3166

Qy  241 ATTCAACCAATTGGTGCACCT 263

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Db 3167 ATTCAACCAATTGGTGCACCT 3189

RESULT 10

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LOCUS      Cloning vector RCAS-L14 DNA, complete sequence.
DEFINITION      AB105370
ACCESSION      AB105370
VERSION        AB105370.1 GI:28971911
KEYWORDS
SOURCE      Cloning vector RCAS-L14
ORGANISM      Cloning vector RCAS-L14
              artificial sequences; vectors.
REFERENCE      1
              Nohno,T.
              Konaguchi,C., Kawakami,Y. and Nohno,T.
              Nucleotide sequence of retroviral cloning vector, RCAS-L14
              Published Only in Database (2003)
              2 (bases 1 to 11572)
              Nohno,T.
              Direct Submission
              Submitted (10-MAR-2003) Teutomu Nohno, Kawasaki Medical School,
              Department of Molecular Biology; 577 Matsushima, Kurashiki, Okayama
              701-0192, Japan [E-mail:nohno@cc.kawasaki-m.ac.jp,
              Tel:81-86-462-1111(ex.83501), fax:81-86-462-1199]
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ORIGIN

Query Match 99.0%; Score 261.4; DB 12; Length 11572;
 Best Local Similarity 99.6%; Pred. No. 4.7e-65;
 Matches 262; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 AATGTAGCTTTATGCAATACCTCTCTGTAGTCTTGGCAACATGTAACGATGAGTACCA 60
 Db 139 AATGTAGCTTTATGCAATACCTCTCTGTAGTCTTGGCAACATGTAACGATGAGTACCA 198
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 Qy 121 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGGAATTGGACGACCACTAAAT 180
 Db 259 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGGAATTGGACGACCACTAAAT 318
 Qy 181 CGGCATTTGACGAGATTTGATTTTAAATGCTGCTAGCTGATACCAATAAAGCCATTGACC 240
 Db 319 CGGCATTTGACGAGATTTGATTTTAAATGCTGCTAGCTGATACCAATAAAGCCATTGACC 378
 Qy 241 ATTCAACCACTTGGTGTCACT 263
 Db 379 ATTCAACCACTTGGTGTCACT 401

RESULT 11
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 LOCUS
 DEFINITION Methods and compositions useful for modulation of angiogenesis

using tyrosine kinase Src.
 BD261584
 VERSION BD261584.1 GI:33071352
 KEYWORDS JP 2002516344-A/1.
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1 (bases 1 to 11627)
 AUTHORS Cheresih,D.A., Eliceiri,B. and Schwartzberg,P.L.
 TITLE Methods and compositions useful for modulation of angiogenesis
 JOURNAL using tyrosine kinase Src
 COMMENT Patent: JP 2002516344-A 1 04-JUN-2002;
 THE SCRIPPS RESEARCH INSTITUTE,THE UNITED STATES OF AMERICA
 OS Artificial Sequence
 PN JP 2002516344-A/1
 PD 04-JUN-2002
 PF 28-MAY-1999 JP 2000550976
 PR 29-MAY-1998 US 60/087220
 PI DAVID A CHERESH,BRIAN ELICEIRI,PAMELA L SCHWARTZBERG PC
 A61K38/00,A61K45/00,A61K48/00,A61P19/02,A61P29/00, PC
 A61P35/00,
 PC A61P35/02,A61P43/00,C12N9/12,C12N15/09,A61K37/02,C12N15/00 CC
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 sarcoma virus
 CC pBR322 sequences
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 CC upstream (numbering begins at the upstream R) CC U3
 CC R
 CC U5
 CC downstream
 CC U3
 CC U3
 CC R
 CC U5
 CC PPT
 CC splice donor (AGGT)
 CC env splice acceptor (AGGC)
 CC ClalI splice acceptor (AGGA)
 CC gag p19
 CC gag p10
 CC gag p12
 CC gag p27
 CC gag p15
 CC gag stop
 CC pol RT
 CC pol IN
 CC pol stop
 CC env gp85
 CC env gp37
 CC env stop
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 CC and does not
 CC cut.
 Location/Qualifiers
 PH Key
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 (7649)..(11258)
 (7166)..(7494)
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 FT misc_feature
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DB 7286 TCGTGCTTATTAAGAGGCAACAGACGCGTCTGACATGATTCGACGACCACTAAAT 7345

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DB 7346 CCGCATTGACAGATATTTGATTTAAGTGCCTAGCTCGATACATAAAGCCATTTGACC 7405

QY 241 ATTCACACATTTGGTGGACCT 263
DB 7406 ATTCACACATTTGGTGGACCT 7428

RESULT 12
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LOCUS AX643582 2245 bp DNA linear PAT 24-FEB-2003
DEFINITION Sequence 1 from Patent WO02099100.
ACCESSION AX643582
VERSION AX643582.1 GI:28551382
KEYWORDS
SOURCE Mus sp.
ORGANISM Mus sp.
REFERENCE
    1 Al-Rubeai, M. and Shuttleworth, J.
    Method of production of a protein in cells which inducibly express
    the cell cycle inhibitor protein, p21
    Patent: WO 02099100-A 1 12-DEC-2002;
    Lonza Biologics plc (GB)
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    Matches 261; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGCTAACGATGAGTTAGCAACA 60
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QY 61 TGCCTTACAGGAGAGAAAAGACCCGTCATGCGGATTCGTTGGAGTAAAGTGGTACGA 120
DB 365 TGCCTTACAGGAGAGAAAAGACCCGTCATGCGGATTCGTTGGAGTAAAGTGGTACGA 424

QY 121 TCGTGCTTATTAAGAGGCAACAGACGCGTCTGACATGATTCGACGACCACTAAAT 180
DB 425 TCGTGCTTATTAAGAGGCAACAGACGCGTCTGACATGATTCGACGACCACTAAAT 484

QY 181 CCGCATTGACAGATATTTGATTTAAGTGCCTAGCTCGATACATAAAGCCATTTGACC 240
DB 485 CCGCATTGACAGATATTTGATTTAAGTGCCTAGCTCGATACATAAAGCCATTTGACC 544

QY 241 ATTCACACATTTGGTGGACCC 262
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RESULT 13
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LOCUS XXU42373 6289 bp DNA circular SYN 05-JAN-1996
DEFINITION Cloning vector pOP13Cat target vector from Lacswitch System.
ACCESSION U42373
VERSION U42373.1 GI:1147762
KEYWORDS
SOURCE Cloning vector pOP13Cat
ORGANISM Cloning vector pOP13Cat
REFERENCE 1 (bases 1 to 6289)
AUTHORS Marsh, S.
TITLE Direct Submission
JOURNAL Submitted (05-DEC-1995) Sam Marsh, Marketing, Stratagene, 11011
North Torrey Pines Road, La Jolla, CA 92037, USA
FEATURES
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    Best Local Similarity 99.6%; Pred. No. 1e-64;
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QY 1 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGCTAACGATGAGTTAGCAACA 60
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QY 61 TGCCTTACAGGAGAGAAAAGACCCGTCATGCGGATTCGTTGGAGTAAAGTGGTACGA 120
DB 2425 TGCCTTACAGGAGAGAAAAGACCCGTCATGCGGATTCGTTGGAGTAAAGTGGTACGA 2484

QY 121 TCGTGCTTATTAAGAGGCAACAGACGCGTCTGACATGATTCGACGACCACTAAAT 180
DB 2485 TCGTGCTTATTAAGAGGCAACAGACGCGTCTGACATGATTCGACGACCACTAAAT 2544

QY 181 CCGCATTGACAGATATTTGATTTAAGTGCCTAGCTCGATACATAAAGCCATTTGACC 240
DB 2545 CCGCATTGACAGATATTTGATTTAAGTGCCTAGCTCGATACATAAAGCCATTTGACC 2604

QY 241 ATTCACACATTTGGTGGACCC 262
DB 2605 ATTCACACATTTGGTGGACCC 2626

RESULT 14
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LOCUS AX018983 5177 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 1 from Patent WO9942577.
ACCESSION AX018983
VERSION AX018983.1 GI:10043078
KEYWORDS

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ORIGIN

Query Match 97.8%; Score 258.2; DB 14; Length 1016;
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QY 61 TGCCTTACAAGGAGAAAGACACCGTGCATGCCGATGGTGAAGTAAGTGGTACGA 120
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 DB 747 TACCTTACAAGGAGAAAGACACCGTGCATGCCGATGGTGAAGTAAGTGGTACGA 806

QY 121 TCGTGCCTTATAGGAGCAACAGACGGGCTCTGACATGGATTGGAGCAACCACTAAATT 180
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 DB 807 TCGTGCCTTATAGGAGCAACAGACGGGCTCTGACATGGATTGGAGCAACCACTGAATT 866

QY 181 CGCATTTGAGAGATATTGTTATTTAAGTGCCTAGCTGATACAAATAAGCGCATTTGACC 240
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 DB 867 CGCATTCGAGAGATATTGTTATTTAAGTGCCTAGCTGATACAAATAAGCGCATTTGACC 926

QY 241 ATTCAACACATTGGTGCACCT 263
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 DB 927 ATTCAACACATTGGTGCACCT 949

RESULT 17

AR071323
 LOCUS AR071323 4965 bp DNA linear PAT 18-FEB-2000
 DEFINITION Sequence 1 from patent US 5910488.
 ACCESSION AR071323
 VERSION AR071323.1 GI:7222211
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 4965)
 AUTHORS Nabel, G.J., Nabel, E.G., Lew, D. and Marquet, M.
 TITLE Plasmids suitable for gene therapy
 JOURNAL Patent: US 5910488-A 1 08-JUN-1999;
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ORIGIN

Query Match 97.6%; Score 257.6; DB 6; Length 4965;
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QY 1 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAACATGCTTAACGATGAGTTAGCAACA 60
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 DB 260 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAACATGCTTAACGATGAGTTAGCAACA 319

QY 61 TGCCTTACAAGGAGAAAGACACCGTGCATGCCGATGGTGAAGTAAGTGGTACGA 120
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 DB 320 TGCCTTACAAGGAGAAAGACACCGTGCATGCCGATGGTGAAGTAAGTGGTACGA 379

QY 121 TCGTGCCTTATAGGAGCAACAGACGGGCTCTGACATGGATTGGAGCAACCACTAAATT 180
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 DB 380 TCGTGCCTTATAGGAGCAACAGACGGGCTCTGACATGGATTGGAGCAACCACTGAATT 439

QY 181 CGCATTTGAGAGATATTGTTATTTAAGTGCCTAGCTGATACAAATAAGCGCATTTGACC 240
 |||||
 DB 440 CGCATTTGAGAGATATTGTTATTTAAGTGCCTAGCTGATACAAATAAGCGCATTTGACC 499

QY 241 ATTCAACACATTGGTGCACCTC 264
 |||||
 DB 500 ATTCAACACATTGGTGCACCTC 523

RESULT 18

Query Match 97.1%; Score 256.4; DB 6; Length 562;
 Best Local Similarity 99.6%; Pred. No. 2e-63;

AX256413
 LOCUS AX256413 262 bp DNA linear PAT 10-OCT-2001
 DEFINITION Sequence 61 from Patent WO0170816.
 ACCESSION AX256413
 VERSION AX256413.1 GI:16075238
 KEYWORDS
 source
 1..262
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"

ORIGIN

Query Match 97.4%; Score 257.2; DB 6; Length 262;
 Best Local Similarity 98.9%; Pred. No. 1.3e-63;
 Matches 259; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAACATGCTTAACGATGAGTTAGCAACAT 61
 |||||
 DB 1 ATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAACATGCTTAACGATGAGTTAGCAACAT 60

QY 62 GCCTTACAAGGAGAAAGACACCGTGCATGCCGATGGTGAAGTAAGTGGTACGAT 121
 |||||
 DB 61 GCCTTACAAGGAGAAAGACACCGTGCATGCCGATGGTGAAGTAAGTGGTACGAT 120

QY 122 CGTGCTTATTAGGAGCAACAGACGGGCTCTGACATGGATTGGAGCAACCACTAAATT 181
 |||||
 DB 121 CGTGCTTATTAGGAGCAACAGACGGGCTCTGACATGGATTGGAGCAACCACTGAATT 180

QY 182 CGCATTCGAGAGATATTGTTATTTAAGTGCCTAGCTGATACAAATAAGCGCATTTGACCA 241
 |||||
 DB 181 CGCATTCGAGAGATATTGTTATTTAAGTGCCTAGCTGATACAAATAAGCGCATTTGACCA 240

QY 242 TTCACCACTGGTGCACCT 263
 |||||
 DB 241 TTCACCACTGGTGCACCT 262

RESULT 19

AX643583
 LOCUS AX643583 562 bp DNA linear PAT 24-FEB-2003
 DEFINITION Sequence 2 from Patent WO02099100.
 ACCESSION AX643583
 VERSION AX643583.1 GI:28551383
 KEYWORDS
 source
 1..562
 /organism="Mus sp."
 /mol_type="unassigned DNA"
 /db_xref="taxon:10095"
 /note="Rous Sarcoma Virus LTR promoter"

ORIGIN

Query Match 97.1%; Score 256.4; DB 6; Length 562;
 Best Local Similarity 99.6%; Pred. No. 2e-63;

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Matches 257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGGCAATGTAACGATGAGTTAGCAACA 60
Db |||||||
305 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGGCAATGTAACGATGAGTTAGCAACA 364
QY 61 TGCCTTACAAGGAGAGAAAAGACACCGTGCATGCCGATTGGTGGAAAGTAAGTGGTACGA 120
Db |||||||
365 TGCCTTACAAGGAGAGAAAAGACACCGTGCATGCCGATTGGTGGAAAGTAAGTGGTACGA 424
QY 121 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGATTTGGAGCAACCACTAAATT 180
Db |||||||
425 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGATTTGGAGCAACCACTAAATT 484
QY 181 CGCATTTGCAGAGATATTGTAATTTAAGTGCCTAGCTCGATACAATAAAGCGCATTTGACC 240
Db |||||||
485 CGCATTTGCAGAGATATTGTAATTTAAGTGCCTAGCTCGATACAATAAAGCGCATTTGACC 544
QY 241 ATTCACCAATTGGTGTG 258
Db |||||||
545 ATTCACCAATTGGTGTG 562

RESULT 20
AX743954
LOCUS AX743954 4457 bp DNA linear PAT 14-MAY-2003
DEFINITION Sequence 2 from Patent WO03031630.
ACCESSION AX743954
VERSION AX743954.1 GI:30722651
KEYWORDS synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Fazio V., Rinaldi M., Sonzogni L., Tonon G. and Orsini G.
TITLE Multi-cistronic vectors for gene transfer protocols
JOURNAL Patent: WO 03031630-A 2 17-APR-2003;
Keryos Spa (IT)
FEATURES
source
1. .4457
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 95.2%; Score 251.4; DB 6; Length 4457;
Best Local Similarity 99.2%; Pred. No. 4.2e-62;
Matches 263; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGGCAATGTAACGATGAGTTAGCAACA 60
Db |||||||
716 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGGCAATGTAACGATGAGTTAGCAACA 775
QY 61 TGCCTTACAAGGAGAGAAAAGACACCGTGCATGCCGATTGGTGGAAAGTAAGTGGTACGA 120
Db |||||||
776 TGCCTTACAAGGAGAGAAAAGACACCGTGCATGCCGATTGGTGGAAAGTAAGTGGTACGA 835
QY 121 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGATTTGGAGCAACCACTAAATT 180
Db |||||||
836 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGATTTGGAGCAACCACTAAATT 895
QY 181 CGCATTTGCAGAGATATTGTAATTTAAGTGCCTAGCTCGATACAATAAAGCGCATTTGACC 239
Db |||||||
896 CGCATTTGCAGAGATATTGTAATTTAAGTGCCTAGCTCGATACAATAAAGCGCATTTGACC 955
QY 240 CATTCAACCAATTGGTGTGACCTC 264
Db |||||||
956 CATTCAACCAATTGGTGTGACCTC 980

RESULT 21
AX743956/c
LOCUS AX743956 7334 bp DNA linear PAT 14-MAY-2003
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DEFINITION Sequence 4 from Patent WO03031630.
ACCESSION AX743956
VERSION AX743956.1 GI:30722653
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Fazio V., Rinaldi M., Sonzogni L., Tonon G. and Orsini G.
TITLE Multi-cistronic vectors for gene transfer protocols
JOURNAL Patent: WO 03031630-A 4 17-APR-2003;
Keryos Spa (IT)
FEATURES
Location/Qualifiers
source
1. .7334
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 95.2%; Score 251.4; DB 6; Length 7334;
Best Local Similarity 99.2%; Pred. No. 3.9e-62;
Matches 263; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGGCAATGTAACGATGAGTTAGCAACA 60
Db |||||||
2041 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGGCAATGTAACGATGAGTTAGCAACA 1982
QY 61 TGCCTTACAAGGAGAGAAAAGACACCGTGCATGCCGATTGGTGGAAAGTAAGTGGTACGA 120
Db |||||||
1981 TGCCTTACAAGGAGAGAAAAGACACCGTGCATGCCGATTGGTGGAAAGTAAGTGGTACGA 1922
QY 121 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGATTTGGAGCAACCACTAAATT 180
Db |||||||
1921 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGATTTGGAGCAACCACTAAATT 1862
QY 181 CGCATTTGCAGAGATATTGTAATTTAAGTGCCTAGCTCGATACAATAAAGCGCATTTGACC 239
Db |||||||
1861 CGCATTTGCAGAGATATTGTAATTTAAGTGCCTAGCTCGATACAATAAAGCGCATTTGACC 1802
QY 240 CATTCAACCAATTGGTGTGACCTC 264
Db |||||||
1801 CATTCAACCAATTGGTGTGACCTC 1777

RESULT 22
ALVCG
LOCUS ALVCG 7286 bp ss-RNA linear VRL 24-JUL-2000
DEFINITION Avian leukemia virus ALV-RSA genome.
ACCESSION M37980
VERSION M37980.1 GI:210272
KEYWORDS capsid protein; complete genome; envelope polypeptide; integrase; matrix protein; nucleocapsid protein; polymerase; protease; reverse transcriptase; surface protein; trans-acting factor; transmembrane protein.
SOURCE Avian leukemia virus
ORGANISM Avian leukemia virus
REFERENCE 1 (bases 1 to 7286)
AUTHORS Bieth, E. and Darlix, J.L.
TITLE Complete nucleotide sequence of a highly infectious avian leukemia virus
JOURNAL Nucleic Acids Res. 20 (2), 367 (1992)
MEDLINE 92158628
PUBMED 1311072
COMMENT Draft entry and computer-readable sequence for [unpublished (1990)] kindly submitted by E. Bieth, 24-AUG-1990.
CREG du CNRS
118 route de Narbonne
31062 Toulouse Cedex
France.
FEATURES
source
1. .7286
Location/Qualifiers
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/organism="Avian leukosis virus"
/mol_type="genomic RNA"
/db_xref="taxon:11864"
1..371
misc_feature
1..21
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/note="CAP site"
10..41
22..101
/note="U5 region"
91..101
/note="5' imperfect repeat"
102..371
rpt_type=terminal
102..371
/note="leader sequence"
102..120
/bound_moiety="primer"
210..270
/note="dimer promoting sequence"
218..248
/note="encapsidation element"
331..371
RBS
372..6872
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/protein_id="AA91268.1"
/db_xref="GI:210273"
/translation="MEAVIKAFITGYGKTSKDSKKEPLATSKDPEKPLPLTRVN
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MWDEPHEQLLGSLPNTNTAQISGITGCGPRPQGVWYLGNSROEATRELLRH
PESKSTPEPTVTVADENLFWGEVCGAYGFWMXNCQVGRQVRCNARSRRPG
LPEICTRGCKWVNSQELNESPFPTVNTASLGNASGCCGKAGTILPERWVDS
TGSTFKALPAIFALICEDRAWGIPSRPVGGCYLGKJUTMLAPKHTDILKLVNS
STGIRKRSKSHLDLTSDEVLQWGPTRIFASILAPVARAQALREIERLACWSYK
QANLTSLGDLDDVTSIRHAVLQNRAAIDFLLAHGHCEDVAGMCCFNLSHSES
IQKFTQLMKHEVANKI GVDSDPTGSMGLRGFGIGEWAVHLLKGLLGLVILLVCL
PCLLQIVCGNIRKMINNSISYHTEYKYLQKACQPSRLV"
372..2474
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/protein_id="AA91267.1"
/db_xref="GI:210274"
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RRKPHKLELAPLASAEQLAVIAEQPRLLLLMWGVVCLLPWRGSSRRARGVTH
LGGNSQGRSGQTRVWPLGRP"
423..440
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502..511
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512..540
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536..556
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701..792
/gene="trans-acting factor"
/note="negative splicing regulator"

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817..876
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/note="enhancer domain"
837..902
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880..897
/gene="p2"
/bound_moiety="nucleocapsid"
903..1088
/gene="p10"
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/gene="NCp12"
1836..2102
/gene="NCp12"
/note="nucleocapsid protein"
1941..1948
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/bound_moiety="nucleocapsid"
2103..2474
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2103..2474
/gene="Prp15"
/note="neutral protease large subunit"
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/product="polymerase"
/protein_id="AA91269.1"
/db_xref="GI:210275"
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GHIESLSCWNTPVFVIRKASGYRLLDLRVNAKLVFPGAVQOGAPVLSALPRGW
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WQVLEPLRLKPSILMLHYMDLILASSHDGLAAGEVILSLERAGTISPDKIQ
REFQVQYGLKGLTYVAVGLVAPRIALWVQKLVSLQNLRLPALGIPPRMGFF
YEQLRGSDPNEAREWNLDMKMAREIVQLSTTAALRNDPAPLEGAVARCEQAGIG
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FREDLPLEGILLALRGFAGKIRSSDTPSIDLARPLHVSILKVRVTHPVGPTFTD
ASSTHKGVVVRGSPRWIKELADLGASQQLERAVAMALLWPTPTNVVDSAP
VAKLLKMGQGVSTAAAFILLEDALSORSMANVLHVSHSEVGPPTGNDVDSQ
ATFQAYPREAKDLHTALHIGPRALSACNISMQQARVTVQCHCNASAPALAGVNP
RGLGLQIWCQDFTLEPRMAPKSLAVTVDTSASSAIVVTHQGRVTSVAQHWWATAIA
VLGRPKAIDTNSGSCFSTKSTREWLARGLAHTGTIPGNSQQAQVVERNLKDKIR
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4747..4758
/gene="INp32"
/bound_moiety="nucleocapsid"
5244..6260
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5244..6260
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[illegible]

RESULT 23	SYNRSV3MV	SYNRSV3MV	3557 bp	DNA	circular SYN 27-APR-1993
LOCUS					
DEFINITION					
ACCESSION					
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
MEDLINE					
PUBMED					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
MEDLINE					
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REFERENCE					
AUTHORS					
TITLE					

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J. Virol. 63 (4), 1756-1762 (1989)
MEDLINE 89178863
PUBMED 2784508
COMMENT Original
FEATURES
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        1. .3557
        /organism="unidentified cloning vector"
        /mol_type="genomic DNA"
        /db_xref="taxon:45196"
    1. .29
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        /evidence=experimental
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        /citation=[2]
        /evidence=experimental

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ORIGIN

Query Match	94.0%;	Score 248.2;	DB 12;	Length 3557;
Best local Similarity	98.5%;	Pred. No. 3.7e-61;		
Matches 261;	Conservative 0;	Mismatches 3;	Indels 1;	Gaps 1;
QY	1	AATGTAGTCCTTATGCAAACTCTTGTAGTCTTGCACAATGCTAAACGATGAGTTAGCAACA	60	
Db	3289	ANTGTAGTCTTATGCACATACATCTTGTAGTCTTGCACAATGCTAAACGATGAGTTAGCAACA	3348	
QY	61	TGCCTTACAGGAGAGAAAGACACGCTGCATTCGCCGATTTGGTGGAGCTTAAGGTGGTACGA	120	
Db	3349	TGCCTTACAGGAGAGAAAGACACGCTGCATTCGCCGATTTGGTGGAGTAAAGGTGGTACGA	3408	
QY	121	TGTCGCCTTTATTAGGAAGGCACAGACGGGCTCTGCATCTGATTTGCAACCACTAAATT	180	
Db	3409	TGTCGCCTTTATTAGGAAGGCACACAGACGGTCTGCATCTGATTTGCAACCACTGAAATT	3468	
QY	181	CGCGATTCGCGAGAT-ATGTGTAATTAAGTGGCTAGCTCGCATACATTAACGCCATTTCAC	239	
Db	3469	CGCGATTCGCGAGATTAATTGTAATTAAGTGGCTAGCTCGCATACATTAACGCCATTTCAC	3528	
QY	240	CATTCAACCAATTTGGTGTGCACCTC	264	
Db	3529	CATTCAACCAATTTGGTGTGCACCTC	3553	

RESULT 24
AR071324/c
LOCUS AR071324 4059 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 2 from patent US 5910488.
ACCESSION AR071324
VERSION AR071324.1 GI:7222212
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified
1 (bases 1 to 4059)
AUTHORS Nabel,G.J., Nabel,E.G., Lew,D. and Marquet,M.
TITLE Plasmids suitable for gene therapy
JOURNAL Patent: US 5910488-A 2 08-JUN-1999;
Location/Qualifiers
FEATURES
1..4059
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 94.0%; Score 248.2; DB 6; Length 4059;
 Best Local Similarity 98.5%;
 Pred.No. 3.66-61;
 Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1 AATGTAGTCTTTATGCAATACACTTTGTAGTCTTTGCAACATGTAACATGATGTATGCAACA 60
 Db 3156 AATGTAGTCTTTATGCAATACACTTTGTAGTCTTTGCAACATGTAACATGATGTATGCAACA 3097

QY 61 TGCCTTACAGGAGAGAAAAGCACCGTGCATGCGATTGGTGAAGTAAGGTGGTACGA 120
 Db 3096 TGCCTTACAGGAGAGAAAAGCACCGTGCATGCGATTGGTGAAGTAAGGTGGTACGA 3037
 QY 121 TCGTGCCTTATTAGAGAGGCAACAGACGGGTCTGACATGGATTGGAACCACTAAATT 180
 Db 3036 TCGTGCCTTATTAGAGAGGCAACAGACAGGTCTGACATGGATTGGAACCACTAAATT 2977
 QY 181 CCCATTGCAGAGAT-ATTGTTATTTAGTGCCTAGCTCGATACATATAAAGCCATTGAC 239
 Db 2976 CCGCATTTGAGAGATAATTGTTAATTAAGTGCCTAGCTCGATACATATAAAGCCATTGAC 2917
 QY 240 CATTCACCACATTGGTGTGCACCTC 264
 Db 2916 CATTCACCACATTGGTGTGCACCTC 2892

RESULT 25
 A38214
 LOCUS A38214 4341 bp DNA linear PAT 05-MAR-1997
 DEFINITION Sequence 58 from Patent WO9408008.
 ACCESSION A38214
 VERSION A38214.1 GI:2294819
 KEYWORDS
 SOURCE unidentified
 ORGANISM unidentified
 unclassified.
 REFERENCE 1 (bases 1 to 4341)
 AUTHORS Hawkins,R.E., Russell,S.J., Stevenson,F.K. and Winter,G.P.
 TITLE IMPROVEMENTS IN OR RELATING TO IMMUNE RESPONSE MODIFICATION
 JOURNAL Patent: WO 9408008-A 58 14-APR-1994;
 MEDICAL RES COUNCIL (GB)
 COMMENT Other publication CA 2145064 940414
 Other publication AU 4832493 940426
 Other publication JP 8501699T 960227.
 FEATURES
 source Location/Qualifiers
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 /mol_type="unassigned DNA"
 /db_xref="taxon:32644"

Query Match 94.0%; Score 248.2; DB 6; Length 4341;
 Best Local Similarity 98.5%; Pred. No. 3.6e-61;
 Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 QY 1 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGCAACATGCTTAACGATGATTAGCAACA 60
 Db 340 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGCAACATGCTTAACGATGATTAGCAACA 399
 QY 61 TGCCTTACAGGAGAGAAAAGCACCGTGCATGCGATTGGTGAAGTAAGGTGGTACGA 120
 Db 400 TGCCTTACAGGAGAGAAAAGCACCGTGCATGCGATTGGTGAAGTAAGGTGGTACGA 459
 QY 121 TCGTGCCTTATTAGAGAGGCAACAGACGGGTCTGACATGGATTGGAACCACTAAATT 180
 Db 460 TCGTGCCTTATTAGAGAGGCAACAGACAGGTCTGACATGGATTGGAACCACTAAATT 519
 QY 181 CCCATTGCAGAGAT-ATTGTTATTTAGTGCCTAGCTCGATACATATAAAGCCATTGAC 239
 Db 520 CCGCATTTGAGAGATAATTGTTAATTAAGTGCCTAGCTCGATACATATAAAGCCATTGAC 579
 QY 240 CATTCACCACATTGGTGTGCACCTC 264
 Db 580 CATTCACCACATTGGTGTGCACCTC 604

RESULT 26
 AX286570
 LOCUS AX286570 4341 bp DNA linear PAT 21-NOV-2001
 DEFINITION Sequence 1 from Patent WO0179510.
 ACCESSION AX286570

VERSION AX286570.1 GI:17048664
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.
 REFERENCE 1
 AUTHORS Rice,J.H. and Stevenson,F.M.
 TITLE Materials and methods relating to immune responses to fusion proteins
 JOURNAL Patent: WO 0179510-A 1 25-OCT-2001;
 Cancer Research Ventures Limited (GB)
 FEATURES
 source Location/Qualifiers
 1..4341
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Vector pVAC1"

ORIGIN
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 Best Local Similarity 98.5%; Pred. No. 3.6e-61;
 Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 QY 1 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGCAACATGCTTAACGATGATTAGCAACA 60
 Db 340 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGCAACATGCTTAACGATGATTAGCAACA 399
 QY 61 TGCCTTACAGGAGAGAAAAGCACCGTGCATGCGATTGGTGAAGTAAGGTGGTACGA 120
 Db 400 TGCCTTACAGGAGAGAAAAGCACCGTGCATGCGATTGGTGAAGTAAGGTGGTACGA 459
 QY 121 TCGTGCCTTATTAGAGAGGCAACAGACGGGTCTGACATGGATTGGAACCACTAAATT 180
 Db 460 TCGTGCCTTATTAGAGAGGCAACAGACAGGTCTGACATGGATTGGAACCACTAAATT 519
 QY 181 CCGCATTTGAGAGAT-ATTGTTATTTAGTGCCTAGCTCGATACATATAAAGCCATTGAC 239
 Db 520 CCGCATTTGAGAGATAATTGTTAATTAAGTGCCTAGCTCGATACATATAAAGCCATTGAC 579
 QY 240 CATTCACCACATTGGTGTGCACCTC 264
 Db 580 CATTCACCACATTGGTGTGCACCTC 604

RESULT 27
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 LOCUS SYNRSV5GPT 4839 bp DNA circular SYN 16-MAR-2000
 DEFINITION Cloning vector RSV.5 (gpt).
 ACCESSION M83236
 VERSION M83236.1 GI:209304
 KEYWORDS cDNA expression vector.
 SOURCE Cloning vector pUC19
 ORGANISM Cloning vector pUC19
 artificial sequences; vectors.
 REFERENCE 1 (bases 1 to 4839)
 AUTHORS Long,E.O., Rosen-Bronson,S., Karp,D.R., Malnati,M., Sekaly,R.P. and Jaraquemada,D.
 TITLE Efficient cDNA expression vectors for stable and transient expression of HLA-DR in transfected fibroblast and lymphoid cells
 JOURNAL Hum. Immunol. 31 (4), 229-235 (1991)
 MEDLINE 92011006
 PUBMED 1655683
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 /mol_type="genomic DNA"
 /db_xref="taxon:31851"
 /focus

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 1..29
 /organism="Cloning vector pUC12"
 /mol_type="genomic DNA"
 /db_xref="taxon:83674"
 /note="HindIII to BamHI fragment of pUC12"

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source
30..872
/organism="Simian virus 40"
/mol_type="genomic DNA"
/db_xref="taxon:10633"
/notes="Bi-directional SV40 termination and
poly-adenylation sequences."
873..1929
/organism="Escherichia coli"
/mol_type="genomic DNA"
/db_xref="taxon:562"
1930..2273
/organism="Simian virus 40"
/mol_type="genomic DNA"
/db_xref="taxon:10633"
/notes="SV40 early promoter and origin of replication."
2274..4311
/organism="Cloning vector pBR322"
/mol_type="genomic DNA"
/db_xref="taxon:47470"
/notes="Ampicillin resistance gene and origin of replication
from the vector pBR322."
4312..4839
/organism="Rous sarcoma virus"
/mol_type="genomic DNA"
/db_xref="taxon:11086"
/notes="5' long terminal repeat."
misc_feature
1..29
/function="polylinker"
/evidence=experimental
misc_feature
/product="guanine-hypoxanthine phosphoribosyltransferase"
/standard_name="gpt"
/notes="gpt gene from E. coli, putative mature peptide -
contains internal stop codons; putative"
2274..4311
/function="ampicillin resistance and origin of
replication"
/evidence=experimental

ORIGIN

Query Match 94.0%; Score 248.2; DB 12; Length 4839;
Best Local Similarity 98.5%; Pred. No. 3.5e-61;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1 AATGCTACTCTTATGCAATACCTCTGTAGTCTTGCACATGCTAAACGATGAGTTAGCAACA 60
Db |||||||
Qy 4571 AATGCTACTCTTATGCAATACCTCTGTAGTCTTGCACATGCTAAACGATGAGTTAGCAACA 4630
Db |||||||
Qy 61 TGCCTTACAGGAGAGAAAAAGCACCGCTGCATGCCGATTTGGTGGAAAGTAAAGTGTGACGA 120
Db |||||||
Qy 121 TCGTGCCTTATAGGAGGACACAGCGGTCTGTGACATGCTTGCACGACCACTAAATT 180
Db |||||||
Qy 4691 TCGTGCCTTATAGGAGGACACAGCGGTCTGTGACATGCTTGCACGACCACTAAATT 4750
Db |||||||
Qy 181 CGCANTGACAGAT-ATTGTATTAAAGTGCCTACGATACATATAACGCCATTGAC 239
Db |||||||
Qy 4751 CGCANTGACAGATATTGTATTAAAGTGCCTACGATACATATAACGCCATTGAC 4810
Db |||||||
Qy 240 CATTACACACATTTGGTGTGCCTC 264
Db |||||||
Qy 4811 CATTACACACATTTGGTGTGCCTC 4835
Db |||||||

RESULT 28
SYNRSV5NEO
LOCUS 5108 bp DNA linear STN 06-APR-2001
DEFINITION cDNA expression vector RSV.5 (neo).
ACCESSION M83237
VERSION M83237.1 GI:209305
KEYWORDS cDNA expression vector.
SOURCE Expression vector RSV.5 (neo)

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ORGANISM Expression vector RSV.5 (neo)
artificial sequences; vectors.
REFERENCE 1 (bases 1 to 5108)
AUTHORS Long, E.O., Rothen-Bronson, S., Karp, D.R., Malnati, M., Sekaly, R.P. and
Jaraquemada, D.
TITLE Efficient cDNA expression vectors for stable and transient
expression of HLA-DR in transfected fibroblast and lymphoid cells
JOURNAL Hum. Immunol. 31 (4), 229-235 (1991)
MEDLINE 92011006
PUBMED 1655683
FEATURES
Location/Qualifiers
1..5108
/organism="Expression vector RSV.5 (neo)"
/mol_type="genomic DNA"
/db_xref="taxon:118308"
/focus
1..29
/organism="unidentified cloning vector"
/mol_type="genomic DNA"
/db_xref="taxon:45196"
/notes="HindIII to BamHI fragment of pUC12."
30..872
/organism="Simian virus 40"
/mol_type="genomic DNA"
/db_xref="taxon:10633"
/notes="Bi-directional SV40 termination and
poly-adenylation sequence."
873..879
/organism="unidentified cloning vector"
/mol_type="genomic DNA"
/db_xref="taxon:45196"
/notes="Remnant of gpt gene from the cDNA expression vector
RSV.5 (gpt)."
880..2197
/organism="Cloning vector pSV2neo"
/mol_type="genomic DNA"
/db_xref="taxon:31846"
/notes="TN5 neomycin-resistance gene from cloning vector
pSV2neo."
2198..2542
/organism="Simian virus 40"
/mol_type="genomic DNA"
/db_xref="taxon:10633"
/notes="SV40 early promoter and origin of replication."
2543..4580
/organism="Cloning vector pBR322"
/mol_type="genomic DNA"
/db_xref="taxon:47470"
/notes="Ampicillin resistance gene and origin of
replication from pBR322."
4581..5108
/organism="Rous sarcoma virus"
/mol_type="genomic DNA"
/db_xref="taxon:11886"
/notes="5' long terminal repeat of Rous Sarcoma virus."
1..29
/function="polylinker"
/evidence=experimental
misc_feature
complement (880..2197)
/notes="neomycin resistance gene from pSV2neo, putative
mature peptide - contains internal stop codons; putative"
2543..4580
/product="ampicillin resistance"
/function="ampicillin resistance and origin of
replication"
/evidence=experimental
LTR
4581..5108
/standard_name="5' LTR of Rous Sarcoma Virus"
/function="promoter"
/evidence=experimental

ORIGIN

Query Match 94.0%; Score 248.2; DB 12; Length 5108;

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DEFINITION Sequence 1 from patent US 5733543.
ACCESSION 195540
VERSION 195540.1 GI:3940010
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 5653)
AUTHORS Nabel,G.J., Woffendin,C., Yang,N.-S. and Sheehy,M.J.
TITLE Introduction of HIV-protective genes into cells by
particle-mediated gene transfer
JOURNAL Patent: US 5733543-A 1 31-MAR-1998;
FEATURES
source
1..5653
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 94.0%; Score 248.2; DB 6; Length 5653;
Best Local Similarity 98.5%; Pred. No. 3.4e-61;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
Qy 1 AATGTAGTCTTATGCAATACACTTTGTAGTCTTGTGCAACATCGTAACGATGAGTTAGCAACA 60
Db 340 AATGTAGTCTTATGCAATACACTTTGTAGTCTTGTGCAACATCGTAACGATGAGTTAGCAACA 399
Qy 61 TGCCTTACAGGAGAGAAAAGCAACCGTCGATCGCGATTGGTGGAGTAAGTGTGACGA 120
Db 400 TGCCTTACAGGAGAGAAAAGCAACCGTCGATCGCGATTGGTGGAGTAAGTGTGACGA 459
Qy 121 TCGTGCCTTATTAGGAGGCAACAGCGGTCTGCATGATGAGTGGAGCAACCAATAATT 180
Db 460 TCGTGCCTTATTAGGAGGCAACAGCGGTCTGCATGATGAGTGGAGCAACCACTGATT 519
Qy 181 CCGCATTGCGAGAGAT-ATTGTATTAAAGTGCCTAGCTAGTCATACATAAAGCCCAATTGAC 239
Db 520 CCGCATTGCGAGAGATATTGTATTAAAGTGCCTAGCTAGTCATACATAAAGCCCAATTGAC 579
Qy 240 CATTACCAACATTGGTGTGCACCTC 264
Db 580 CATTACCAACATTGGTGTGCACCTC 604
RESULT 32
SYNPRSVNEO/c
LOCUS SYNPRSVNEO 5736 bp DNA circular SYN 27-APR-1993
DEFINITION PRSVNeo cloning vector for high efficiency gene transfer into
mammalian cells.
ACCESSION M77786
VERSION M77786.1 GI:209147
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 5736)
AUTHORS Gilbert,W.
TITLE Obtained from VecBase 3.0
JOURNAL Unpublished (1991)
COMMENT Original source text: Synthetic construct DNA.
These data and their annotation were supplied to GenBank by Will
Gilbert under the auspices of the GenBank Curator Program. PRSVNeo
- Cloning Vector for High Efficiency Gene Transfer into Mammalian
Cells
ENTRY PRSVNEO #TYPE DNA CIRCULAR TITLE PRSVNeo -
Cloning Vector for High Efficiency Gene Transfer
into Mammalian Cells
DATE 06-JUN-1986
#sequence 16-DEC-1986
ACCESSION V80064
SOURCE artificial
COLLECTION ATCC 37198
REFERENCE
#number 1

#authors Gorman C.
#book 'DNA cloning Volume II, a practical approach', pp.
143-190,
edited by D. M. Glover, IRL Press, (1986),
eds. D. Rickwood and B. D. Hames
COMMENT
Entered by William Gilbert, Whitaker College, MIT, 02-APR-1986
Revised 16-DEC-1986 by F. Pfeiffer:
1012/3 'AT' to 'TA' to match revised sequence of PBR322 KEYWORDS
CROSSREFERENCE
#parent
VecBase (3): PBR322, GenBank (50): SV4CG,
GenBank (50): ALRPOLTB,
GenBank (50): Trn5Neo, GenBank (50): Trn5IR1
PARENT
Features of PRSVNeo (5736 bp)
residue source
6- 529 550- 27 (c) Rous Sarcoma Virus (GenBank (50):
ALRPOLTB)
6- 529 3189-2667 (c) GenBank (50): ALRPOLTB (6 mutations)
529-2644 2248-4363 PBR322
2641-3634 1781-2774 SV40
3631-4244 4100-4713 SV40
4248-5533 1286- 1 (c) Trn5 (GenBank (50): TRNSNEO)
5251-5736 1720-1235 (c) Trn5 (GenBank (50): TRNSIR1)
Conflict (cfl) and Mutations (mut): none
FEATURE
1579-2367 789-1 (c) Ap-R; b-lactamase
4589-5383 791-1 (c) Neo-R
POLYLINKER
SELECTION #resistance Ap
SUMMARY PRSVNeo #length 5736 #checksum 3569.
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 94.0%; Score 248.2; DB 12; Length 5736;
Best Local Similarity 98.5%; Pred. No. 3.4e-61;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
Qy 1 AATGTAGTCTTATGCAATACACTTTGTAGTCTTGTGCAACATCGTAACGATGAGTTAGCAACA 60
Db 269 AATGTAGTCTTATGCAATACACTTTGTAGTCTTGTGCAACATCGTAACGATGAGTTAGCAACA 210
Qy 61 TGCCTTACAGGAGAGAAAAGCAACCGTCGATCGCGATTGGTGGAGTAAGTGTGACGA 120
Db 209 TGCCTTACAGGAGAGAAAAGCAACCGTCGATCGCGATTGGTGGAGTAAGTGTGACGA 150
Qy 121 TCGTGCCTTATTAGGAGGCAACAGCGGTCTGCATGATGAGTGGAGCAACCAATAATT 180
Db 149 TCGTGCCTTATTAGGAGGCAACAGCGGTCTGCATGATGAGTGGAGCAACCACTGATT 90
Qy 181 CCGCATTGCGAGAGAT-ATTGTATTAAAGTGCCTAGCTAGTCATACATAAAGCCCAATTGAC 239
Db 89 CCGCATTGCGAGAGATATTGTATTAAAGTGCCTAGCTAGTCATACATAAAGCCCAATTGAC 30
Qy 240 CATTACCAACATTGGTGTGCACCTC 264
Db 29 CATTACCAACATTGGTGTGCACCTC 5
RESULT 33
AR215114
LOCUS AR215114 6836 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 18 from patent US 6410266.
ACCESSION AR215114
VERSION AR215114.1 GI:23313242
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.
REFERENCE 1 (bases 1 to 6836)
AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.
TITLE Compositions and methods for non-targeted activation of endogenous genes
JOURNAL Patent: US 6410266-A 18 25-JUN-2002;
FEATURES Location/Qualifiers
source 1..6836
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 94.0%; Score 248.2; DB 6; Length 6836;
Best Local Similarity 98.5%; Pred. No. 3.4e-61;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 1 AATGTAGTCTTATGCAATACACTTGTAGTCTTGCACATGGTAAACGATGAGTTAGCAACA 60
Db 1558 AATGTAGTCTTATGCAATACACTTGTAGTCTTGCACATGGTAAACGATGAGTTAGCAACA 1617
QY 61 TGCCTTACAGGAGAGAAAAGCACCGTGCATGCCGATTTGGTGAAGTAAGTGGTACGA 120
Db 1618 TGCCTTACAGGAGAGAAAAGCACCGTGCATGCCGATTTGGTGAAGTAAGTGGTACGA 1677
QY 121 TCGTGCCTTATTAGAGAGCAACAGACGGGTCTGACATGGATTGGACGAACCACTAAATT 180
Db 1678 TCGTGCCTTATTAGAGAGCAACAGACGGGTCTGACATGGATTGGACGAACCACTAAATT 1737
QY 181 CCCATTGCAGAGAT-ATTCTATTATTAAGTGCCTAGCTCGATACATATAAGCCATTGGAC 239
Db 1738 CCCATTGCAGAGAT-ATTCTATTATTAAGTGCCTAGCTCGATACATATAAGCCATTGGAC 1797
QY 240 CATTACCAACATTTGGTGTGCACCTC 264
Db 1798 CATTACCAACATTTGGTGTGCACCTC 1822

RESULT 34
AR302356
LOCUS AR302356 6836 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 18 from patent US 6541221.
ACCESSION AR302356
VERSION AR302356.1 GI:31690610
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 6836)
AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.
TITLE Compositions and methods for non-targeted activation of endogenous genes
JOURNAL Patent: US 6541221-A 18 01-APR-2003;
FEATURES Location/Qualifiers
source 1..6836
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 94.0%; Score 248.2; DB 6; Length 6836;
Best Local Similarity 98.5%; Pred. No. 3.4e-61;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 1 AATGTAGTCTTATGCAATACACTTGTAGTCTTGCACATGGTAAACGATGAGTTAGCAACA 60
Db 1558 AATGTAGTCTTATGCAATACACTTGTAGTCTTGCACATGGTAAACGATGAGTTAGCAACA 1617
QY 61 TGCCTTACAGGAGAGAAAAGCACCGTGCATGCCGATTTGGTGAAGTAAGTGGTACGA 120
Db 1618 TGCCTTACAGGAGAGAAAAGCACCGTGCATGCCGATTTGGTGAAGTAAGTGGTACGA 1677
QY 121 TCGTGCCTTATTAGAGAGCAACAGACGGGTCTGACATGGATTGGACGAACCACTAAATT 180
Db 1678 TCGTGCCTTATTAGAGAGCAACAGACGGGTCTGACATGGATTGGACGAACCACTAAATT 1737

QY 181 CGCATTGCAGAGAT-ATTGTATTTAAGTGCCTAGCTCGATACATAAAGCCATTGGAC 239
Db 1738 CGCATTGCAGAGAT-ATTGTATTTAAGTGCCTAGCTCGATACATAAAGCCATTGGAC 1797
QY 240 CATTACCAACATTTGGTGTGCACCTC 264
Db 1798 CATTACCAACATTTGGTGTGCACCTC 1822

RESULT 35
AR373228
LOCUS AR373228 6836 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 18 from patent US 6602686.
ACCESSION AR373228
VERSION AR373228.1 GI:40075236
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 6836)
AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.
TITLE Compositions and method for non-targeted activation of endogenous genes
JOURNAL Patent: US 6602686-A 18 05-AUG-2003;
FEATURES Location/Qualifiers
source 1..6836
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 94.0%; Score 248.2; DB 6; Length 6836;
Best Local Similarity 98.5%; Pred. No. 3.4e-61;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 1 AATGTAGTCTTATGCAATACACTTGTAGTCTTGCACATGGTAAACGATGAGTTAGCAACA 60
Db 1558 AATGTAGTCTTATGCAATACACTTGTAGTCTTGCACATGGTAAACGATGAGTTAGCAACA 1617
QY 61 TGCCTTACAGGAGAGAAAAGCACCGTGCATGCCGATTTGGTGAAGTAAGTGGTACGA 120
Db 1618 TGCCTTACAGGAGAGAAAAGCACCGTGCATGCCGATTTGGTGAAGTAAGTGGTACGA 1677
QY 121 TCGTGCCTTATTAGAGAGCAACAGACGGGTCTGACATGGATTGGACGAACCACTAAATT 180
Db 1678 TCGTGCCTTATTAGAGAGCAACAGACGGGTCTGACATGGATTGGACGAACCACTAAATT 1737
QY 181 CGCATTGCAGAGAT-ATTGTATTTAAGTGCCTAGCTCGATACATAAAGCCATTGGAC 239
Db 1738 CGCATTGCAGAGAT-ATTGTATTTAAGTGCCTAGCTCGATACATAAAGCCATTGGAC 1797
QY 240 CATTACCAACATTTGGTGTGCACCTC 264
Db 1798 CATTACCAACATTTGGTGTGCACCTC 1822

RESULT 36
AR401614
LOCUS AR401614 6836 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 18 from patent US 6623958.
ACCESSION AR401614
VERSION AR401614.1 GI:40149062
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 6836)
AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.
TITLE Compositions and methods for non-targeted activation of endogenous genes
JOURNAL Patent: US 6623958-A 18 23-SEP-2003;
FEATURES Location/Qualifiers
source 1..6836

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ORIGIN
Query Match          94.0%; Score 248.2; DB 6; Length 6836;
Best Local Similarity 98.5%; Pred. No. 3.4e-61;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGAGCTTTATGCAATACCTCTTGAGTCTTGGCAATGCTTAACGATGAGTTAGCAACA 60
DB 1558 AATGAGCTTTATGCAATACCTCTTGAGTCTTGGCAATGCTTAACGATGAGTTAGCAACA 1617

QY 61 TGCCTTACAGGAGAGAAAAGACCGCTGCATGCCGATTTGGTGGAAAGTAAGTGGTACGA 120
DB 1618 TGCCTTACAGGAGAGAAAAGACCGCTGCATGCCGATTTGGTGGAAAGTAAGTGGTACGA 1677

QY 121 TCGTGCCTTATTAGCAAGGCAACAGACGGGTCTGCATGCCGATTTGGTGGAAAGTAAGTGGTACGA 180
DB 1678 TCGTGCCTTATTAGCAAGGCAACAGACGGGTCTGCATGCCGATTTGGTGGAAAGTAAGTGGTACGA 1737

QY 121 TCGTGCCTTATTAGCAAGGCAACAGACGGGTCTGCATGCCGATTTGGTGGAAAGTAAGTGGTACGA 180
DB 1678 TCGTGCCTTATTAGCAAGGCAACAGACGGGTCTGCATGCCGATTTGGTGGAAAGTAAGTGGTACGA 1737

QY 181 CCGCATTCGACAGAT-ATTGATTTAAGTGCTAGCTCGATACATAATAAAGCCATTGAC 239
DB 1738 CCGCATTCGACAGAT-ATTGATTTAAGTGCTAGCTCGATACATAATAAAGCCATTGAC 1797

QY 240 CATTCCACCATGTTGTGCACCTC 264
DB 1798 CATTCCACCATGTTGTGCACCTC 1822

RESULT 37
AF346624
LOCUS             AF346624             6836 bp    DNA    circular SYN 30-AUG-2001
DEFINITION       RAGE vector pRIG1, complete sequence.
ACCESSION        AF346624
VERSION          AF346624.1 GI:15383987
KEYWORDS
SOURCE           RAGE vector pRIG1
ORGANISM         RAGE vector pRIG1
REFERENCE        1 (bases 1 to 6836)
AUTHORS          Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
                  Cain,S., Leventhal,C., Thornton,M., Ramachandran,R.,
                  Whittington,J., Lerner,T., Costanzo,D., McElligott,K., Booser,S.,
                  Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K.,
                  Offenbacher,J., Danzig,J. and Ducar,M.
                  Creation of genome-wide protein expression libraries using random
                  activation of gene expression
JOURNAL          Nat. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE          21227151
PUBMED           11329013
REFERENCE        2 (bases 1 to 6836)
AUTHORS          Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
                  Cain,S., Dahl,T., Thornton,M., Ramachandran,R., Whittington,J.,
                  Lerner,L., Krashoc,D., McElligott,K., Clark,S., Mays,R., Smith,B.,
                  Veloso,N., Hess,J., Cothren,K., Lo,K., Offenbacher,J., Danzig,J.
                  and Ducar,M.
                  Direct Submission
JOURNAL          Submitted (06-FEB-2001) Athersys, Inc., 3201 Carnegie Ave.,
                  Cleveland, OH 44115, USA
FEATURES
source           1..6836
                  /organism="RAGE vector pRIG1"
                  /mol_type="genomic DNA"
                  /db_xref="taxon:161236"

ORIGIN
Query Match          94.0%; Score 248.2; DB 12; Length 6836;
Best Local Similarity 98.5%; Pred. No. 3.4e-61;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGAGCTTTATGCAATACCTCTTGAGTCTTGGCAATGCTTAACGATGAGTTAGCAACA 60
DB 1558 AATGAGCTTTATGCAATACCTCTTGAGTCTTGGCAATGCTTAACGATGAGTTAGCAACA 1617

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QY 61 TGCCTTACAGGAGAGAAAAGACCGCTGCATGCCGATTTGGTGGAAAGTAAGTGGTACGA 120
DB 1618 TGCCTTACAGGAGAGAAAAGACCGCTGCATGCCGATTTGGTGGAAAGTAAGTGGTACGA 1677

QY 121 TCGTGCCTTATTAGCAAGGCAACAGACGGGTCTGCATGCCGATTTGGTGGAAAGTAAGTGGTAC 180
DB 1678 TCGTGCCTTATTAGCAAGGCAACAGACGGGTCTGCATGCCGATTTGGTGGAAAGTAAGTGGTAC 1737

QY 181 CCGCATTCGACAGAT-ATTGATTTAAGTGCTAGCTCGATACATAATAAAGCCATTGAC 239
DB 1738 CCGCATTCGACAGAT-ATTGATTTAAGTGCTAGCTCGATACATAATAAAGCCATTGAC 1797

QY 240 CATTCCACCATGTTGTGCACCTC 264
DB 1798 CATTCCACCATGTTGTGCACCTC 1822

RESULT 38
XXUI9931
LOCUS             XXUI9931             6864 bp    DNA    linear SYN 30-MAR-1995
DEFINITION       Cloning vector pGlacRSV, complete sequence.
ACCESSION        UI9931
VERSION          UI9931.1 GI:644834
KEYWORDS         Cloning vector pGlacRSV
SOURCE           Cloning vector pGlacRSV
ORGANISM         Cloning vector pGlacRSV
REFERENCE        1 (bases 1 to 6864)
AUTHORS          Gottgens,B.B.
TITLE            A versatile lacZ reporter vector
JOURNAL          Unpublished
VERSION          2 (bases 641 to 4011)
AUTHORS          Ravid,K., Beeler,D.L., Rabin,M.S., Ruley,H.B. and Rosenberg,R.D.
TITLE            Selective targeting of gene products with the megakaryocyte
                  platelet factor 4 promoter
JOURNAL          Proc. Natl. Acad. Sci. U.S.A. 88 (4), 1521-1525 (1991)
MEDLINE          91142205
PUBMED           1899930
REFERENCE        3 (bases 1 to 6864)
AUTHORS          Gottgens,B.B.
TITLE            Direct Submission
JOURNAL          Submitted (18-JAN-1995) Berthold B. Gottgens, Hematology, Cambridge
                  University, MRC Centre, Hills Road, Cambridge, UK, CB2 2QH
                  Location/Qualifiers
FEATURES
source           1..6864
                  /organism="Cloning vector pGlacRSV"
                  /mol_type="genomic DNA"
                  /db_xref="taxon:39038"
misc_feature     1..37
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misc_feature     38..631
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misc_feature     632..6864
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misc_feature     641..4011
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                  /citation=[2]
gene            662..3727
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CDS              662..3727
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                  /protein_id="AA04569.1"
                  /db_xref="GI:644835"
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misc_feature
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 YSPVTEKHLTDGMRELCSAAITMSDNTAANLLTTGGPKELTAPLHNMGDHTRL
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 ETGASLIKHW"

ORIGIN

Query Match 94.0%; Score 248.2; DB 12; Length 6864;
 Best Local Similarity 98.5%; Pred. No. 3.4e-61;
 Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAACATGCTTAACGATGAGTTAGCAACA 60
 DB 365 AATGTAGTCTTATGCAATCACTTGTAGTCTTGTGCAACATGCTTAACGATGAGTTAGCAACA 424

QY 61 TGCCTTACAAGGAGAGAAAAAGCACCGTGCATGCCGATTTGGTGAAGTAAGGTGCTACGA 120
 DB 425 TGCCTTACAAGGAGAGAAAAAGCACCGTGCATGCCGATTTGGTGAAGTAAGGTGCTACGA 484

QY 121 TCGTGCCTTATTAGGAGGCAACAGACCGGCTCTGACATGATGATGAGCAACCACTAAATT 180
 DB 485 TCGTGCCTTATTAGGAGGCAACAGACCGGCTCTGACATGATGATGAGCAACCACTAAATT 544

QY 181 CCGCATTGCAGAGAT-ATTGTATTAAAGTGCCTGATCGATACATAAAGCCATTGTGAC 239
 DB 545 CCGCATTGCAGAGATATTGTATTAAAGTGCCTGATCGATACATAAAGCCATTGTGAC 604

QY 240 CATTCAACCACTTGTGTGCACCTC 264
 DB 605 CATTCAACCACTTGTGTGCACCTC 629

RESULT 39
 158322
 LOCUS I58322 8591 bp DNA linear PAT 07-OCT-1997
 DEFINITION Sequence 6 from patent US 5652092.
 ACCESSION I58322
 VERSION I58322.1 GI:2477560
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 Vitek, M. Peter, and Jacobsen, J. Steven.
 Amyloid precursor proteins and method of using same to assess
 agents which down-regulate formation of .beta.-amyloid peptide
 Patent: US 5652092-A 8 29-JUL-1997;
 Location/Qualifiers
 1..8591
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 94.0%; Score 248.2; DB 6; Length 8591;
 Best Local Similarity 98.5%; Pred. No. 3.3e-61;
 Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAACATGATGATGAGTTAGCAACA 60
 DB 4975 AATGTAGTCTTATGCAATCACTTGTAGTCTTGTGCAACATGATGATGAGTTAGCAACA 5034

QY 61 TGCCTTACAAGGAGAGAAAAAGCACCGTGCATGCCGATTTGGTGAAGTAAGGTGCTACGA 120
 DB 5035 TGCCTTACAAGGAGAGAAAAAGCACCGTGCATGCCGATTTGGTGAAGTAAGGTGCTACGA 5094

QY 121 TCGTGCCTTATTAGGAGGCAACAGACCGGCTCTGACATGATGATGAGCAACCACTAAATT 180
 DB 5095 TCGTGCCTTATTAGGAGGCAACAGACCGGCTCTGACATGATGATGAGCAACCACTAAATT 5154

QY 181 CCGCATTGCAGAGAT-ATTGTATTAAAGTGCCTGATCGATACATAAAGCCATTGTGAC 239

TITLE Amyloid precursor proteins and method of using same to assess
 agents which down-regulate formation of .beta.-amyloid peptide
 JOURNAL Patent: US 5652092-A 6 29-JUL-1997;
 FEATURES Location/Qualifiers
 source 1..8591
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN

Query Match 94.0%; Score 248.2; DB 6; Length 8591;
 Best Local Similarity 98.5%; Pred. No. 3.3e-61;
 Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAACATGATGATGAGTTAGCAACA 60
 DB 4975 AATGTAGTCTTATGCAATCACTTGTAGTCTTGTGCAACATGATGATGAGTTAGCAACA 5034

QY 61 TGCCTTACAAGGAGAGAAAAAGCACCGTGCATGCCGATTTGGTGAAGTAAGGTGCTACGA 120
 DB 5035 TGCCTTACAAGGAGAGAAAAAGCACCGTGCATGCCGATTTGGTGAAGTAAGGTGCTACGA 5094

QY 121 TCGTGCCTTATTAGGAGGCAACAGACCGGCTCTGACATGATGATGAGCAACCACTAAATT 180
 DB 5095 TCGTGCCTTATTAGGAGGCAACAGACCGGCTCTGACATGATGATGAGCAACCACTAAATT 5154

QY 181 CCGCATTGCAGAGAT-ATTGTATTAAAGTGCCTGATCGATACATAAAGCCATTGTGAC 239
 DB 5215 CATTCAACCACTTGTGTGCACCTC 5239

RESULT 40
 158323
 LOCUS I58323 8591 bp DNA linear PAT 07-OCT-1997
 DEFINITION Sequence 8 from patent US 5652092.
 ACCESSION I58323
 VERSION I58323.1 GI:2477561
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 Vitek, M. Peter, and Jacobsen, J. Steven.
 Amyloid precursor proteins and method of using same to assess
 agents which down-regulate formation of .beta.-amyloid peptide
 Patent: US 5652092-A 8 29-JUL-1997;
 Location/Qualifiers
 1..8591
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 94.0%; Score 248.2; DB 6; Length 8591;
 Best Local Similarity 98.5%; Pred. No. 3.3e-61;
 Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAACATGATGATGAGTTAGCAACA 60
 DB 4975 AATGTAGTCTTATGCAATCACTTGTAGTCTTGTGCAACATGATGATGAGTTAGCAACA 5034

QY 61 TGCCTTACAAGGAGAGAAAAAGCACCGTGCATGCCGATTTGGTGAAGTAAGGTGCTACGA 120
 DB 5035 TGCCTTACAAGGAGAGAAAAAGCACCGTGCATGCCGATTTGGTGAAGTAAGGTGCTACGA 5094

QY 121 TCGTGCCTTATTAGGAGGCAACAGACCGGCTCTGACATGATGATGAGCAACCACTAAATT 180
 DB 5095 TCGTGCCTTATTAGGAGGCAACAGACCGGCTCTGACATGATGATGAGCAACCACTAAATT 5154

QY 181 CCGCATTGCAGAGAT-ATTGTATTAAAGTGCCTGATCGATACATAAAGCCATTGTGAC 239


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Db      5155 CCGCATTGCAGAGATAATTGTTAATTAAGTGCCTAGCTCGATACATAAAGCCATTGGAC 5214
Qy      240 CATTACCAACATTGGTGTGCACCTC 264
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Db      5215 CATTACCAACATTGGTGTGCACCTC 5239

RESULT 41
160508
LOCUS      I60508      8591 bp      DNA      linear      PAT 07-OCT-1997
DEFINITION      Sequence 6 from patent US 5656477.
ACCESSION      I60508
VERSION      I60508.1 GI:2478953
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 8591)
AUTHORS      Vitek M.Peter, and Jacobsen J.Steven.
TITLE      Amyloid precursor proteins and method of using same to assess
      agents which down-regulate formation of .beta.-amyloid peptide
JOURNAL      Patent: US 5656477-A 6 12-AUG-1997;
FEATURES
      Location/Qualifiers
      source
      1..8591
      /organism="unknown"
      /mol_type="unassigned DNA"

ORIGIN
Query Match      94.0%; Score 248.2; DB 6; Length 8591;
Best Local Similarity 98.5%; Pred. No. 3.3e-61;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy      1 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGTGCAACATGTAACGATGAGTTAGCAACA 60
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Db      4975 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGTGCAACATGTAACGATGAGTTAGCAACA 5034

Qy      61 TGCCTTACAGGAGAGAAAAAGCACCGTGCATGCCGANTGCTGGAAGTAAAGTGGTACGA 120
      |||||
Db      5035 TGCCTTACAGGAGAGAAAAAGCACCGTGCATGCCGANTGCTGGAAGTAAAGTGGTACGA 5094

Qy      121 TCGTGCCTTATTAGGAAGGCAACAGACAGGCTCTGACATGATGGACGACCACTAAATT 180
      |||||
Db      5095 TCGTGCCTTATTAGGAAGGCAACAGACAGGCTCTGACATGATGGACGACCACTAAATT 5154

Qy      181 CGCATTGCAGAGAT-ATTGTATTAAAGTGCCTAGCTCGATACATAAAGCCATTGGAC 239
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Db      5155 CGCATTGCAGAGATATTGTATTAAAGTGCCTAGCTCGATACATAAAGCCATTGGAC 5214

Qy      240 CATTACCAACATTGGTGTGCACCTC 264
      |||||
Db      5215 CATTACCAACATTGGTGTGCACCTC 5239

RESULT 42
160509
LOCUS      I60509      8591 bp      DNA      linear      PAT 07-OCT-1997
DEFINITION      Sequence 8 from patent US 5656477.
ACCESSION      I60509
VERSION      I60509.1 GI:2478954
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 8591)
AUTHORS      Vitek M.Peter, and Jacobsen J.Steven.
TITLE      Amyloid precursor proteins and method of using same to assess
      agents which down-regulate formation of .beta.-amyloid peptide
JOURNAL      Patent: US 5656477-A 8 12-AUG-1997;
FEATURES
      Location/Qualifiers
      source
      1..8591
      /organism="unknown"
      /mol_type="unassigned DNA"

ORIGIN
Query Match      94.0%; Score 248.2; DB 6; Length 8591;
Best Local Similarity 98.5%; Pred. No. 3.3e-61;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy      1 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGTGCAACATGTAACGATGAGTTAGCAACA 60
      |||||
Db      4975 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGTGCAACATGTAACGATGAGTTAGCAACA 5034

Qy      61 TGCCTTACAGGAGAGAAAAAGCACCGTGCATGCCGANTGCTGGAAGTAAAGTGGTACGA 120
      |||||
Db      5035 TGCCTTACAGGAGAGAAAAAGCACCGTGCATGCCGANTGCTGGAAGTAAAGTGGTACGA 5094

Qy      121 TCGTGCCTTATTAGGAAGGCAACAGACAGGCTCTGACATGATGGACGACCACTAAATT 180
      |||||
Db      5095 TCGTGCCTTATTAGGAAGGCAACAGACAGGCTCTGACATGATGGACGACCACTAAATT 5154

Qy      181 CGCATTGCAGAGAT-ATTGTATTAAAGTGCCTAGCTCGATACATAAAGCCATTGGAC 239
      |||||
Db      5155 CGCATTGCAGAGATATTGTATTAAAGTGCCTAGCTCGATACATAAAGCCATTGGAC 5214

Qy      240 CATTACCAACATTGGTGTGCACCTC 264
      |||||
Db      5215 CATTACCAACATTGGTGTGCACCTC 5239

RESULT 43
177052
LOCUS      I77052      8591 bp      DNA      linear      PAT 03-APR-1998
DEFINITION      Sequence 6 from patent US 5693478.
ACCESSION      I77052
VERSION      I77052.1 GI:3013206
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 8591)
AUTHORS      Vitek M.Peter, and Jacobsen J.Steven.
TITLE      Method of detecting amyloid precursor proteins
JOURNAL      Patent: US 5693478-A 6 02-DEC-1997;
FEATURES
      Location/Qualifiers
      source
      1..8591
      /organism="unknown"
      /mol_type="unassigned DNA"

ORIGIN
Query Match      94.0%; Score 248.2; DB 6; Length 8591;
Best Local Similarity 98.5%; Pred. No. 3.3e-61;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy      1 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGTGCAACATGTAACGATGAGTTAGCAACA 60
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Db      4975 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGTGCAACATGTAACGATGAGTTAGCAACA 5034

Qy      61 TGCCTTACAGGAGAGAAAAAGCACCGTGCATGCCGANTGCTGGAAGTAAAGTGGTACGA 120
      |||||
Db      5035 TGCCTTACAGGAGAGAAAAAGCACCGTGCATGCCGANTGCTGGAAGTAAAGTGGTACGA 5094

Qy      121 TCGTGCCTTATTAGGAAGGCAACAGACAGGCTCTGACATGATGGACGACCACTAAATT 180
      |||||
Db      5095 TCGTGCCTTATTAGGAAGGCAACAGACAGGCTCTGACATGATGGACGACCACTAAATT 5154

Qy      181 CGCATTGCAGAGAT-ATTGTATTAAAGTGCCTAGCTCGATACATAAAGCCATTGGAC 239
      |||||
Db      5155 CGCATTGCAGAGATATTGTATTAAAGTGCCTAGCTCGATACATAAAGCCATTGGAC 5214

Qy      240 CATTACCAACATTGGTGTGCACCTC 264
      |||||
Db      5215 CATTACCAACATTGGTGTGCACCTC 5239

RESULT 44
177053

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Db	5035	TGCCTTTACAGGAGAGAAAAAGACCGTGCATGCGGATTTGGTGGAGGTAAAGTGGTACGA	5094		
QY	121	TGGTGCCCTTTATTAGGAAGCGCAAGACGGGTCTGCATCATGATTTGCACGAACCACTAAATT	180		
Db	5095	TGGTGCCCTTTATTAGGAGCGCAAGACAGGTCTGCATCATGATTTGCACGAACCACTGAATT	5154		
QY	181	CGCATTTGCAGAGAT-ATTGTATTAAATGTCCTAGCTGCATACAAATAAACGCCATTGCAC	239		
Db	5155	CGCATTTGCAGAGATAATTGTATTAAATGTCCTAGCTGCATACAAATAAACGCCATTGCAC	5214		
QY	240	CATTACACCAATTTGGTGTGCACCTC	264		
Db	5215	CATTACCAATTTGGTGTGCACCTC	5239		
RESULT 46					
LOCUS	187174	8591 bp	DNA linear PAT 10-JUN-1998		
DEFINITION	Sequence 8 from patent US 5703209.				
ACCESSION	187174				
VERSION	187174.1	GI:3206892			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 8591)				
AUTHORS	Vitek,M.Peter. and Jacobsen,J.Steven.				
TITLE	Amyloid precursor proteins and method of using same to assess agents which down-regulate formation of .beta.-amyloid peptide				
JOURNAL	Patent: US 5703209-A 8 30-DEC-1997;				
FEATURES	Location/Qualifiers				
source	1..8591				
	/organism="unknown"				
	/mol_type="unassigned DNA"				
ORIGIN					
Query Match	94.0%; Score 248.2; DB 6; Length 8591;				
Best Local Similarity	98.5%; Pred. No. 3.3e-61;				
Matches	261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;				
QY	1	AATGTAGTCTTATGCAATACACTCTTGTAGTCTTGCACATGTTACGATGATGTAGCAACA	60		
Db	4975	AATGTAGTCTTATGCAATACACTCTTGTAGTCTTGCACATGTTACGATGATGTAGCAACA	5034		
QY	61	TGCCTTTACAGGAGAGAAAAAGACCGTGCATGCGGATTTGGTGGAGGTAAAGTGGTACGA	120		
Db	5035	TGCCTTTACAGGAGAGAAAAAGACCGTGCATGCGGATTTGGTGGAGGTAAAGTGGTACGA	5094		
QY	121	TGGTGCCCTTTATTAGGAAGCGCAAGACGGGTCTGCATCATGATTTGCACGAACCACTAAATT	180		
Db	5095	TGGTGCCCTTTATTAGGAAGCGCAAGACAGGTCTGCATCATGATTTGCACGAACCACTGAATT	5154		
QY	181	CGCATTTGCAGAGAT-ATTGTATTAAATGTCCTAGCTGCATACAAATAAACGCCATTGCAC	239		
Db	5155	CGCATTTGCAGAGATAATTGTATTAAATGTCCTAGCTGCATACAAATAAACGCCATTGCAC	5214		
QY	240	CATTACACCAATTTGGTGTGCACCTC	264		
Db	5215	CATTACCAATTTGGTGTGCACCTC	5239		
RESULT 47					
LOCUS	AR215118	9737 bp	DNA linear PAT 25-SEP-2002		
DEFINITION	Sequence 22 from patent US 6410266.				
ACCESSION	AR215118				
VERSION	AR215118.1	GI:23313246			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 9737)				
Unclassified.					

AUTHORS Harrington,J.J. and Rundlett,S.
TITLE Compositions and methods for non-targeted activation of endogenous genes
JOURNAL Patent: US 6410266-A 22 25-JUN-2002;
FEATURES Location/Qualifiers
source 1..9737
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 94.0%; Score 248.2; DB 6; Length 9737;
Best Local Similarity 98.5%; Pred. No. 3.2e-61;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGTGCAACATGCTAAACGATGAGTTAGCAACA 60
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Db 1411 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGTGCAACATGCTAAACGATGAGTTAGCAACA 1470
|||||

QY 61 TGCCTTACAAGGAGAGAAAAAGCACCCTGTCATGCGATTGGTGAAGTAAGTGTGTACGA 120
|||||
Db 1471 TGCCTTACAAGGAGAGAAAAAGCACCCTGTCATGCGATTGGTGAAGTAAGTGTGTACGA 1530
|||||

QY 121 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGATGGAAGCAACCACTAAATT 180
|||||
Db 1531 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGATGGAAGCAACCACTAAATT 1590
|||||

QY 181 CGCATTTGCAGAGAT-ATTGTATTTAAGTGCCTAGCTCGATACATAATAAACGCCATTTGAC 239
|||||

Db 1591 CGCATTTGCAGAGAT-ATTGTATTTAAGTGCCTAGCTCGATACATAATAAACGCCATTTGAC 1650
|||||

QY 240 CATTCACACATTTGGTGTGCACCTC 264
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Db 1651 CATTCACACATTTGGTGTGCACCTC 1675
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RESULT 48

AR215119
LOCUS AR215119 9737 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 23 from patent US 6410266.
ACCESSION AR215119
VERSION AR215119.1 GI:23313247
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 9737)
AUTHORS Harrington,J.J. and Rundlett,S.
TITLE Compositions and methods for non-targeted activation of endogenous genes
JOURNAL Patent: US 6410266-A 23 25-JUN-2002;
FEATURES Location/Qualifiers
source 1..9737
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 94.0%; Score 248.2; DB 6; Length 9737;
Best Local Similarity 98.5%; Pred. No. 3.2e-61;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGTGCAACATGCTAAACGATGAGTTAGCAACA 60
|||||
Db 1411 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGTGCAACATGCTAAACGATGAGTTAGCAACA 1470
|||||

QY 61 TGCCTTACAAGGAGAGAAAAAGCACCCTGTCATGCGATTGGTGAAGTAAGTGTGTACGA 120
|||||
Db 1471 TGCCTTACAAGGAGAGAAAAAGCACCCTGTCATGCGATTGGTGAAGTAAGTGTGTACGA 1530
|||||

QY 121 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGATGGAAGCAACCACTAAATT 180
|||||
Db 1531 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGATGGAAGCAACCACTAAATT 1590
|||||

QY 181 CGCATTTGCAGAGAT-ATTGTATTTAAGTGCCTAGCTCGATACATAATAAACGCCATTTGAC 239
|||||

Db 1591 CGCATTTGCAGAGAT-ATTGTATTTAAGTGCCTAGCTCGATACATAATAAACGCCATTTGAC 1650
|||||

QY 240 CATTCACACATTTGGTGTGCACCTC 264
|||||
Db 1651 CATTCACACATTTGGTGTGCACCTC 1675
|||||

RESULT 49

AR215124
LOCUS AR215124 9737 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 28 from patent US 6410266.
ACCESSION AR215124
VERSION AR215124.1 GI:23313252
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 9737)
AUTHORS Harrington,J.J. and Rundlett,S.
TITLE Compositions and methods for non-targeted activation of endogenous genes
JOURNAL Patent: US 6410266-A 28 25-JUN-2002;
FEATURES Location/Qualifiers
source 1..9737
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 94.0%; Score 248.2; DB 6; Length 9737;
Best Local Similarity 98.5%; Pred. No. 3.2e-61;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGTGCAACATGCTAAACGATGAGTTAGCAACA 60
|||||
Db 1411 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGTGCAACATGCTAAACGATGAGTTAGCAACA 1470
|||||

QY 61 TGCCTTACAAGGAGAGAAAAAGCACCCTGTCATGCGATTGGTGAAGTAAGTGTGTACGA 120
|||||
Db 1471 TGCCTTACAAGGAGAGAAAAAGCACCCTGTCATGCGATTGGTGAAGTAAGTGTGTACGA 1530
|||||

QY 121 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGATGGAAGCAACCACTAAATT 180
|||||
Db 1531 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGATGGAAGCAACCACTAAATT 1590
|||||

QY 181 CGCATTTGCAGAGAT-ATTGTATTTAAGTGCCTAGCTCGATACATAATAAACGCCATTTGAC 239
|||||

Db 1591 CGCATTTGCAGAGAT-ATTGTATTTAAGTGCCTAGCTCGATACATAATAAACGCCATTTGAC 1650
|||||

QY 240 CATTCACACATTTGGTGTGCACCTC 264
|||||
Db 1651 CATTCACACATTTGGTGTGCACCTC 1675
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RESULT 50

AR302360
LOCUS AR302360 9737 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 22 from patent US 6541221.
ACCESSION AR302360
VERSION AR302360.1 GI:31690614
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 9737)
AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.
TITLE Compositions and methods for non-targeted activation of endogenous genes
JOURNAL Patent: US 6541221-A 22 01-APR-2003;
FEATURES Location/Qualifiers
source 1..9737
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 94.0%; Score 248.2; DB 6; Length 9737;
Best Local Similarity 98.5%; Pred. No. 3.2e-61;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGTGCAACATGCTAAACGATGAGTTAGCAACA 60
|||||
Db 1411 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGTGCAACATGCTAAACGATGAGTTAGCAACA 1470
|||||

QY 61 TGCCTTACAAGGAGAGAAAAAGCACCCTGTCATGCGATTGGTGAAGTAAGTGTGTACGA 120
|||||
Db 1471 TGCCTTACAAGGAGAGAAAAAGCACCCTGTCATGCGATTGGTGAAGTAAGTGTGTACGA 1530
|||||

QY 121 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGATGGAAGCAACCACTAAATT 180
|||||
Db 1531 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGATGGAAGCAACCACTAAATT 1590
|||||

QY 181 CGCATTTGCAGAGAT-ATTGTATTTAAGTGCCTAGCTCGATACATAATAAACGCCATTTGAC 239
|||||

Db 1591 CGCATTTGCAGAGAT-ATTGTATTTAAGTGCCTAGCTCGATACATAATAAACGCCATTTGAC 1650
|||||

QY 240 CATTCACACATTTGGTGTGCACCTC 264
|||||
Db 1651 CATTCACACATTTGGTGTGCACCTC 1675
|||||

Query Match		94.0%;	Score 248.2;	DB 6;	Length 9737;
Best Local Similarity		98.5%;	Pred. No. 3.2e-61;		
Matches	261;	Conservative	0;	Mismatches	3;
				Indels	1;
				Gaps	1;
Qy	1	AATGTAGCTTTATGCAATPACTCTTTGAGTCTTGTGCAACATGGTAAACGATGAGTTAGCAACA	60		
Db	1411	AATGTAGCTTTATGCAATPACACTTGTAGTCTTGTGCAACATGGTAAACGATGAGTTAGCAACA	1470		
Qy	61	TGCCTTACAGAGAGAGAGAAAGACACCGTGCATGCCGATTTGGTGCAATAGAGTGTGACGA	120		
Db	1471	TGCCTTACAGAGAGAGAAAGACACCGTGCATGCCGATTTGGTGCAATAGAGTGTGACGA	1530		
Qy	121	TCGTGCCTTTATTAGAGAGCGAACAGACAGCGGGTCTGCATCGATTGGAGCAACACCTAAATT	180		
Db	1531	TCGTGCCTTTATTAGAGAGCGAACAGACAGCGGGTCTGCATCGATTGGAGCAACACCTAAATT	1590		
Qy	181	CGCGATTTCGACAGAT-AATTGTATTAACTGGCTAGCTTCGATCAATAAAGCCGCACTTGAC	239		
Db	1591	CGCGATTTCGACAGATTAATTGTATTAACTGGCTAGCTTCGATCAATAAAGCCGCACTTGAC	1650		
Qy	240	CATTACCAACATGGTGTGCACCTC	264		
Db	1651	CATTACCAACATGGTGTGCACCTC	1675		

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RESULT 53
AR373232
LOCUS          AR373232          9737 bp      DNA      linear      PAT 18-DEC-2003
DEFINITION     Sequence 22 from patent US 6602686.
ACCESSION      AR373232
VERSION        AR373232.1  GI:40075240
KEYWORDS       .
SOURCE         Unknown.
ORGANISM       Unknown.
               Unclassified.
REFERENCE      1 (bases 1 to 9737)
AUTHORS       Harrington,J., Sherf,B. and Rundlett,S.
TITLE         Compositions and method for non-targeted activation of endogenous
               genes
JOURNAL       Patent: US 6602686-A 22 05-AUG-2003;
FEATURES       Location/Qualifiers
               1..9737
               /organism="unknown"
               /mol_type="genomic DNA"

ORIGIN
Query Match          94.08;  Score 248.2;  DB 6;  Length 9737;
Best Local Similarity 98.58;  Pred. No. 3.2e-61;
Matches 461;  Conservative 0;  Mismatches 3;  Indels 1;  Gaps 1;

1  AATGTAGTCTTATGCAATATCTTCTAGTCTTTCGAACATGGTAAACGATGAGTTAGCAACA 60

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Db 1411 AATGTAGTCTTATGCAATACACTTGTAGTCTTGGCAATGTAACGATGAGTTAGCAACA 1470

QY 61 TGCCTTACAAGGAGAGAAAAGACACCGTGCATGCCGATTGGTGGAGTAAGTGTGACGA 120

Db 1471 TGCCTTACAAGGAGAGAAAAGACACCGTGCATGCCGATTGGTGGAGTAAGTGTGACGA 1530

QY 121 TCGTGCCTTATTAGGAAGCAACAGACAGCGGTCTGACATGGATTGGCAAGCAACCACTAAAT 180

Db 1531 TCGTGCCTTATTAGGAAGCAACAGACAGCGGTCTGACATGGATTGGCAAGCAACCACTAAAT 1590

QY 181 CCGCATTCGACAGAT-ATTGTATTAAAGTGCCTAGCTCGATACATATAACCCATTGGAC 239

Db 1591 CCGCATTCGACAGAT-ATTGTATTAAAGTGCCTAGCTCGATACATATAACCCATTGGAC 1650

QY 240 CATTCAACCATTTGGTGTGCACCTC 264

Db 1651 CATTCAACCATTTGGTGTGCACCTC 1675

RESULT 54

AR373233

LOCUS AR373233 9737 bp DNA linear PAT 18-DEC-2003

DEFINITION Sequence 23 from patent US 6602686.

ACCESSION AR373233

VERSION AR373233.1 GI:40075241

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 9737)

AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.

TITLE Compositions and method for non-targeted activation of endogenous genes

JOURNAL Patent: US 6602686-A 23 05-AUG-2003;

FEATURES Location/Qualifiers

source 1..9737

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Query Match 94.0%; Score 248.2; DB 6; Length 9737;

Best Local Similarity 98.5%; Pred. No. 3.2e-61;

Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATACACTTGTAGTCTTGGCAATGTAACGATGAGTTAGCAACA 60

Db 1411 AATGTAGTCTTATGCAATACACTTGTAGTCTTGGCAATGTAACGATGAGTTAGCAACA 1470

QY 61 TGCCTTACAAGGAGAGAAAAGACACCGTGCATGCCGATTGGTGGAGTAAGTGTGACGA 120

Db 1471 TGCCTTACAAGGAGAGAAAAGACACCGTGCATGCCGATTGGTGGAGTAAGTGTGACGA 1530

QY 121 TCGTGCCTTATTAGGAAGCAACAGACAGCGGTCTGACATGGATTGGCAAGCAACCACTAAAT 180

Db 1531 TCGTGCCTTATTAGGAAGCAACAGACAGCGGTCTGACATGGATTGGCAAGCAACCACTAAAT 1590

QY 181 CCGCATTCGACAGAT-ATTGTATTAAAGTGCCTAGCTCGATACATATAACCCATTGGAC 239

Db 1591 CCGCATTCGACAGAT-ATTGTATTAAAGTGCCTAGCTCGATACATATAACCCATTGGAC 1650

QY 240 CATTCAACCATTTGGTGTGCACCTC 264

Db 1651 CATTCAACCATTTGGTGTGCACCTC 1675

RESULT 55

AR373238

LOCUS AR373238 9737 bp DNA linear PAT 18-DEC-2003

DEFINITION Sequence 28 from patent US 6602686.

ACCESSION AR373238

VERSION AR373238.1 GI:40075246

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 9737)

AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.

TITLE Compositions and method for non-targeted activation of endogenous genes

JOURNAL Patent: US 6602686-A 28 05-AUG-2003;

FEATURES Location/Qualifiers

source 1..9737

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Query Match 94.0%; Score 248.2; DB 6; Length 9737;

Best Local Similarity 98.5%; Pred. No. 3.2e-61;

Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATACACTTGTAGTCTTGGCAATGTAACGATGAGTTAGCAACA 60

Db 1411 AATGTAGTCTTATGCAATACACTTGTAGTCTTGGCAATGTAACGATGAGTTAGCAACA 1470

QY 61 TGCCTTACAAGGAGAGAAAAGACACCGTGCATGCCGATTGGTGGAGTAAGTGTGACGA 120

Db 1471 TGCCTTACAAGGAGAGAAAAGACACCGTGCATGCCGATTGGTGGAGTAAGTGTGACGA 1530

QY 121 TCGTGCCTTATTAGGAAGCAACAGACAGCGGTCTGACATGGATTGGCAAGCAACCACTAAAT 180

Db 1531 TCGTGCCTTATTAGGAAGCAACAGACAGCGGTCTGACATGGATTGGCAAGCAACCACTAAAT 1590

QY 181 CCGCATTCGACAGAT-ATTGTATTAAAGTGCCTAGCTCGATACATATAACCCATTGGAC 239

Db 1591 CCGCATTCGACAGAT-ATTGTATTAAAGTGCCTAGCTCGATACATATAACCCATTGGAC 1650

QY 240 CATTCAACCATTTGGTGTGCACCTC 264

Db 1651 CATTCAACCATTTGGTGTGCACCTC 1675

RESULT 56

AR401618

LOCUS AR401618 9737 bp DNA linear PAT 18-DEC-2003

DEFINITION Sequence 22 from patent US 6623958.

ACCESSION AR401618

VERSION AR401618.1 GI:40149066

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 9737)

AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.

TITLE Compositions and methods for non-targeted activation of endogenous genes

JOURNAL Patent: US 6623958-A 22 23-SEP-2003;

FEATURES Location/Qualifiers

source 1..9737

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Query Match 94.0%; Score 248.2; DB 6; Length 9737;

Best Local Similarity 98.5%; Pred. No. 3.2e-61;

Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATACACTTGTAGTCTTGGCAATGTAACGATGAGTTAGCAACA 60

Db 1411 AATGTAGTCTTATGCAATACACTTGTAGTCTTGGCAATGTAACGATGAGTTAGCAACA 1470

QY 61 TGCCTTACAAGGAGAGAAAAGACACCGTGCATGCCGATTGGTGGAGTAAGTGTGACGA 120

Db 1471 TGCCTTACAAGGAGAGAAAAGACACCGTGCATGCCGATTGGTGGAGTAAGTGTGACGA 1530

QY 121 TCGTGCCTTATTAGGAAGCAACAGACAGCGGTCTGACATGGATTGGCAAGCAACCACTAAAT 180

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Db 1531 TCGTGCTTTATTAGGAAGGCAACAGACAGAGTCTGCATGGAATTGGACGAACCACTGAATT 1590
Qy 181 CCSCATTGCAGAGAT-ATTGCTATTAAAGTCCTAGCTCGATACATTAATAGCCATTGGAC 239
Db 1591 CCGCATTGCAGAGATTAATTGTTAAAGTCCTAGCTCGATACATTAATAGCCATTGGAC 1650
Qy 240 CATTACCAACATTGGTGTGCACCTC 264
Db 1651 CATTACCAACATTGGTGTGCACCTC 1675

RESULT 57
AR401619
LOCUS AR401619 9737 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 23 from patent US 6623958.
ACCESSION AR401619
VERSION AR401619.1 GI:40149067
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 9737)
AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.
TITLE Compositions and methods for non-targeted activation of endogenous genes
JOURNAL Patent: US 6623958-A 23 23-SEP-2003;
FEATURES
source Location/Qualifiers
1..9737
/mol_type="genomic DNA"

ORIGIN
Query Match 94.0%; Score 248.2; DB 6; Length 9737;
Best Local Similarity 98.5%; Pred. No. 3.2e-61;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGCACATGGTAACGATGAGTTAGCAACA 60
Db 1411 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGCACATGGTAACGATGAGTTAGCAACA 1470
Qy 61 TGCCTTACAGGAGAGAAAAGCAGCGTGCATGCGGATGCTGGAAGTAAGTGGTACGA 120
Db 1471 TGCCTTACAGGAGAGAAAAGCAGCGTGCATGCGGATGCTGGAAGTAAGTGGTACGA 1530
Qy 121 TCGTGCTTTATTAGGAAGGCAACAGACGCGGTCTGCATGGAATGGACGAACCACTAAATT 180
Db 1531 TCGTGCTTTATTAGGAAGGCAACAGACGCGGTCTGCATGGAATGGACGAACCACTAAATT 1590
Qy 181 CCGCATTGCAGAGAT-ATTGCTATTAAAGTCCTAGCTCGATACATTAATAGCCATTGGAC 239
Db 1591 CCGCATTGCAGAGATTAATTGTTAAAGTCCTAGCTCGATACATTAATAGCCATTGGAC 1650
Qy 240 CATTACCAACATTGGTGTGCACCTC 264
Db 1651 CATTACCAACATTGGTGTGCACCTC 1675

RESULT 58
AR401624
LOCUS AR401624 9737 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 28 from patent US 6623958.
ACCESSION AR401624
VERSION AR401624.1 GI:40149072
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 9737)
AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.
TITLE Compositions and methods for non-targeted activation of endogenous genes
JOURNAL Patent: US 6623958-A 28 23-SEP-2003;
FEATURES
source Location/Qualifiers
1..9737
/mol_type="genomic DNA"

ORIGIN
Query Match 94.0%; Score 248.2; DB 6; Length 9871;
Best Local Similarity 98.5%; Pred. No. 3.2e-61;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGCACATGGTAACGATGAGTTAGCAACA 60
Db 1545 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGCACATGGTAACGATGAGTTAGCAACA 1604
Qy 61 TGCCTTACAGGAGAGAAAAGCAGCGTGCATGCGGATGCTGGAAGTAAGTGGTACGA 120
Db 1605 TGCCTTACAGGAGAGAAAAGCAGCGTGCATGCGGATGCTGGAAGTAAGTGGTACGA 1664
Qy 121 TCGTGCTTTATTAGGAAGGCAACAGACGCGGTCTGCATGGAATGGACGAACCACTAAATT 180
Db 1665 TCGTGCTTTATTAGGAAGGCAACAGACGCGGTCTGCATGGAATGGACGAACCACTAAATT 1724
Qy 181 CCGCATTGCAGAGAT-ATTGCTATTAAAGTCCTAGCTCGATACATTAATAGCCATTGGAC 239
Db 1725 CCGCATTGCAGAGATTAATTGTTAAAGTCCTAGCTCGATACATTAATAGCCATTGGAC 1784
Qy 240 CATTACCAACATTGGTGTGCACCTC 264
Db 1651 CATTACCAACATTGGTGTGCACCTC 1675
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source 1..9737
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 94.0%; Score 248.2; DB 6; Length 9737;
Best Local Similarity 98.5%; Pred. No. 3.2e-61;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGCACATGGTAACGATGAGTTAGCAACA 60
Db 1411 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGCACATGGTAACGATGAGTTAGCAACA 1470
Qy 61 TGCCTTACAGGAGAGAAAAGCAGCGTGCATGCGGATGCTGGAAGTAAGTGGTACGA 120
Db 1471 TGCCTTACAGGAGAGAAAAGCAGCGTGCATGCGGATGCTGGAAGTAAGTGGTACGA 1530
Qy 121 TCGTGCTTTATTAGGAAGGCAACAGACGCGGTCTGCATGGAATGGACGAACCACTAAATT 180
Db 1531 TCGTGCTTTATTAGGAAGGCAACAGACGCGGTCTGCATGGAATGGACGAACCACTAAATT 1590
Qy 181 CCGCATTGCAGAGAT-ATTGCTATTAAAGTCCTAGCTCGATACATTAATAGCCATTGGAC 239
Db 1591 CCGCATTGCAGAGATTAATTGTTAAAGTCCTAGCTCGATACATTAATAGCCATTGGAC 1650
Qy 240 CATTACCAACATTGGTGTGCACCTC 264
Db 1651 CATTACCAACATTGGTGTGCACCTC 1675

RESULT 59
AR215120
LOCUS AR215120 9871 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 24 from patent US 6410266.
ACCESSION AR215120
VERSION AR215120.1 GI:23313248
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 9871)
AUTHORS Harrington,J.J. and Rundlett,S.
TITLE Compositions and methods for non-targeted activation of endogenous genes
JOURNAL Patent: US 6410266-A 24 25-JUN-2002;
FEATURES
source Location/Qualifiers
1..9871
/mol_type="genomic DNA"

ORIGIN
Query Match 94.0%; Score 248.2; DB 6; Length 9871;
Best Local Similarity 98.5%; Pred. No. 3.2e-61;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGCACATGGTAACGATGAGTTAGCAACA 60
Db 1545 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGCACATGGTAACGATGAGTTAGCAACA 1604
Qy 61 TGCCTTACAGGAGAGAAAAGCAGCGTGCATGCGGATGCTGGAAGTAAGTGGTACGA 120
Db 1605 TGCCTTACAGGAGAGAAAAGCAGCGTGCATGCGGATGCTGGAAGTAAGTGGTACGA 1664
Qy 121 TCGTGCTTTATTAGGAAGGCAACAGACGCGGTCTGCATGGAATGGACGAACCACTAAATT 180
Db 1665 TCGTGCTTTATTAGGAAGGCAACAGACGCGGTCTGCATGGAATGGACGAACCACTAAATT 1724
Qy 181 CCGCATTGCAGAGAT-ATTGCTATTAAAGTCCTAGCTCGATACATTAATAGCCATTGGAC 239
Db 1725 CCGCATTGCAGAGATTAATTGTTAAAGTCCTAGCTCGATACATTAATAGCCATTGGAC 1784
Qy 240 CATTACCAACATTGGTGTGCACCTC 264
Db 1651 CATTACCAACATTGGTGTGCACCTC 1675
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Db      1785 CATTCAACCACTTGGTGTGCACCTC 1809

RESULT 60
LOCUS   AR302362
DEFINITION Sequence 24 from patent US 6541221.
ACCESSION AR302362
VERSION  AR302362.1 GI:31690616
KEYWORDS
SOURCE  Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 9871)
AUTHORS  Harrington,J.J., Sherf,B. and Rundlett,S.
TITLE    Compositions and methods for non-targeted activation of endogenous
genes
JOURNAL  Patent: US 6541221-A 24 01-APR-2003;
FEATURES Location/Qualifiers
source   1..9871
         /organism="unknown"
         /mol_type="genomic DNA"

ORIGIN
Query Match 94.0%; Score 248.2; DB 6; Length 9871;
Best Local Similarity 98.5%; Pred. No. 3.2e-61;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy      1 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGGCAACATGTAACGATGAGTTAGCAACA 60
        |||
Db      1545 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGGCAACATGTAACGATGAGTTAGCAACA 1604

Qy      61 TGCCTTACAAGGAGAGAAAAGACCGTGCATGCCGATTGGTGAAGTAAGTGGTACGA 120
        |||
Db      1605 TGCCTTACAAGGAGAGAAAAGACCGTGCATGCCGATTGGTGAAGTAAGTGGTACGA 1664

Qy      121 TCGTGCCTTATTAGGAAGGCAACAGACGGGTCTGCATGATGGATTGGACGACCACTAAATT 180
        |||
Db      1665 TCGTGCCTTATTAGGAAGGCAACAGACGGGTCTGCATGATGGATTGGACGACCACTAAATT 1724

Qy      181 CGCATTTGCAGAGAT-ATTGTATTATTAAAGTGCCTAGCTCGATACATAATAAAGCCATTTCAC 239
        |||
Db      1725 CGCATTTGCAGAGATTAATTGTATTAAAGTGCCTAGCTCGATACATAATAAAGCCATTTCAC 1784

Qy      240 CATTCAACCACTTGGTGTGCACCTC 264
        |||
Db      1785 CATTCAACCACTTGGTGTGCACCTC 1809

RESULT 62
LOCUS   AR401620
DEFINITION Sequence 24 from patent US 6623958.
ACCESSION AR401620
VERSION  AR401620.1 GI:40149068
KEYWORDS
SOURCE  Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 9871)
AUTHORS  Harrington,J.J., Sherf,B. and Rundlett,S.
TITLE    Compositions and methods for non-targeted activation of endogenous
genes
JOURNAL  Patent: US 6623958-A 24 23-SEP-2003;
FEATURES Location/Qualifiers
source   1..9871
         /organism="unknown"
         /mol_type="genomic DNA"

ORIGIN
Query Match 94.0%; Score 248.2; DB 6; Length 9871;
Best Local Similarity 98.5%; Pred. No. 3.2e-61;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy      1 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGGCAACATGTAACGATGAGTTAGCAACA 60
        |||
Db      1545 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGGCAACATGTAACGATGAGTTAGCAACA 1604

Qy      61 TGCCTTACAAGGAGAGAAAAGACCGTGCATGCCGATTGGTGAAGTAAGTGGTACGA 120
        |||
Db      1605 TGCCTTACAAGGAGAGAAAAGACCGTGCATGCCGATTGGTGAAGTAAGTGGTACGA 1664

Qy      121 TCGTGCCTTATTAGGAAGGCAACAGACGGGTCTGCATGATGGATTGGACGACCACTAAATT 180
        |||
Db      1665 TCGTGCCTTATTAGGAAGGCAACAGACGGGTCTGCATGATGGATTGGACGACCACTAAATT 1724

Qy      181 CGCATTTGCAGAGAT-ATTGTATTATTAAAGTGCCTAGCTCGATACATAATAAAGCCATTTCAC 239
        |||
Db      1725 CGCATTTGCAGAGATTAATTGTATTAAAGTGCCTAGCTCGATACATAATAAAGCCATTTCAC 1784

Qy      240 CATTCAACCACTTGGTGTGCACCTC 264
        |||
Db      1785 CATTCAACCACTTGGTGTGCACCTC 1809

RESULT 63
LOCUS   AR215121
DEFINITION Sequence 25 from patent US 6410266.
ACCESSION AR215121

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Qy      1 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGGCAACATGTAACGATGAGTTAGCAACA 60
        |||
Db      1545 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGGCAACATGTAACGATGAGTTAGCAACA 1604

Qy      61 TGCCTTACAAGGAGAGAAAAGACCGTGCATGCCGATTGGTGAAGTAAGTGGTACGA 120
        |||
Db      1605 TGCCTTACAAGGAGAGAAAAGACCGTGCATGCCGATTGGTGAAGTAAGTGGTACGA 1664

Qy      121 TCGTGCCTTATTAGGAAGGCAACAGACGGGTCTGCATGATGGATTGGACGACCACTAAATT 180
        |||
Db      1665 TCGTGCCTTATTAGGAAGGCAACAGACGGGTCTGCATGATGGATTGGACGACCACTAAATT 1724

Qy      181 CGCATTTGCAGAGAT-ATTGTATTATTAAAGTGCCTAGCTCGATACATAATAAAGCCATTTCAC 239
        |||
Db      1725 CGCATTTGCAGAGATTAATTGTATTAAAGTGCCTAGCTCGATACATAATAAAGCCATTTCAC 1784

Qy      240 CATTCAACCACTTGGTGTGCACCTC 264
        |||
Db      1785 CATTCAACCACTTGGTGTGCACCTC 1809

RESULT 63
LOCUS   AR215121
DEFINITION Sequence 25 from patent US 6410266.
ACCESSION AR215121

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Qy	121	TGTCGCTTATTAGAGGCAACAGACGGGTCTGACATGATGTGACGAACCACTAAATT	180
Db	1854	TGTCGCTTATTAGAGGCAACAGACGGGTCTGACATGATGTGACGAACCACTAAATT	1913
Qy	181	CGCATTTGCAGAGAT-ATTGTATTTAAGTGGCTAGCTCGATACATTAACGCCATTTCAC	239
Db	1914	CGCATTTGCAGAGATATTGTATTTAAGTGGCTAGCTCGATACATTAACGCCATTTCAC	1973
Qy	240	CATTCAACACATTGGTGTGCACCTC	264
Db	1974	CATTCAACACATTGGTGTGCACCTC	1998
RESULT 65			
AR373235			
LOCUS	AR373235	10060 bp	DNA
DEFINITION	Sequence 25 from patent US 6602686.		
ACCESSION	AR373235		
VERSION	AR373235.1	GI:40075243	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 10060)		
AUTHORS	Harrington,J.J., Sherif,B. and Rundlett,S.		
TITLE	Compositions and method for non-targeted activation of endogenous genes		
JOURNAL	Patent: US 6602686-A 25 05-AUG-2003;		
FEATURES	Location/Qualifiers		
source	1..10060		
	/organism="unknown"		
	/mol_type="genomic DNA"		
ORIGIN			
Query Match	94.0%; Score 248.2; DB 6; Length 10060;		
Best Local Similarity	98.5%; Pred. No. 3.2e-61;		
Matches	261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;		
Qy	1	AATGTAGTCTTATGCAATACACTCTTTAGTCTTTGCAACATGCTAACGATGAGTTAGCAACA	60
Db	1734	AATGTAGTCTTATGCAATACACTTTAGTCTTTGCAACATGCTAACGATGAGTTAGCAACA	1793
Qy	61	TGCCTTACAGCAGAGAAAAAGCACCGTGATCGCATCCGATTGGTGGAACTAAGTGGTACGA	120
Db	1794	TGCCTTACAGCAGAGAAAAAGCACCGTGATCGCATCCGATTGGTGGAACTAAGTGGTACGA	1853
Qy	121	TGTCGCTTATTAGAGGCAACAGACGGGTCTGACATGATTTGACGAACCACTAAATT	180
Db	1854	TGTCGCTTATTAGAGGCAACAGACGGGTCTGACATGATTTGACGAACCACTAAATT	1913
Qy	181	CGCATTTGCAGAGAT-ATTGTATTTAAGTGGCTAGCTCGATACATTAACGCCATTTCAC	239
Db	1914	CGCATTTGCAGAGATATTGTATTTAAGTGGCTAGCTCGATACATTAACGCCATTTCAC	1973
Qy	240	CATTCAACACATTGGTGTGCACCTC	264
Db	1974	CATTCAACACATTGGTGTGCACCTC	1998
RESULT 66			
AR401621			
LOCUS	AR401621	10060 bp	DNA
DEFINITION	Sequence 25 from patent US 6623958.		
ACCESSION	AR401621		
VERSION	AR401621.1	GI:40149069	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 10060)		
AUTHORS	Harrington,J.J., Sherif,B. and Rundlett,S.		
TITLE	Compositions and methods for non-targeted activation of endogenous		


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/db_xref="taxon:31805"

Query Match          94.0%; Score 248.2; DB 12; Length 10737;
Best Local Similarity 98.5%; Pred. No. 3.2e-61;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1 AATGTAGTCTTATGCAATACCTCTGTAGTCTTGCACAATGCTAAACGATGATTAGCAACA 60
    |||||
Db 407 AATGTAGTCTTATGCAATACACTTGTAGTCTTGCACAATGCTAAACGATGATTAGCAACA 465

Qy 61 TGCCTTACAGGAGAGAAAGAACACCGTGCATGCCGATTCGTTGGTGAAGTAAAGTGTGACGA 120
    |||||
Db 467 TGCCTTACAGGAGAGAAAGAACACCGTGCATGCCGATTCGTTGGTGAAGTAAAGTGTGACGA 526

Qy 121 TGTGSCCTTTATTAGGAAGGCAACAGACAGCGGTCTGACATGATGATTCGACGACCACTTAATTT 180
    |||||
Db 527 TGTGSCCTTTATTAGGAGGCAACAGACAGGCTGACATGATTCGACGACCACTGATTT 586

Qy 181 CCGCATTCGACAGAT-ATTGTATTTAAGTGGCTAGCTCGATACATAAAGCCATTTCAC 239
    |||||
Db 587 CCGCATTCGACAGATAAATTGTATTTAAGTGGCTAGCTCGATACATAAAGCCATTTCAC 646

Qy 240 CATTCAACCAATTGGTGTGACCTC 264
    |||||
Db 647 CATTCAACCAATTGGTGTGACCTC 671

RESULT 68
U02455
LOCUS
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UN02455
ACCESSION
UN02455.1 GI:413821
VERSION
KEYWORDS
SOURCE
ORGANISM
Cloning vector rpDR2
Cloning vector rpDR2
artificial sequences; vectors.
REFERENCE
1 (bases 1 to 10850)
AUTHORS
Kitts,P.A.
TITLE
CLONTECH Vectors On Disc version 1.3
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 10850)
AUTHORS
Murphy,A.J., Kung,A.L., Swirski,R.A. and Schinke,R.T.
TITLE
cDNA expression cloning in human cells using the pIamodaDR2
episonal vector system
JOURNAL
Methods: A Companion to Methods in Enzymology 4, 111-131 (1992)
REFERENCE
3 (bases 1 to 10850)
AUTHORS
Kitts,P.A.
TITLE
Direct Submission
JOURNAL
Submitted (07-OCT-1993) Paul A. Kitts, CLONTECH Laboratories, Inc.,
1020 East Meadow Circle, Palo Alto, CA 94303, USA
COMMENT
Lambda DR2 can be obtained from CLONTECH Laboratories, Inc., 1020
East Meadow Circle, Palo Alto, CA 94303, USA. To place an order
call (415) 424-8222 or (800) 662-2566, extension 1. International
customers, please contact your local distributor. For technical
information, call (415) 424- 8222 or (800) 662-2566, extension 3.
This sequence was compiled by Andrew Murphy and revised at
CLONTECH. If you suspect there is an error in this sequence, please
contact CLONTECH's Technical Service Department at (415) 424-8222
or (800) 662-2566, extension 3 or E-mail TECH@CLONTECH.COM.
FEATURES
source
1..10850
/organism="Cloning vector rpDR2"
/mol_type="genomic DNA"
/db_xref="taxon:31858"
/note="Plasmid released from lambda DR2"
ORIGIN
Query Match 94.0%; Score 248.2; DB 12; Length 10850;
Best Local Similarity 98.5%; Pred. No. 3.2e-61;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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QY 1 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGTGCAACATGTAACGATGAGTTAGCAACA 60
 Db 407 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGTGCAACATGTAACGATGAGTTAGCAACA 466
 QY 61 TGCCTTACAGGAGAGAAAAGCACCCTGTCATGCCGATTTGTCGAAGTAAAGTGGTAGCA 120
 Db 467 TGCCTTACAGGAGAGAAAAGCACCCTGTCATGCCGATTTGTCGAAGTAAAGTGGTAGCA 526
 QY 121 TCGTGCCTTATTAGGAAGGCAACAGACCGGCTCTGACATGATTTGGACGAACCACTAAATT 180
 Db 527 TCGTGCCTTATTAGGAAGGCAACAGACCGGCTCTGACATGATTTGGACGAACCACTAAATT 586
 QY 181 CGCATTTGACAGAT-ATTGTATTAAAGTCCCTAGTCCGATGATACATATAAAGCCATTGAC 239
 Db 587 CGCATTTGACAGATATTGTATTAAAGTCCCTAGTCCGATGATACATATAAAGCCATTGAC 646
 QY 240 CATTACACCATTTGGTGGCACCTC 264
 Db 647 CATTACACCATTTGGTGGCACCTC 671

RESULT 69
 AX031159
 LOCUS 11265 bp DNA circular PAT 20-SEP-2000
 DEFINITION Sequence 1 from Patent WO9844129.
 ACCESSION AX031159
 VERSION AX031159.1 GI:10278512
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 1
 AUTHORS
 TITLE
 JOURNAL

Lew, A.M., Boyle, J.S. and Brady, J.L.
 Enhancement of immune response using targeting molecules
 Patent: WO 9844129-A 1 08-OCT-1998;
 INST MEDICAL W & E HALL (AU); QUEENSLAND INST MED RES (AU); CSL
 LTD (AU); LEW ANDREW MARK (AU); UNIV MELBOURNE (AU); BOYLE
 JEFFREY STEPHEN (AU); BRADY JAMIE LOUISE (AU); COMM SCIENT IND
 RES ORG (AU)

FEATURES
 source

1. .11265
 /organism="unidentified"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32644"

ORIGIN

Query Match 94.0%; Score 248.2; DB 6; Length 11265;
 Best Local Similarity 98.5%; Pred. No. 3.2e-61;
 Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGTGCAACATGTAACGATGAGTTAGCAACA 60
 Db 369 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGTGCAACATGTAACGATGAGTTAGCAACA 428
 QY 61 TGCCTTACAGGAGAGAAAAGCACCCTGTCATGCCGATTTGTCGAAGTAAAGTGGTAGCA 120
 Db 429 TGCCTTACAGGAGAGAAAAGCACCCTGTCATGCCGATTTGTCGAAGTAAAGTGGTAGCA 488
 QY 121 TCGTGCCTTATTAGGAAGGCAACAGACCGGCTCTGACATGATTTGGACGAACCACTAAATT 180
 Db 489 TCGTGCCTTATTAGGAAGGCAACAGACCGGCTCTGACATGATTTGGACGAACCACTAAATT 548
 QY 181 CGCATTTGACAGAT-ATTGTATTAAAGTCCCTAGTCCGATGATACATATAAAGCCATTGAC 239
 Db 549 CGCATTTGACAGATATTGTATTAAAGTCCCTAGTCCGATGATACATATAAAGCCATTGAC 608
 QY 240 CATTACACCATTTGGTGGCACCTC 264
 Db 609 CATTACACCATTTGGTGGCACCTC 633

RESULT 70
 BD084805

LOCUS BD084805
 DEFINITION Enhancement of immune response using targeting molecules.
 ACCESSION BD084805
 VERSION BD084805.1 GI:22630415
 KEYWORDS JP 2001522235-A/1.
 SOURCE
 ORGANISM

REFERENCE
 1 (bases 1 to 11265)
 AUTHORS Boyle, J.S., Brady, J.L. and Lew, A.M.
 TITLE Enhancement of immune response using targeting molecules
 JOURNAL Patent: JP 2001522235-A 1 13-NOV-2001;
 THE COUNCIL OF THE QUEENSLAND INSTITUTE OF MEDICAL RESEARCH, THE
 COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION, THE
 UNIVERSITY OF MELBOURNE, THE WALTER AND ELIZA HALL INSTITUTE OF
 MEDICAL RESEARCH, CSL LTD

COMMENT

OS Unidentified
 PN JP 2001522235-A/1
 PD 13-NOV-2001
 PF 26-MAR-1998 JP 1998540989
 PR 27-MAR-1997 AU POS891,13-FEB-1998 AU PP 1830 PI
 JEFFREY STEPHEN BOYLE, JAMIE LOUISE BRADY, ANDREW MARK LEW PC
 CL215/62, C07K19/00, A61K39/00, A61K48/00
 CC Strandedness: Double;
 CC Topology: Circular;
 CC Enhancement of immune response using targeting molecules PH
 Key source Location/Qualifiers
 FT 1. .11265
 FT /organism="Unidentified".

FEATURES
 source

1. .11265
 /organism="unidentified"
 /mol_type="genomic DNA"
 /db_xref="taxon:32644"

ORIGIN

Query Match 94.0%; Score 248.2; DB 6; Length 11265;
 Best Local Similarity 98.5%; Pred. No. 3.2e-61;
 Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGTGCAACATGTAACGATGAGTTAGCAACA 60
 Db 369 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGTGCAACATGTAACGATGAGTTAGCAACA 428
 QY 61 TGCCTTACAGGAGAGAAAAGCACCCTGTCATGCCGATTTGTCGAAGTAAAGTGGTAGCA 120
 Db 429 TGCCTTACAGGAGAGAAAAGCACCCTGTCATGCCGATTTGTCGAAGTAAAGTGGTAGCA 488
 QY 121 TCGTGCCTTATTAGGAAGGCAACAGACCGGCTCTGACATGATTTGGACGAACCACTAAATT 180
 Db 489 TCGTGCCTTATTAGGAAGGCAACAGACCGGCTCTGACATGATTTGGACGAACCACTAAATT 548
 QY 181 CGCATTTGACAGAT-ATTGTATTAAAGTCCCTAGTCCGATGATACATATAAAGCCATTGAC 239
 Db 549 CGCATTTGACAGATATTGTATTAAAGTCCCTAGTCCGATGATACATATAAAGCCATTGAC 608
 QY 240 CATTACACCATTTGGTGGCACCTC 264
 Db 609 CATTACACCATTTGGTGGCACCTC 633

RESULT 71

AX665480
 LOCUS 16958 bp DNA linear PAT 26-MAR-2003
 DEFINITION Sequence 3 from Patent WO03002735.
 ACCESSION AX665480
 VERSION AX665480.1 GI:29290565

KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 1
 AUTHORS Lanctot, C., Gingras, R. and Gaumond, M.-H.

synthetic construct
 synthetic construct
 artificial sequences.

```

QY      181  CGCATGTCGAGAGT-ATTGTAATTAAGTGGCTAGCTGATACATATAACGCCATTTCAC 239
      28328  CGCATGTCGAGAGTAAATTTGTAATTAAGTGGCTAGCTGATACATATAACGCCATTTCAC
QY      240  CATTCAACCATTTGGTGTGCACCTC 264
      28388  CATTCAACCATTTGGTGTGCACCTC 28412

RESULT 73
LOCUS      ALRPOLITE                               633 bp ss-RNA      linear      VRL 28-APR-1993
DEFINITION Rous sarcoma virus (Schmidt-Rupplin), proviral, 3' LTR on 21S mRNA.
ACCESSION  J02025 J02022
VERSION     J02025.1 GI:210255
KEYWORDS   C-myc proto-oncogene; long terminal repeat (LTR); src oncogene.
SOURCE     Rous sarcoma virus
ORGANISM   Rous sarcoma virus
REFERENCE  1 (sites)
           Viruses; Retroviridae; Retroviridae; Alpharetrovirus.
AUTHORS   Yamamoto,T., de Crombrughe,B. and Pastan,I.
TITLE     Identification of a functional promoter in the long terminal repeat
           of Rous sarcoma virus
JOURNAL   Cell 22 (3), 787-797 (1980)
MEDLINE   81112147
PUBMED    6257399
REFERENCE  2 (bases 1 to 633)
           Yamamoto,T., Tyagi,J.S., Pagan,J.B., Jay,G., deCrombrughe,B. and
AUTHORS   Pastan,I.
TITLE     Molecular mechanism for the capture and excision of the
           transforming gene of avian sarcoma virus as suggested by analysis
           of recombinant clones
JOURNAL   J. Virol. 35 (2), 436-443 (1980)
MEDLINE   81072438
PUBMED    6255184
REFERENCE  3 (bases 319 to 633)
           Yamamoto,T., Jay,G. and Pastan,I.
TITLE     Unusual features in the nucleotide sequence of a cDNA clone derived
           from the common region of avian sarcoma virus messenger RNA
JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 77 (1), 176-180 (1980)
MEDLINE   80145590
PUBMED    6244542
COMMENT   Original source text: Rous sarcoma virus (Schmidt-Rupplin strain,
           subgroup D) provirus, cDNA to 21S mRNA from infected chicken
           embryonic fibroblasts, clone pSR1.
           [1] sites; mRNA start.
           Original figure in [2] included 24 'g's on 5' end and 16 'c's on 3'
           end that were cDNA synthesis artifacts.
           [2] also sequenced a defective clone, pSR2, with the src gene
           deleted (see separate entry).
           [1] demonstrated the mRNA transcription initiation site shown in
           the Sites table using pSR1 as a template. However, this is the 3'
           LTR, and the functional mRNA start site would be assumed to be on
           the 5' LTR at the homologous site.
FEATURES   Location/Qualifiers
           1..633
            /organism="Rous sarcoma virus"
            /mol_type="genomic RNA"
            /db_xref="taxon:11886"
misc_RNA   <1..517
            /note="viral genomic RNA"
LTR        211..>633
            /note="3' LTR"
mRNA       517..>633
            /note="in vitro mRNA [1]; see comment"
repeat_region 517..536
            /note="terminally redundant repeat"
ORIGIN     20 bp upstream of PstI site.

Query Match          93.6%; Score 247.2; DB 14; Length 633;
Best Local Similarity 98.5%; Pred. No. 8.9e-61;
Matches 260; Conservative 0; Mis-matches 3; Indels 1; Gaps 1;

```


GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 11, 2004, 03:02:06 ; Search time 227.972 Seconds
(without alignments)
4919.575 Million cell updates/sec

Title: US-09-733-368a-1_COPY_349_612

Perfect score: 264
Sequence: 1 aatgtagtcttatgcaatac.....accacattggtgcaactc 264

Scoring table: IDENTITY NUC
Gapex 10.0, Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues
Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :
1: Geneseqn23jan04:*
2: Geneseqn1980s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002s:*
7: Geneseqn2003as:*
8: Geneseqn2003bs:*
9: Geneseqn2003cs:*
10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	264	100.0	648	AAH43951	Aah43951 Rous sarc
2	262.4	99.4	2187	AAA14722	Aaa14722 Nucleotid
3	262.4	99.4	2829	AAZ93333	Aaz93333 Partial s
4	262.4	99.4	2878	AAZ93078	Aaz93078 Partial s
5	262.4	99.4	3310	AAZ93331	Aaz93331 Partial s
6	262.4	99.4	3311	AAZ933079	Aaz933079 Partial s
7	262.4	99.4	3385	AAZ99169	Aaz99169 ADRSV-bet
8	262.4	99.4	4487	AAA09085	Aaa09085 ADRSV-bet
9	262.4	99.4	7086	ADD35600	Add35600 Tricistron
10	262.4	99.4	8238	AAA59078	Aaa59078 Nucleotid
11	262.4	99.4	33622	AAAL56867	Aal56867 DNA seque
12	262.4	99.4	34302	AAZ94163	Aaz94163 Adenoviru
13	262.4	99.4	35211	AAAL56866	Aal56866 DNA seque
14	261.4	99.0	11627	AAZ29699	Aaz29699 Viral exp
15	260.4	98.6	2245	7 ABZ23249	Abz23249 Lac repre
16	259.2	98.2	5177	2 AAZ09997	Aaz09997 Bovine sc
17	257.6	97.6	4965	2 AAQ75973	Aaq75973 pHLA-B7/b
18	257.2	97.4	262	4 AAS15665	Aas15665 Human res
19	256.4	97.1	562	7 ABZ23250	Abz23250 Nucleotid
20	251.4	95.2	4457	9 ADD35599	Add35599 Bictistron
21	251.4	95.2	7334	9 ADD35601	Add35601 Tetractist
22	248.2	94.0	397	3 AAZ94161	Aaz94161 395 Nucle
23	248.2	94.0	397	3 AAA14719	Aaa14719 Nucleotid

Aaz931077	Rous Sarc
Aaq75974	pHLA-B7 e
Aaq62391	Vector pv
Aas17704	Vector pv
Abn81143	Plasmid p
Aat02998	RSV tar R
Aat76802	RSV tar R
Aaq43814	pRLD3D4 C
Aaq43813	pRLD2D3D4 C
Aaq43812	pRLD1D1D2D3
Aaa53869	Expressio
Aat84562	Plasmid p
Aat84561	Plasmid p
Aat87083	Plasmid p
Aat87084	Plasmid p
Aav04866	CDNA enco
Aav04865	CDNA enco
Aav05850	APP-REP 7
Aav05849	APP-REP 7
Ab157333	Vector pl
Aaa53873	Expressio
Aaa53879	Expressio
Aaa53874	Expressio
Aaa53875	Expressio
Aaa53876	Expressio
Aav59501	Plasmid p
Aal55269	DNA of ex
Aax02780	Vector pm
Aat62602	Luciferas
Aat71261	Rous sarc
Aaz60824	Nucleotid
Aad28311	LSRNL vec
Aad28272	LSRNL vec
AcD27899	pdmT2 vec
Aaq06310	Sequence
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Aaq06313	Sequence
Aaq06312	Sequence
Aac92489	Fragment
Aax77359	Polynucle
Aaa90391	987Bneuo
Aad27850	Complete
Aad04741	Alphavira
Aaf84024	Complete
Abk10062	Expressio
Aad53272	MESV2/EGF
Aad53270	MESV2/ACT
Aad53271	MESV2/IRE
Aad14296	MESV2/EGF
Aad13899	Recombina
Ab94279	Nucleotid
Ab94279	Nucleotid
Aal56865	DNA seque
Aad53274	MESV2/EGF
Aad53290	MESV2/EGF
Aad53293	MESV2/EGF
Aad53282	MESV2/EGF
Aad53273	MESV2/EGF
Aad53289	MESV2/EGF
Aad53291	MESV2/EGF
Aad14199	MESV2/EGF
Aad14203	MESV2/EGF
Ab190071	Human pol
Ab159286	Nucleotid
Ab159285	Nucleotid
Ab159276	Nucleotid
Ab159280	Nucleotid
Ab159277	Nucleotid
Ab159284	Nucleotid
Ab159283	Nucleotid
Ab159278	Nucleotid

97 93.8 35.5 97 6 ABL59281 Nucleotid
98 88 33.3 101 4 AAF84457 Rous sarc
99 87 33.0 92 6 ABL59282 Nucleotid
100 82.6 31.3 149 6 ABL59279 Nucleotid

ALIGNMENTS

RESULT 1
AAH43951
ID AAH43951 standard; DNA; 648 BP.
XX
AC AAH43951;
XX
DT 06-SEP-2001 (first entry)
XX
DE Rous sarcoma virus promoter nucleotide sequence SEQ ID NO:1.
XX
KW Rous sarcoma virus; promoter; enhancer; RSV; primate; gene expression;
KW transgene; genetic engineering; gene therapy; immunisation; ds.
XX
OS Rous sarcoma virus.
XX
FN WO200142444-A2.
XX
PD 14-JUN-2001.
XX
PF 08-DEC-2000; 2000WO-US033256.
XX
PR 10-DEC-1999; 99US-0170019P.
XX
PA (ARIA-) ARIAD GENE THERAPEUTICS INC.
PA (TYPE-) UNIV PENNSYLVANIA.
XX
PI Rivera V, Zoltick P, Wilson JM;
XX WPI; 2001-381673/40.
XX
DR Genetically engineering a primate for expression of a desired gene,
PT comprises introducing into the primate a transgene comprising Rous
PT Sarcoma Virus (RSV) promoter and a nucleic acid sequence heterologous to
PT RSV promoter.
XX
PS Claim 7; Page 44; 64pp; English.

XX The present invention describes a method for genetically engineering a
CC primate for expression of a desired gene comprising introducing into the
CC primate a transgene comprising an Rous Sarcoma Virus (RSV) promoter and a
CC nucleic acid sequence heterologous to RSV promoter. Also described is a
CC primate cell (I) containing and capable of expressing a transgene
CC comprising an RSV promoter operably linked to a recombinant nucleic acid
CC encoding one or more fusion proteins, where the fusion proteins bind to a
CC ligand and in the presence of the ligand modulate(s) the expression level
CC of a target gene. The method can be used for high level expression of
CC genes in primates or for engineering primate cells. It is useful for
CC increasing the efficacy of many gene therapy strategies, and for
CC increasing the efficacy of intracellular immunisation agents, molecules
CC like ribozymes, antisense RNA, and dominant negative proteins, that act
CC either stoichiometrically, or by competition. The method increases the
CC efficacy of many gene therapy strategies by substantially elevating the
CC expression of an exogenous therapeutic gene, and allowing expression to
CC reach therapeutically effective levels. The present sequence represents a
CC specifically claimed RSV enhancer/promoter nucleotide sequence from the
CC present invention

XX Sequence 648 BP; 163 A; 135 C; 179 G; 171 T; 0 U; 0 Other;

Query Match 100.0%; Score 264; DB 4; Length 648;

Best Local Similarity 100.0%; Pred. No. 2.2e-82;
Matches 264; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGATAGTCTTATGCAATACCTTGTAGTCTTGCACATCGGTAAAGTAGTTAGCAACA 60

Db 349 AATGATAGTCTTATGCAATACCTTGTAGTCTTGCACATCGGTAAAGTAGTTAGCAACA 408
QY 61 TGCCTTACAAGGAGAGAAAAAGCACCGTGCAATGCCGATTTGGTGAAGTAAGGTGGTACGA 120
Db 409 TGCCTTACAAGGAGAGAAAAAGCACCGTGCAATGCCGATTTGGTGAAGTAAGGTGGTACGA 468
QY 121 TCGTGCCTTATTAGGAGGCAAGACGCGGTCTGCATGGAATTGGACGAACCACTAAATT 180
Db 469 TCGTGCCTTATTAGGAGGCAAGACGCGGTCTGCATGGAATTGGACGAACCACTAAATT 528
QY 181 CGCATTTGCAGAGATATTGTATTTAAGTGCCTAGCTCGATACATATAAAGCCATTGACC 240
Db 529 CGCATTTGCAGAGATATTGTATTTAAGTGCCTAGCTCGATACATATAAAGCCATTGACC 588
QY 241 ATTACACACATTTGGTGTGCACCTC 264
Db 589 ATTACACACATTTGGTGTGCACCTC 612

RESULT 2

AAH14722
ID AAH14722 standard; DNA; 2187 BP.
XX
AC AAH14722;
XX
DT 06-AUG-2003 (revised)
DT 08-AUG-2000 (first entry)
XX
DE Nucleotide sequence of region A of vector Ad5RSVbeta-lactamase.

XX Cellular cytotoxicity; tumor cell; expression vector; beta-lactamase;
KW replication-deficient adenovirus type 5; suicide gene therapy;
KW cancer cell; chemotherapy; beta-lactamase produg enzyme; produg TCM;
KW anticancer; tumor; leukemia; breast cancer; Wilms' tumor;
KW small cell lung carcinoma; Ewing's sarcoma; colon carcinoma;
KW papillary adenocarcinoma; ss.

XX Synthetic.

OS Rous sarcoma virus.

OS Mastadenovirus.

XX WO2000020608-A1.

PN 13-APR-2000.

XX 01-OCT-1999; 99WO-US020908.

XX 02-OCT-1998; 98US-00165321.

XX (GENO-) GENOTHERAPEUTICS INC.

PI Steiner MS;

XX WPI; 2000-303788/26.

DR Treating cancer using viral vectors which encode enzymes that convert
XX inactive drugs to active cytotoxic agents, expression of the enzyme is
PT tissue specific therefore targeting the effects of the drug to tumor
PT cells.

PS Disclosure; Fig 10; 130pp; English.

XX The specification describes a method for inducing cellular cytotoxicity
CC in tumor cells using replication-deficient adenovirus type 5 expression
CC vectors. The vectors comprise a sequence encoding a beta-lactamase under
CC the control of a Rous Sarcoma virus in combination with a produg
CC conjugated to a toxic agent. Tissue specific expression of the enzyme
CC converts the inactive drugs into active cancer killing agents. The
CC adenovirus genome has a deletion in an E1 and/or E3 region, and the beta-
CC lactamase sequence is inserted within this region. The vectors are used
CC for suicide gene therapy. This involves introducing genes into cancer
CC cells that encode enzymes capable of converting inactive drugs into

CC active cancer killing agents. If tissue specific promoters are coupled to
 CC the prodrug enzymes, then production of the prodrug will be tissue
 CC specific and targeted to the tumor. Therefore the cancer cells act as
 CC their own factories to activate chemotherapy agents and commit suicide.
 CC Beta-lactamase prodrug enzymes convert prodrug TCM into an active
 CC anticancer agent which is cytotoxic to cancer cells PPC-1. The method is
 CC used to treat patients with cancers of the brain, bladder or prostate. It
 CC may also be used to treat a range of other tumors such as leukemia,
 CC breast cancer, Wilms tumor, small cell lung carcinoma, Ewing's sarcoma,
 CC colon carcinoma and papillary adenocarcinomas. The present sequence
 CC represents region A of vector Ad5RSVbeta-lactamase, a vector of the
 CC invention. (Updated on 06-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 2187 BP; 562 A; 477 C; 592 G; 556 T; 0 U; 0 Other;

Query Match 99.4%; Score 262.4; DB 3; Length 2187;
 Best Local Similarity 99.6%; Pred. No. 1.4e-81;
 Matches 263; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGCAATGTTAAAGATGATTAGCAACA 60
 Db 541 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGCAATGTTAAAGATGATTAGCAACA 600
 QY 61 TGCCTTACAGGAGAGAAAAGCAACCGTGCATGCCGATTTGGTGAAGTAAGTGGTACGA 120
 Db 601 TGCCTTACAGGAGAGAAAAGCAACCGTGCATGCCGATTTGGTGAAGTAAGTGGTACGA 660
 QY 121 TCGTGCCCTTATTAGGAGGCAACAGACGGGTCTGCATGATGTTGAACCACTTAATTT 180
 Db 661 TCGTGCCCTTATTAGGAGGCAACAGACGGGTCTGCATGATGTTGAACCACTTAATTT 720
 QY 181 CCGCATTTGCAGAGATATTGTATTAAAGTGCCTAGCTCGATACATAAAGCGCACTTTGACC 240
 Db 721 CCGCATTTGCAGAGATATTGTATTAAAGTGCCTAGCTCGATACATAAAGCGCACTTTGACC 780

QY 241 ATTCACCACTTTGGTGTGCACCTC 264
 Db 781 ATTCACCACTTTGGTGTGCACCTC 804

RESULT 3
 AAZ93333
 ID AAZ93333 standard; DNA; 2829 BP.
 AC AAZ93333;
 XX
 DT 04-JUL-2000 (first entry)
 XX
 DE Partial sequence of replication deficient adenoviral vector Ad5RSV2C9.
 XX Adenovirus; vector; E1; E3; cytochrome; NADPH cytochrome reductase;
 KW Rous Sarcoma virus; RSV; chemotoxicity; transfection; sensitisation;
 KW prodrug; nicotinamide adenine dinucleotide phosphatase; ss.
 XX Synthetic.

OS
 XX WO200014256-A1.
 PN
 XX 16-MAR-2000.
 PD
 XX
 PF 03-SEP-1999; 99WO-US018834.
 XX
 XX 04-SEP-1998; 98US-00148275.
 XX
 XX (GENO-) GENOTHERAPEUTICS INC.
 PA
 XX
 FI Steiner MS, Lu Y;
 XX
 XX WPI; 2000-257001/22.
 DR
 XX
 XX
 PT Replication-deficient adenovirus type 5 expression vectors used for gene
 ET therapy of cancer, especially prostate cancer, comprising an insertion of
 ET nucleic acid encoding cytochrome p450 genes.

XX
 PS Claim 16; Fig 11A; 110pp; English.
 XX
 CC Replication-deficient adenovirus type 5 expression vectors comprise an
 CC adenovirus genome with a deletion in the E1 and E2 region of the genome
 CC and an insertion within the region under the control of a Rous Sarcoma
 CC Virus promoter can be used to induce chemotoxicity in tumour cells. Three
 CC such expression vectors are described, the inserted nucleic acids in each
 CC being the following: Vector (I) has an insertion of a nucleic acid
 CC encoding a cytochrome 2C9 p450 and is designated Ad5RSV2C9 (ATCC VR-
 CC 2628). Vector (II) has an insertion of a nucleic acid encoding a
 CC cytochrome 3A4 p450 and is designated Ad5RSV3A4 (ATCC VR-2629). Vector
 CC (III) has an insertion of a nucleic acid encoding a nicotinamide adenine
 CC dinucleotide phosphatase (NADPH) cytochrome p450 reductase and is
 CC designated Ad5RSVRED (ATCC VR-2630). The chemotoxicity of a tumor cell
 CC can be induced by administering (I) and (II) or (II) and (III) into the
 CC tumor cell (e.g. a prostate tumor cell) to selectively sensitize the cell
 CC to a prodrug and then administering the prodrug which kills the cell,
 CC inducing its chemotoxicity. The method uses gene-directed enzyme prodrug
 CC therapy to transfer a drug susceptibility gene to the tumor which
 CC activates a nontoxic prodrug intratumorally so the released drug can kill
 CC the tumor cells containing the drug susceptibility gene. This sequence is
 CC designated region A of the vector Ad5RSV2C9 and is the sequence of the
 CC cytochrome 2C9 p450
 XX

SQ Sequence 2829 BP; 748 A; 633 C; 707 G; 741 T; 0 U; 0 Other;

Query Match 99.4%; Score 262.4; DB 3; Length 2829;
 Best Local Similarity 99.6%; Pred. No. 1.6e-81;
 Matches 263; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGCAATGTTAAAGATGATTAGCAACA 60
 Db 541 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGCAATGTTAAAGATGATTAGCAACA 600
 QY 61 TGCCTTACAGGAGAGAAAAGCAACCGTGCATGCCGATTTGGTGAAGTAAGTGGTACGA 120
 Db 601 TGCCTTACAGGAGAGAAAAGCAACCGTGCATGCCGATTTGGTGAAGTAAGTGGTACGA 660
 QY 121 TCGTGCCCTTATTAGGAGGCAACAGACGGGTCTGCATGATGTTGAACCACTTAATTT 180
 Db 661 TCGTGCCCTTATTAGGAGGCAACAGACGGGTCTGCATGATGTTGAACCACTTAATTT 720
 QY 181 CCGCATTTGCAGAGATATTGTATTAAAGTGCCTAGCTCGATACATAAAGCGCACTTTGACC 240
 Db 721 CCGCATTTGCAGAGATATTGTATTAAAGTGCCTAGCTCGATACATAAAGCGCACTTTGACC 780
 QY 241 ATTCACCACTTTGGTGTGCACCTC 264
 Db 781 ATTCACCACTTTGGTGTGCACCTC 804

RESULT 4
 AAZ933078
 ID AAZ933078 standard; DNA; 2878 BP.
 AC AAZ933078;
 XX
 DT 04-JUL-2000 (first entry)
 XX
 DE Partial sequence of replication deficient adenoviral vector Ad5RSV3A4.
 XX Adenovirus; vector; E1; E3; cytochrome; NADPH cytochrome reductase;
 KW Rous Sarcoma virus; RSV; chemotoxicity; transfection; sensitisation;
 KW prodrug; nicotinamide adenine dinucleotide phosphatase; ss.
 XX Synthetic.
 OS
 XX WO200014256-A1.
 PN
 XX 16-MAR-2000.
 PD
 XX
 PF 03-SEP-1999; 99WO-US018834.

XX 04-SEP-1998; 98US-00148275.
 XX (GENO-) GENOTHERAPEUTICS INC.
 XX Steiner MS, Lu Y;
 XX WPI; 2000-257001/22.
 XX Replication-deficient adenovirus type 5 expression vectors used for gene
 PT therapy of cancer, especially prostate cancer, comprising an insertion of
 PT nucleic acid encoding cytochrome p450 genes.
 XX Claim 17; Fig 11B; 110pp; English.
 XX Replication-deficient adenovirus type 5 expression vectors comprise an
 CC adenovirus genome with a deletion in the E1 and E2 region of the genome
 CC and an insertion within the region under the control of a Rous Sarcoma
 CC Virus promoter can be used to induce chemotoxicity in tumour cells. Three
 CC such expression vectors are described, the inserted nucleic acids in each
 CC being the following: Vector (I) has an insertion of a nucleic acid
 CC encoding a cytochrome 2C9 p450 and is designated Ad5RSV2C9 (ATCC VR-
 CC 2628). Vector (II) has an insertion of a nucleic acid encoding a
 CC cytochrome 3A4 p450 and is designated Ad5RSV3A4 (ATCC VR-2629). Vector
 CC (III) has an insertion of a nucleic acid encoding a nicotinamide adenine
 CC dinucleotide phosphatase (NADPH) cytochrome p450 reductase and is
 CC designated Ad5RSVRED (ATCC VR-2630). The chemotoxicity of a tumor cell
 CC can be induced by administering (I) and (III) or (II) and (III) into the
 CC tumor cell (e.g. a prostate tumor cell) to selectively sensitise the cell
 CC to a prodrug and then administering the prodrug which kills the cell,
 CC inducing its chemotoxicity. The method uses gene-directed enzyme prodrug
 CC therapy to transfer a drug susceptibility gene to the tumor which
 CC activates a nontoxic prodrug intratumorally so the released drug can kill
 CC the tumor cells containing the drug susceptibility gene. This sequence is
 CC designated region A of the vector Ad5RSV3A4 and is the sequence of the
 CC cytochrome 3A4 p450
 XX
 SQ Sequence 2878 BP; 786 A; 609 C; 710 G; 773 T; 0 U; 0 Other;
 Query Match 99.4%; Score 262.4; DB 3; Length 2878;
 Best Local Similarity 99.6%; Pred. No. 1.6e-81;
 Matches 263; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 AATGTAGTCTTATGCAATCTCTTTAGTCTTGTGCAATGCTTAACGATGAGTACGACA 60
 Db |||||||
 541 AATGTAGTCTTATGCAATCTCTTTAGTCTTGTGCAATGCTTAACGATGAGTACGACA 600
 QY 61 TGCCTTACAGGAGAGAAAAGCAACCGTGCATGCGGATTTGGTGAAGTAAAGTGTACGA 120
 Db |||||||
 601 TGCCTTACAGGAGAGAAAAGCAACCGTGCATGCGGATTTGGTGAAGTAAAGTGTACGA 660
 QY 121 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGGATTTGGACCAACCACTAAATT 180
 Db |||||||
 661 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGGATTTGGACCAACCACTAAATT 720
 QY 181 CCGCATTTGCAGAGATATTGTTAATTAAGTGCCTAGCTGATACATAAAGCGCAATTTGACC 240
 Db |||||||
 721 CCGCATTTGCAGAGATATTGTTAATTAAGTGCCTAGCTGATACATAAAGCGCAATTTGACC 780
 QY 241 ATTCACCAATTTGGTGTGCACCTC 264
 Db |||||||
 781 ATTCACCAATTTGGTGTGCACCTC 804
 RESULT 5
 AA293331
 ID AA293331 standard; DNA; 3310 BP.
 XX
 AC AA293331;
 XX
 DT 04-JUL-2000 (first entry)
 XX
 DE Partial sequence of replication deficient adenoviral vector Ad5RSVRed.

XX Adenovirus; vector: E1; E3; cytochrome; NADPH cytochrome reductase;
 KW Rous Sarcoma virus; RSV; chemotoxicity; transfection; sensitisation;
 KW prodrug; nicotinamide adenine dinucleotide phosphatase; ss.
 XX Synthetic.
 XX WO200014256-A1.
 PN
 XX 16-MAR-2000.
 PD
 XX 03-SEP-1999; 99WO-US018834.
 PF
 XX 04-SEP-1998; 98US-00148275.
 PR
 XX (GENO-) GENOTHERAPEUTICS INC.
 PA Steiner MS, Lu Y;
 XX WPI; 2000-257001/22.
 DR Replication-deficient adenovirus type 5 expression vectors used for gene
 PT therapy of cancer, especially prostate cancer, comprising an insertion of
 PT nucleic acid encoding cytochrome p450 genes.
 XX Disclosure; Fig 10; 110pp; English.
 XX Replication-deficient adenovirus type 5 expression vectors comprise an
 CC adenovirus genome with a deletion in the E1 and E2 region of the genome
 CC and an insertion within the region under the control of a Rous Sarcoma
 CC Virus promoter can be used to induce chemotoxicity in tumour cells. Three
 CC such expression vectors are described, the inserted nucleic acids in each
 CC being the following: Vector (I) has an insertion of a nucleic acid
 CC encoding a cytochrome 2C9 p450 and is designated Ad5RSV2C9 (ATCC VR-
 CC 2628). Vector (II) has an insertion of a nucleic acid encoding a
 CC cytochrome 3A4 p450 and is designated Ad5RSV3A4 (ATCC VR-2629). Vector
 CC (III) has an insertion of a nucleic acid encoding a nicotinamide adenine
 CC dinucleotide phosphatase (NADPH) cytochrome p450 reductase and is
 CC designated Ad5RSVRED (ATCC VR-2630). The chemotoxicity of a tumor cell
 CC can be induced by administering (I) and (III) or (II) and (III) into the
 CC tumor cell (e.g. a prostate tumor cell) to selectively sensitise the cell
 CC to a prodrug and then administering the prodrug which kills the cell,
 CC inducing its chemotoxicity. The method uses gene-directed enzyme prodrug
 CC therapy to transfer a drug susceptibility gene to the tumor which
 CC activates a nontoxic prodrug intratumorally so the released drug can kill
 CC the tumor cells containing the drug susceptibility gene. This sequence is
 CC designated region A of the vector Ad5RSVRed
 XX
 SQ Sequence 3310 BP; 755 A; 881 C; 980 G; 694 T; 0 U; 0 Other;
 Query Match 99.4%; Score 262.4; DB 3; Length 3310;
 Best Local Similarity 99.6%; Pred. No. 1.7e-81;
 Matches 263; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 AATGTAGTCTTATGCAATCTCTTTAGTCTTGTGCAATGCTTAACGATGAGTACGACA 60
 Db |||||||
 541 AATGTAGTCTTATGCAATCTCTTTAGTCTTGTGCAATGCTTAACGATGAGTACGACA 600
 QY 61 TGCCTTACAGGAGAGAAAAGCAACCGTGCATGCGGATTTGGTGAAGTAAAGTGTACGA 120
 Db |||||||
 601 TGCCTTACAGGAGAGAAAAGCAACCGTGCATGCGGATTTGGTGAAGTAAAGTGTACGA 660
 QY 121 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGGATTTGGACCAACCACTAAATT 180
 Db |||||||
 661 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGGATTTGGACCAACCACTAAATT 720
 QY 181 CCGCATTTGCAGAGATATTGTTAATTAAGTGCCTAGCTGATACATAAAGCGCAATTTGACC 240
 Db |||||||
 721 CCGCATTTGCAGAGATATTGTTAATTAAGTGCCTAGCTGATACATAAAGCGCAATTTGACC 780
 QY 241 ATTCACCAATTTGGTGTGCACCTC 264
 Db |||||||
 781 ATTCACCAATTTGGTGTGCACCTC 804

RESULT 6
 AA293079
 ID AA293079 standard; DNA; 3311 BP.
 XX
 AC
 AC
 AA293079;
 DT 04-JUL-2000 (first entry)
 XX
 DE Partial sequence of replication deficient adenoviral vector AdRSVRred.
 XX
 KW Adenovirus; vector; E1; E3; cytochrome; NADPH cytochrome reductase;
 KW Rous Sarcoma virus; RSV; chemotoxicity; transfection; sensitisation;
 KW prodrug; nicotinamide adenine dinucleotide phosphatase; ss.
 XX
 OS Synthetic.
 XX
 FN WO200014256-A1.
 XX
 PD 16-MAR-2000.
 XX
 PF 03-SEP-1999; 99WO-US018934.
 XX
 PR 04-SEP-1998; 98US-00148275.
 XX
 PA (GENO-) GENOTHERAPEUTICS INC.
 XX
 PI Steiner MS, Lu Y;
 XX
 XX WPI; 2000-257001/22.
 XX
 PT Replication-deficient adenovirus type 5 expression vectors used for gene
 PT therapy of cancer, especially prostate cancer, comprising an insertion of
 PT nucleic acid encoding cytochrome p450 genes.
 XX
 PS Claim 18; Fig 11C; 110pp; English.
 XX
 CC Replication-deficient adenovirus type 5 expression vectors comprise an
 CC adenovirus genome with a deletion in the E1 and E2 region of the genome
 CC and an insertion within the region under the control of a Rous Sarcoma
 CC Virus promoter can be used to induce chemotoxicity in tumour cells. Three
 CC such expression vectors are described, the inserted nucleic acids in each
 CC being the following: Vector (I) has an insertion of a nucleic acid
 CC encoding a cytochrome 2C9 p450 and is designated AdRSRV2C9 (ATCC VR-
 CC 2628). Vector (II) has an insertion of a nucleic acid encoding a
 CC cytochrome 3A4 p450 and is designated AdRSRV3A4 (ATCC VR-2629). Vector
 CC (III) has an insertion of a nucleic acid encoding a nicotinamide adenine
 CC dinucleotide phosphatase (NADPH) cytochrome p450 reductase and is
 CC designated AdRSVRred (ATCC VR-2630). The chemotoxicity of a tumor cell
 CC can be induced by administering (I) and (III) or (II) and (III) into the
 CC tumor cell (e.g. a prostate tumor cell) to selectively sensitize the cell
 CC to a prodrug and then administering the prodrug which kills the cell,
 CC inducing its chemotoxicity. The method uses gene-directed enzyme prodrug
 CC therapy to transfer a drug susceptibility gene to the tumor which
 CC activates a nontoxic prodrug intratumorally so the released drug can kill
 CC the tumor cells containing the drug susceptibility gene. This sequence is
 CC designated region A of the vector AdRSVRred and is the sequence of the
 CC cytochrome NADPH p450 reductase
 XX
 SQ Sequence 3311 BP; 755 A; 881 C; 981 G; 694 T; 0 U; 0 Other;
 Query Match 99.4%; Score 262.4; DB 3; Length 3311;
 Best Local Similarity 99.6%; Pred. No. 1.7e-81;
 Matches 263; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAATCGTAAACGATGATAGCAACA 60
 DB 541 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAATCGTAAACGATGATAGCAACA 600
 QY 61 TGCCTTACAGAGAGAAAAGACCGTGCATGCCGATGGTGGAGTGGTGGTACGA 120
 DB 601 TGCCTTACAGAGAGAAAAGACCGTGCATGCCGATGGTGGAGTGGTGGTACGA 660

QY 121 TCGTGCCTTATTAGGAGGCAACAGACGGGCTTGACATGGATTGGACGACCACTAAATT 180
 DB 661 TCGTGCCTTATTAGGAGGCAACAGACGGGCTTGACATGGATTGGACGACCACTAAATT 720
 QY 181 CGCATTTGCAGAGATATTGTATTATTAAGTCCCTAGCTGATACATAAAGCGCATTTGACC 240
 DB 721 CGCATTTGCAGAGATATTGTATTATTAAGTCCCTAGCTGATACATAAAGCGCATTTGACC 780
 QY 241 ATTCAACCATTTGGTGTGCACCTC 264
 DB 781 ATTCAACCATTTGGTGTGCACCTC 804
 RESULT 7
 AAC89169
 ID AAC89169 standard; DNA; 3885 BP.
 XX
 AC AAC89169;
 XX
 DT 08-MAR-2001 (first entry)
 XX
 DE AdRSVpHYDE region A coding sequence.
 XX
 KW p-HYDE; cytostatic; gene therapy; apoptosis; leukaemia; prostate;
 KW tumour suppressor gene; DNA repair; cancer; melanoma; lymphoma;
 KW colorectal; pancreatic; breast; brain; gastric carcinoma; ds.
 XX
 OS Unidentified.
 XX
 FN WO200071564-A2.
 XX
 PD 30-NOV-2000.
 XX
 PF 01-MAY-2000; 2000WO-US011456.
 XX
 PR 29-APR-1999; 99US-00302457.
 PR 29-APR-1999; 99US-0131607P.
 PR 08-FEB-2000; 2000US-00499817.
 XX
 PA (UYTE-) UNIV TENNESSEE RES CORP.
 XX
 PI Steiner MS, Wang C, Rinaldy A, Menon R;
 XX
 XX WPI; 2001-032016/04.
 XX
 PT New isolated nucleic acid encoding a mammalian p-Hyde protein of the p-
 PT Hyde family is useful for treating cancer, e.g. prostate cancer.
 XX
 PS Disclosure; Fig 10; 171pp; English.
 XX
 CC The present sequence is region A of AdRSVpHYDE. AdRSVpHYDE is an
 CC adenovirus vector expressing p-HYDE. p-HYDE induces susceptibility of a
 CC cancer cell to cell death. The p-HYDE gene is associated with the
 CC regression of tumour growth in vivo, the induction to susceptibility to
 CC apoptosis caused by UV or chemotherapy induced DNA damage and prevention
 CC of DNA repair with the upregulation of apoptosis as the result of UV
 CC damage and the failure to repair DNA. The present sequence may be used to
 CC treat cancer, preferably melanoma, lymphoma, leukaemia, prostate,
 CC colorectal, pancreatic, breast, brain or gastric carcinoma
 XX
 SQ Sequence 3885 BP; 847 A; 1039 C; 1063 G; 936 T; 0 U; 0 Other;
 Query Match 99.4%; Score 262.4; DB 4; Length 3885;
 Best Local Similarity 99.6%; Pred. No. 1.8e-81;
 Matches 263; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAATCGTAAACGATGATAGCAACA 60
 DB 541 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAATCGTAAACGATGATAGCAACA 600
 QY 61 TGCCTTACAGAGAGAAAAGACCGTGCATGCCGATGGTGGAGTGGTGGTACGA 120

PD 31-JUL-2003.
 XX
 XX
 XX 24-JAN-2003; 2003WO-US002295.
 XX
 XX
 XX 24-JAN-2002; 2002US-0350388P.
 PR 26-JUN-2002; 2002US-0391967P.
 XX
 XX
 XX (SRI) SCRIPPS RES INST.
 PA (NOVS) NOVARTIS AG.
 XX
 XX Kaleko M, Nemerow GR, Smith T, Stevenson SC;
 PI WPI; 2003-627459/59.
 XX
 DR
 XX
 XX New modified adenovirus capsid protein, useful as a base vector for
 PT producing redirected adenoviruses.
 XX
 XX Example 1; Page 156-165; 132pp; English.
 XX
 XX This invention relates to novel fibre shaft modifications in adenoviral
 CC vectors. Adenoviral vector-mediated gene therapy aims to transduce a
 CC specific targeted tissue or organ, accordingly gene therapy requires the
 CC ablation of normal virus tropism. If successful, systemic vector delivery
 CC into a peripheral vein would be targeted to the desired location in the
 CC body without any associated side effects, which would permit lower, less
 CC toxic vector doses that are also potentially less immunogenic. The
 CC present invention describes capsid modifications, specifically fibre
 CC shaft mutations that when expressed on adenoviral particles ablates
 CC binding to heparin sulphate proteoglycans (HSP) thus providing de-targeted
 CC vectors. Furthermore, when this is combined with modifications of other
 CC adenoviral proteins involved in the cell entry pathway such as the fibre
 CC knob, penton or CAR (coxsackie adenovirus receptor) proteins, the vectors
 CC become fully de-targeted. As such, these fully ablated particles can be
 CC used in vivo as base vectors for producing redirected adenoviruses with
 CC the desired cell specificity. This polynucleotide sequence is the
 CC recombinant E1, E2a and E3-deleted adenoviral vector (Av3nBg) that
 CC encodes a nuclear localising beta-galactosidase, used in the
 CC exemplification of the invention
 XX
 XX Sequence 33622 BP; 7857 A; 9539 C; 9277 G; 6949 T; 0 U; 0 Other;
 SQ
 Query Match 99.4%; Score 262.4; DB 8; Length 33622;
 Best Local Similarity 99.6%; Pred. No. 4.6e-81;
 Matches 263; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 AATGCTCTTATGCAATCTTTGTAGTCTTGTGCAACATGTAACGATGAGTTAGCAACA 60
 DB 533 AATGCTCTTATGCAATCTTTGTAGTCTTGTGCAACATGTAACGATGAGTTAGCAACA 592
 QY 61 TGCCTTACAAGGAGAGAAAAGCACCCTGTCATGCCGATTTGGTGAAGTAAGTGTTAGCA 120
 DB 593 TGCCTTACAAGGAGAGAAAAGCACCCTGTCATGCCGATTTGGTGAAGTAAGTGTTAGCA 652
 QY 121 TCGTGCCTTATAGGAGGCAACAGACGGGCTGACATGATTTGGACGACCACTAAATT 180
 DB 653 TCGTGCCTTATAGGAGGCAACAGACGGGCTGACATGATTTGGACGACCACTAAATT 712
 QY 181 CGCATTTGCAGAGATTTGTTATTTAAGTCGTAGCTGCATACATAAAGCCATTTCAC 240
 DB 713 CGCATTTGCAGAGATTTGTTATTTAAGTCGTAGCTGCATACATAAAGCCATTTCAC 772
 QY 241 ATTCCACACATTTGGTGTGCACCTC 264
 DB 773 ATTCCACACATTTGGTGTGCACCTC 796
 RESULT 12
 AAZ94163
 ID AAZ94163 standard; DNA; 34302 BP.
 XX
 AC AAZ94163;
 XX
 XX 15-SEP-2003 (revised)
 DT

DT 19-JUN-2000 (first entry)
 XX
 DE Adenovirus vector Ad5RSVP16 used for prostate cancer gene therapy.
 XX
 KW Ad5RSVP16; adenovirus; vector; RSV; promoter; human; p16;
 KW tumour suppressor gene; prostate cancer; gene therapy; ds.
 XX
 OS Human adenovirus type 5.
 OS Rous sarcoma virus.
 OS Homo sapiens.
 OS Chimeric.
 XX
 FH Key Location/Qualifiers
 FT promoter 410..805
 FT /*tag= a
 FT misc_feature 1055..2014
 FT /*tag= b
 FT /*note= "p16 sense cDNA"
 XX
 PN WO200014211-A1.
 XX
 XX 16-MAR-2000.
 PD
 XX 02-SEP-1999; 99WO-US018833.
 PF
 XX 02-SEP-1998; 98US-00145729.
 PR
 XX (GENO-) GENOTHERAPEUTICS INC.
 PA
 XX Steiner MS, Lu Y;
 FI WPI; 2000-256967/22.
 XX
 DR
 XX Replication-deficient adenovirus type 5 expression vector, useful in gene
 PT therapy of prostate cancer, comprises a nucleic acid encoding p16 under
 PT the control of a Rous Sarcoma virus promoter.
 XX
 XX Disclosure; Fig 13; 118pp; English.
 PS
 XX The present sequence is that of replication-deficient adenovirus vector
 CC Ad5RSVP16, deposited as ATCC VR 2626. The vector is a type 5 adenovirus
 CC in which the E1 and E3 regions of the genome have been removed, and a p16
 CC tumour suppressor gene (see AAZ94162) has been inserted under control of
 CC a Rous sarcoma virus (RSV) promoter (see AAZ94161). Ad5RSVP16 can be used
 CC in the gene therapy of prostate cancer to replace a missing, mutated or
 CC inactivated p16 gene. In vitro, PC3 cells which were stably transfected
 CC with the vector showed a 70% reduction in cell number. The vector also
 CC inhibited growth of prostate cancer cells PPC-1, DU145 and PC3 in
 CC culture. PPC-1 tumours grown in nude mice treated by a single injection
 CC of Ad5RSVP16 had a marked reduction in tumour size when compared to
 CC untreated control. The mice also survived for longer. Transduction rates
 CC were over 90%, with transgene expression detectable in tumours for up to
 CC 2 wk. (Updated on 15-SEP-2003 to standardise OS field)
 XX
 XX Sequence 34302 BP; 7995 A; 9797 C; 9303 G; 7207 T; 0 U; 0 Other;
 SQ
 Query Match 99.4%; Score 262.4; DB 3; Length 34302;
 Best Local Similarity 99.6%; Pred. No. 4.6e-81;
 Matches 263; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 AATGCTCTTATGCAATCTTTGTAGTCTTGTGCAACATGTAACGATGAGTTAGCAACA 60
 DB 541 AATGCTCTTATGCAATCTTTGTAGTCTTGTGCAACATGTAACGATGAGTTAGCAACA 600
 QY 61 TGCCTTACAAGGAGAGAAAAGCACCCTGTCATGCCGATTTGGTGAAGTAAGTGTTAGCA 120
 DB 601 TGCCTTACAAGGAGAGAAAAGCACCCTGTCATGCCGATTTGGTGAAGTAAGTGTTAGCA 660
 QY 121 TCGTGCCTTATAGGAGGCAACAGACGGGCTGACATGATTTGGACGACCACTAAATT 180
 DB 661 TCGTGCCTTATAGGAGGCAACAGACGGGCTGACATGATTTGGACGACCACTAAATT 720
 QY 181 CGCATTTGCAGAGATTTGTTATTTAAGTCGTAGCTGCATACATAAAGCCATTTCAC 240

```
Db 721 CCGCATGCGAGGATATGTTATTAAGTGGCTAGTCGATACATTAACGCCATTGACC 780
QY 241 ATTACACACATTTGGTGGACCTC 264
Db 781 ATTACACACATTTGGTGGACCTC 804

RESULT 13
AAL56866
ID AAL56866 standard; DNA; 35211 BP.
AC AAL56866;
XX
XX 06-NOV-2003 (first entry)
XX
XX DNA sequence of the recombinant adenoviral AvinBg vector.
XX
XX Fibre shaft modification; adenoviral vector; cell entry pathway; penton;
XX CAR; coxsackie adenovirus receptor; heparin sulphate proteoglycan; HSP;
XX gene therapy; fibre knob; AvinBg; ds.
XX
XX Human adenovirus type 5.
XX Unidentified.
XX
XX WO2003062400-A2.
XX
XX 31-JUL-2003.
XX
XX 24-JAN-2003; 2003WO-US002295.
XX
XX 24-JAN-2002; 2002US-0350388P.
XX
XX 26-JUN-2002; 2002US-0391967P.
XX
XX (SRI ) SCRIPPS RBS INST.
XX
XX (NOVS ) NOVARTIS AG.
XX
XX Kaleko M, Nemerow GR, Smith T, Stevenson SC;
XX
XX WPI; 2003-627459/59.
XX
XX New modified adenovirus capsid protein, useful as a base vector for
XX producing redirected adenoviruses.
XX
XX Example 1; Page 146-156; 132pp; English.
XX
XX This invention relates to novel fibre shaft modifications in adenoviral
XX vectors. Adenoviral vector-mediated gene therapy aims to transduce a
XX specific targeted tissue or organ, accordingly gene therapy requires the
XX ablation of normal virus tropism. If successful, systemic vector delivery
XX into a peripheral vein would be targeted to the desired location in the
XX body without any associated side effects, which would permit lower, less
XX toxic vector doses that are also potentially less immunogenic. The
XX present invention describes capsid modifications, specifically fibre
XX shaft mutations that when expressed on adenoviral particles ablates
XX binding to heparin sulphate proteoglycans (HSP) thus providing detargeted
XX vectors. Furthermore, when this is combined with modifications of other
XX adenoviral proteins involved in the cell entry pathway such as the fibre
XX knob, penton or CAR (coxsackie adenovirus receptor) proteins, the vectors
XX become fully detargeted. As such, these fully ablated particles can be
XX used in vivo as base vectors for producing redirected adenoviruses with
XX the desired cell specificity. This polynucleotide sequence is the
XX recombinant E1 and E3-deleted adenoviral vector (AvinBg) that encodes a
XX nuclear localising beta-galactosidase, used in the exemplification of the
XX invention
XX
XX Sequence 35211 BP; 8136 A; 10028 C; 9704 G; 7343 T; 0 U; 0 Other;
XX
XX Query Match 99.4%; Score 262.4; DB 8; Length 35211;
XX Best Local Similarity 99.6%; Pred. No. 4.7e-81;
XX Matches 263; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 AATGTAGTCTTATGCAATACTCTTGTGAGTCTTGGCAATGGTAAAGTATGACCA 60
```

```
FT mat_peptide 2501..4216
FT /tag= l
FT /label= Polymerase_pol_pt
FT 4217..5186
FT /tag= m
FT /label= Polymerase_pol_in
FT 5075..5078
FT /tag= n
FT /note= "env splice acceptor site"
FT 5245..6882
FT /tag= o
FT /product= "Envelope protein (env)"
FT 5245..6264
FT /tag= p
FT /label= env_gp85_peptide
FT 6265..6879
FT /tag= q
FT /label= env_gp37_peptide
FT 6983..6986
FT /tag= r
FT /note= "Clal splice acceptor site"
FT 7154..7165
FT /tag= s
FT /label= PPT
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FT 7166..7394
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FT /note= "3'end unique sequence"
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FT /tag= v
FT /rpt_type= DIRECT
FT 7416..7494
FT /tag= w
FT /note= "5'end unique sequence"
FT 7649..11258
FT /tag= x
FT /label= pBR322_vector
FT 11394..11623
FT /tag= y
FT /note= "3'end unique sequence"
XX
FN WO9961590-A1.
XX
XX
PD 02-DEC-1999.
XX
XX
XX 28-MAY-1999; 99WO-US011780.
XX
XX 29-MAY-1998; 98US-0087220P.
XX
XX (SCRI ) SCRIPPS RES INST.
XX
XX Cheresch DA, Eliceiri B, Schwartzberg PL;
XX
XX WPI; 2000-116335/10.
XX
XX Using tyrosine kinase Src for modulating angiogenesis in tissues useful
XX in, e.g. treatment of chronic articular rheumatism.
XX
XX Claim 15; Page 59-66; 80pp; English.
XX
CC The present DNA sequence is the viral expression vector, RCASBP(A)
CC construct. This vector is based on a replication competent avian sarcoma
CC virus with an enhanced Bryan polymerase (BP) and is specific for the 'A'
CC type envelope glycoprotein expressed on normal avian cells. The vector
CC expresses Src protein or modified Src, that can be used to modulate
CC angiogenesis. When the Src protein is inactivated, angiogenesis is
CC inhibited, while when it is activated, angiogenesis is potentiated. This
CC modified or mutant Src can be used to treat inflammatory diseases like,
CC arthritis, rheumatoid arthritis, diabetic retinopathy, restenosis,
CC osteoporosis and cancer associated disorders
XX
XX Sequence 11627 BP; 2796 A; 2808 C; 3324 G; 2699 T; 0 U; 0 Other;
```

```
Query Match 99.0%; Score 261.4; DB 3; Length 11627;
Best Local Similarity 99.6%; Pred. No. 6.5e-81;
Matches 262; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AATGTAGTCTTATGCAATCTCTTGTAGTCTTTGCAACATGTAACGATGAGTTAGCAACA 60
Db 7166 AATGTAGTCTTATGCAATCTCTTGTAGTCTTTGCAACATGTAACGATGAGTTAGCAACA 7225

Qy 61 TGCCTTACAGGAGAGAAAAGACCCGTCATGCGATTGTTGGAGTAAGTGGTACGA 120
Db 7226 TGCCTTACAGGAGAGAAAAGACCCGTCATGCGATTGTTGGAGTAAGTGGTACGA 7285

Qy 121 TCGTGCCTTATTAGGAAGCAACAGACGGGCTCGACATGATGGACGAACCACTAAATT 180
Db 7286 TCGTGCCTTATTAGGAAGCAACAGACGGGCTCGACATGATGGACGAACCACTGAATT 7345

Qy 181 CCGCATTGCAGAGATATTGATTAAAGTGCCTAGCTCGATACATTAACACGCAATTGACC 240
Db 7346 CCGCATTGCAGAGATATTGATTAAAGTGCCTAGCTCGATACATTAACACGCAATTGACC 7405

Qy 241 ATTCACACATTTGTTGCACCT 263
Db 7406 ATTCACACATTTGTTGCACCT 7428

RESULT 15
ABZ23249
ID ABZ23249 standard; DNA; 2245 BP.
XX
XX AC ABZ23249;
XX
DT 24-MAR-2003 (first entry)
XX
DE Lac repressor operated p21-expression cassette and RSV-LTR promoter.
XX
XX Lac repressor; p21; RSV; LTR promoter; cell cycle inhibitor protein;
XX protein production; anchorage-independent producer cell line; ss.
XX OS Synthetic.
XX
XX Key Location/Qualifiers
XX promoter 1..563
XX /tag= a
XX /note= "RSV-LTR promoter"
XX intron 564..1051
XX /tag= b
XX /note= "SV40 small t antigen intron"
XX misc_feature 1052..1907
XX /tag= c
XX /note= "p21 coding sequence"
XX polyA_signal 1908..2245
XX /tag= d
XX /note= "thymidine kinase polyA site"
XX
XX WO200299100-A2.
XX
XX 12-DEC-2002.
XX
XX 03-JUN-2002; 2002WO-EP006054.
XX
XX 01-JUN-2001; 2001GB-00013318.
XX (LONZ ) LONZA BIOLOGICS PLC.
XX
XX Al-Rubeai M, Shuttleworth J;
XX WPI; 2003-148669/14.
XX
XX Producing recombinant protein, particularly for maximizing or enhancing
XX e.g. therapeutic protein production, by co-expressing protein with
XX recombinant cell cycle inhibitor protein (p21) in producer cell line.
XX
```


FT oligonucleotide which modifies this regulatory sequence
 FT to effect a higher level of expression of downstream
 FT sequences. The oligonucleotide removes a polyadenylation
 FT signal sequence originally found in the RSV DNA
 FT sequence."
 FT 531..534
 FT /tag= b
 FT /label= consensus_Kozak_signal_sequence
 FT CDS 535..1620
 FT /tag= c
 FT /note= "HLA-B7 heavy chain open reading frame"
 FT 535..606
 FT /tag= d
 FT /note= "encodes putative signal peptide of the HLA-B7
 FT heavy chain"
 FT mat_peptide 607..1620
 FT /tag= e
 FT /note= "encodes putative HLA-B7 heavy chain mature
 FT peptide"
 FT 1621..1853
 FT /tag= f
 FT /note= "3' untranslated sequence of HLA-B7 heavy chain
 FT mRNA"
 FT 1854..1888
 FT /tag= g
 FT /note= "multiple cloning site, forms a junction between
 FT the HLA-B7 sequence and the EMCV-CITE sequence, and is
 FT used to facilitate subcloning"
 FT RBS 1889..2479
 FT /tag= h
 FT /note= "murine encephalomyocarditis CAP-independent
 FT translational enhancer (EMCV-CITE); taken from
 FT nucleotides 255-843 of cloned EMCV genomic DNA. It is a
 FT non-coding regulatory sequence functioning as an internal
 FT entry point for the eukaryotic ribosomal subunits when
 FT located within a mRNA mol. It enables the translational
 FT start codon of the beta-2 microglobulin, downstream of
 FT the HLA-B7 stop codon on this bicistronic mRNA to be
 FT recognised by the ribosome"
 FT 2480..2839
 FT /tag= i
 FT /note= "encodes beta-2 microglobulin; this cDNA is deriv.
 FT from chimpanzee (differs to the human cDNA by only 4
 FT bases)"
 FT 2840..2846
 FT /tag= j
 FT /note= "3' untranslated region of the beta-2
 FT microglobulin mRNA"
 FT 2847..2870
 FT /tag= k
 FT /note= "synthetic linker"
 FT 2879..2984
 FT /tag= l
 FT 3112..3151
 FT /tag= m
 FT /note= "synthetic linker to facilitate cloning"
 FT complement(3151..3967)
 FT /tag= n
 FT /note= "kanamycin resistance gene open reading frame; the
 FT gene is taken from the transposable element Tn903"
 FT 4014..4965
 FT /tag= o
 FT /note= "pBR322 backbone contg. bacterial origin of
 FT replication, it represents nucleotides 2244-3193"
 FT XX WO9429469-A2.
 FT 22-DEC-1994.
 FT 27-MAY-1994;
 FT 94WO-US006069.
 FT 07-JUN-1993;
 FT 93US-00074344.
 FT XX

PA (VICA-) VICAL INC.
 PA (UNMI) UNIV MICHIGAN.
 XX Nabel GJ, Nabel EG, Lew D, Marquet M;
 XX WPI; 1995-036494/05.
 XX
 XX New vectors for gene therapy, partic for tumours - comprising genetic
 XX material encoding one or more cistron(s) which express immunogenic or
 XX therapeutic peptide(s).
 XX
 XX Claim 8; Page 41-42; 50pp; English.
 XX
 XX The pHLA-B7/beta-2 microglobulin plasmid expression vector, in addition
 XX to the kanamycin resistance gene, contains the plasmid DNA encoding the
 XX heavy (human HLA-B7) and light (beta-2 microglobulin) proteins of a class
 XX I major histocompatibility complex (MHC) antigen. The plasmid is
 XX designed to express these two proteins via a bicistronic mRNA in
 XX eukaryotic cells. Initiation of transcription of the mRNA is dependent on
 XX a Rous Sarcoma Virus (RSV) promoter sequence deriv. from the 3' long
 XX terminal repeat. Termination of transcription is dependent upon the
 XX polyadenylation signal sequence deriv. from the bovine growth hormone
 XX gene. Eukaryotic cell translation of the heavy chain is regulated by the
 XX 5' cap-dependent protein start site. Translation of the light chain is
 XX controlled by the CITE. Finally the replication of the plasmid in
 XX bacterial cells is controlled by the presence of a bacterial origin of
 XX replication. The vector is used partic. for the treatment of neoplastic
 XX disease, eg. melanoma, and provides enhanced gene delivery and expression
 XX in vivo. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 XX Sequence 4965 BP; 1171 A; 1293 C; 1338 G; 1163 T; 0 U; 0 Other;
 XX
 XX Query Match 97.6%; Score 257.6; DB 2; Length 4965;
 XX Best Local Similarity 98.5%; Pred. No. 9.8e-80;
 XX Matches 260; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 AATGATGCTTATGCAATPACTCTTGTAGTCTTGGCAATGTAACGATGAGTTAGCAACA 60
 DB 260 AATGATGCTTATGCAATPACTCTTGTAGTCTTGGCAATGTAACGATGAGTTAGCAACA 319
 QY 61 TGCCTTACAAGGAGAGAAAGACCGTGCATGCGGATTTGGTGAAGTAAGTGGTACGA 120
 DB 320 TGCCTTACAAGGAGAGAAAGACCGTGCATGCGGATTTGGTGAAGTAAGTGGTACGA 379
 QY 121 TCGTGCCCTTATAGGAGGCAACAGACGGGCTGACATGGAATTGGACGACCACTAAATT 180
 DB 380 TCGTGCCCTTATAGGAGGCAACAGACGGGCTGACATGGAATTGGACGACCACTAAATT 439
 QY 181 CGCATTTGCAGAGATATTGTATTAAAGTCCCTAGCTGCATCAATAAAGCCATTTCACC 240
 DB 440 CGCATTTGCAGAGATATTGTATTAAAGTCCCTAGCTGCATCAATAAAGCCATTTCACC 499
 QY 241 ATTCACCAATTTGGTGCACCTC 264
 DB 500 ATTCACCAATTTGGTGCACCTC 523
 XX
 XX RESULT 18
 XX AAS15665
 XX ID AAS15665 standard; DNA; 262 BP.
 XX AC AAS15665;
 XX XX
 XX 29-JAN-2002 (first entry)
 XX
 XX Human respiratory syncytial virus promoter.
 XX
 XX Ecdysone receptor; EGR; ligand binding domain; ds; retinoid X receptor;
 XX RXRalpha; DNA-binding domain; RSV promoter; transactivation domain;
 XX nuclear receptor; ultraspindle; gene therapy; protein production;
 XX antibody production; high throughput screening; HIS; transgenic plant;
 XX transgenic animal.
 XX

OS	Human respiratory syncytial virus.
XX	
FN	WO200170816-A2.
XX	
PD	27-SEP-2001.
XX	
PF	21-MAR-2001; 2001WO-US0009050.
XX	
PR	22-MAR-2000; 2000US-0191355P.
PR	20-FEB-2001; 2001US-0269799P.
XX	
PA	(ROHM) ROHM & HAAS CO.
XX	
PI	Palli SR, Kapitskaya MZ, Cress DE;
DR	WPI; 2001-656841/75.
XX	
PT	Ecdysone and retinoid X receptor based inducible gene expression systems
PT	for use in e.g. gene therapy, large scale production of proteins and cell
PT	-based high-throughput screening assays.
XX	
PS	Example 1; Page 141; 144pp; English.
XX	
CC	The invention relates to Ecdysone and retinoid X receptor based inducible
CC	gene expression systems useful for modulating gene expression in host
CC	cells. The gene expression system encodes a polypeptide with a DNA-
CC	binding domain recognizes a response element associated with a gene whose
CC	expression is to be modulated and/or a ligand binding domain (LBD)
CC	comprising a LBD from a nuclear receptor and a second gene expression
CC	cassette capable of being repressed in a host cell comprising a
CC	polynucleotide sequence encoding a second polypeptide comprising a trans-
CC	activation domain and/or a LBD comprising a LBD from a nuclear receptor
CC	other than ultraspiracle (USP) (the trans-activation domain is from a
CC	nuclear receptor other than an ecdysone receptor, a retinoid X receptor
CC	or a USP receptor and the LBDs from the first and second polypeptides are
CC	different and dimerize). The ecdysone and retinoid X receptor based
CC	inducible gene expression systems useful for modulating gene expression
CC	in host cells, for use in gene therapy, large scale production of
CC	proteins and antibodies, cell-based high-throughput screening assays
CC	(HTS), functional genomic and regulation of traits in transgenic plants
CC	and animals. The present sequence represents promoter from human
CC	respiratory syncytial virus (RSV) which is used in an inducible gene
CC	expression system of the invention
XX	
SQ	Sequence 262 BP; 79 A; 53 C; 64 G; 66 T; 0 U; 0 Other;

RESULT 19
ABZ23250

ID	AB223250	standard; DNR; 562 BP.
XX	AC	
XX	AB223250;	
XX	AC	
XX	DT	
XX	24-MAR-2003	(first entry)
XX	DE	
XX	DE	Nucleotide sequence of the Rous sarcoma virus (RSV)-LTR promoter.
XX	DE	
XX	DE	p21; RSV; LTR promoter; cell cycle inhibitor protein; protein production;
KW	KW	anchorage-independent producer cell line; ss.
KW	KW	
XX	OS	
XX	OS	Rous sarcoma virus.
XX	PN	
XX	WO200299100-A2.	
XX	PD	
XX	12-DEC-2002.	
XX	XX	
XX	03-JUN-2002;	2002WO-EP006054.
XX	XX	
XX	01-JUN-2001;	2001GB-00013319.
PR	XX	
XX	PA	(LONZ) LONZA BIOLOGICS PLC.
XX	PA	
XX	PI	
XX	PI	Al-Rubeai M, Shuttleworth J;
XX	DR	
XX	DR	WPI; 2003-148669/14.
XX	XX	
XX	XX	Producing recombinant protein, particularly for maximizing or enhancing
PT	PT	e.g. therapeutic protein production, by co-expressing protein with
PT	PT	recombinant cell cycle inhibitor protein (p21) in producer cell line.
XX	XX	
XX	PS	Disclosure; Page 32-33; 33pp; English.
XX	PS	
XX	CC	The present sequence represents the Rous sarcoma virus (RSV)-LTR
XX	CC	promoter. The present sequence is used to produce vectors for use in the
XX	CC	method of the invention. The specification describes a method for
XX	CC	producing a protein, preferably a recombinant protein, in a mammalian
XX	CC	anchorage-independent producer cell line. The method comprises co-
XX	CC	expressing with the protein in the producer cell line a recombinant cell
XX	CC	cycle inhibitor protein (preferably p21). The method is useful for
XX	CC	producing a recombinant protein in a producer cell line. This is
XX	CC	particularly useful for maximizing or enhancing the production of e.g.
XX	CC	therapeutic proteins at an industrial scale
XX	XX	
SQ	Sequence	562 BP; 143 A; 109 C; 163 G; 147 T; 0 U; 0 Other;
Query Match 97.1%; Score 256.4; DB 7; Length 562;		
Best local Similarity 99.8%; Pred. No. 1e-79;		
Matches 257; Conservative 0; Mismatches 1; Indels 0; Gaps 0		
Qy	1	ANTGTAGCTTATGCAATACTCTTGATGCTTGCAACATGTAACGATGAGTTAGCAACA 60
Db	305	AATGTAGCTTATGCAATACTCTTGATGCTTGCAACATGTAACGATGAGTTAGCAACA 364
Qy	61	TGCTTTACAAGGAGAGAAAAGCACCGTGCATGCCGATTCGTGGAAAGTGAAGTGGTACGA 120
Db	365	TGCCTTTACAAGGAGAGAAAAGCACCGTGCATGCCGATTCGTGGAAAGTGAAGTGGTACGA 424
Qy	121	TCGTGCCTTATTAGGAGGCACACAGACGGCTCTGCATGATTCGTCGACGACCACTTAATT 180
Db	425	TCGTGCCTTATTAGGAGGCACACAGACGGGTCTGCATGATTCGTCGACGACCACTTAATT 484
Qy	181	CCGCATTGCAGAGATTTGCTATTTTAAGTGCCTAGCTGCATACATATAAGCCATTTGACC 240
Db	485	CCGCATTGCAGAGATTTGCTATTTTAAGTGCCTAGCTGCATACATATAAGCCATTTGACC 544
Qy	241	ATTCACCACTTTGGTGTG 258
Db	545	ATTCACCACTTTGGTGTG 562

RESULT 20
ADD35599

proteins using host cells transformed with a vector of the invention. The vectors are useful in various biotechnological applications in which the simultaneous expression of two or more genes is necessary, such as gene transfer protocols, DNA immunisation, or for the expression of different molecules in the same cell. They may also be used in gene therapy. The present sequence represents a specifically claimed vector designated PL250, which comprises a cytomegalovirus (CMV) promoter/enhancer, CMV intron A, the encephalomyocarditis virus (EMCV) IRES, an SV40 polyadenylation site, a transcription pause site, a Rous sarcoma virus (RSV) promoter, rabbit beta-globin intron, the hepatitis C virus (HCV) IRES, and a rabbit beta-globin gene mRSG terminator as well as a kanamycin resistance gene.

RESULT 22	
AAZ94161	
ID	AAZ94161 standard; DNA; 397 BP.
XX	
AC	AAZ94161;
XX	
DT	19-JUN-2000 (first entry)
XX	
DE	395 Nucleic acid Rous sarcoma virus promoter.
XX	
KW	Adenovirus; vector; RSV; promoter; prostate cancer; gene therapy;
KW	tumour suppressor gene; p16; ss.
OS	Rous sarcoma virus.
XX	
PN	WO200014211-A1.
XX	
PD	16-MAR-2000.
XX	
PF	02-SEP-1999; 99WO-US018833.
XX	
PR	02-SEP-1998; 98US-00145729.
XX	
PA	(GENO-) GENOTHERAPEUTICS INC.
XX	
PI	Steiner MS, Lu Y;
XX	
DR	WPI; 2000-256967/22.
XX	
PT	Replication-deficient adenovirus type 5 expression vector, useful in gene
PT	therapy of prostate cancer, comprises a nucleic acid encoding p16 under
PT	the control of a Rous Sarcoma virus promoter.
XX	

PS Claim 1; Page 12; 118pp; English.

CC The present sequence is that of 395 nucleic acid Rous sarcoma virus (RSV) promoter. A novel replication-deficient adenovirus type 5 expression vector of the invention, termed AdRSVP16 (see AAZ94163), has a deletion in an E1 and E3 region of the genome and contains a p16 tumour suppressor gene under the control of the RSV promoter. The adenoviral vector is used in the gene therapy of prostate cancer, in which p16 is frequently abnormal. Gene therapy is used to replace a missing, mutated or inactivated p16 tumour suppressor gene, thereby inhibiting the growth and/or progression of the tumour

CC Sequence 397 BP; 108 A; 79 C; 110 G; 100 T; 0 U; 0 Other;

Query Match 94.0%; Score 248.2; DB 3; Length 397;

Best Local Similarity 98.5%; Pred. No. 6.6e-77;

Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATACTCTTTAGTCTTTGCCAATGCTAAACGATGAGTTCAGCA 60

DB 132 AATGTAGTCTTATGCAATACTCTTTAGTCTTTGCCAATGCTAAACGATGAGTTCAGCA 191

QY 61 TGCCTTACAGGAGAGAAAAGACCGTGCATGCCGATTCGGTGGAGTAGTGTTGATACGA 120

DB 192 TGCCTTACAGGAGAGAAAAGACCGTGCATGCCGATTCGGTGGAGTAGTGTTGATACGA 251

QY 121 TCGTGCCCTTATTAGGAAGGCAACAGACGGGCTCGACATGGATTGACGACCACTAAATT 180

DB 252 TCGTGCCCTTATTAGGAAGGCAACAGACGGGCTCGACATGGATTGACGACCACTAAATT 311

QY 181 CGCATTCGACAGAT-ATTGTATTTAAGTGCTAGCTCGATACATTAACGCCATTTCAC 239

DB 312 CGCATTCGACAGATAAATTGTATTTAAGTGCTAGCTCGATACATTAACGCCATTTCAC 371

QY 240 CATTCACCACCAATTCGGTGCACCTC 264

DB 372 CATTCACCACCAATTCGGTGCACCTC 396

RESULT 23

AAAL14719

ID AAAL14719 standard; DNA; 397 BP.

XX

AC AAAL14719;

XX

DT 08-AUG-2000 (first entry)

XX

DE Nucleotide sequence of the Rous Sarcoma virus promoter.

XX

KW Cellular cytotoxicity; tumor cell; expression vector; beta-lactamase; replication-deficient adenovirus type 5; suicide gene therapy;

KW cancer cell; chemotherapy; beta-lactamase producing enzyme; prodrug TCM;

KW anticancer; tumor; leukemia; breast cancer; Wilms' tumor;

KW small cell lung carcinoma; Ewing's sarcoma; colon carcinoma;

KW papillary adenocarcinoma; promoter; ss.

XX

OS Rous sarcoma virus.

XX

XX WO200020608-A1.

PN

XX

PD 13-APR-2000.

XX

PF 01-OCT-1999; 99WO-US020908.

XX

XX

PR 02-OCT-1998; 98US-00165321.

XX

PA (GENO-) GENOTHERAPEUTICS INC.

XX

PI Steiner MS;

XX

XX WPI; 2000-303788/26.

DR

XX

PT Treating cancer using viral vectors which encode enzymes that convert

PT inactive drugs to active cytotoxic agents, expression of the enzyme is
PT tissue specific therefore targeting the effects of the drug to tumor
XX cells.
PS Disclosure; Page 13-14; 130pp; English.
XX
CC The specification describes a method for inducing cellular cytotoxicity
CC in tumor cells using replication-deficient adenovirus type 5 expression
CC vectors. The vectors comprise a sequence encoding a beta-lactamase under
CC the control of a Rous Sarcoma virus in combination with a prodrug
CC conjugated to a toxic agent. Tissue specific expression of the enzyme
CC converts the inactive drugs into active cancer killing agents. The
CC adenovirus genome has a deletion in an E1 and/or E3 region, and the beta-
CC lactamase sequence is inserted within this region. The vectors are used
CC for suicide gene therapy. This involves introducing genes into cancer
CC cells that encode enzymes capable of converting inactive drugs into
CC active cancer killing agents. If tissue specific promoters are coupled to
CC the prodrug enzymes, then production of the prodrug will be tissue
CC specific and targeted to the tumor. Therefore the cancer cells act as
CC their own factories to activate chemotherapy agents and commit suicide.
CC Beta-lactamase prodrug enzymes convert prodrug TCM into an active
CC anticancer agent which is cytotoxic to cancer cells pPC-1. The method is
CC used to treat patients with cancers of the brain, bladder or prostate. It
CC may also be used to treat a range of other tumors such as leukemia,
CC breast cancer, Wilms tumor, small cell lung carcinoma, Ewing's sarcoma,
CC colon carcinoma and papillary adenocarcinomas. The present sequence
CC represents the the Rous Sarcoma virus promoter, which was used to
CC construct vectors of the invention
XX
SQ Sequence 397 BP; 108 A; 79 C; 110 G; 100 T; 0 U; 0 Other;

Query Match 94.0%; Score 248.2; DB 3; Length 397;
Best Local Similarity 98.5%; Pred. No. 6.6e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 1 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGTGCAATGCTTAACGATGAGTTAGCAACA 60
DB 132 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGTGCAATGCTTAACGATGAGTTAGCAACA 191
QY 61 TGCCTTACAGGAGAGAAAAGCAGCGTGCATGCCGATTGGTGAAGTGGTACGA 120
DB 192 TGCCTTACAGGAGAGAAAAGCAGCGTGCATGCCGATTGGTGAAGTGGTACGA 251
QY 121 TCGTGCCCTTATTAGGAGGCAACAGACGCGTCTGCATGCGATTGGACGAACCACTAAATT 180
DB 252 TCGTGCCCTTATTAGGAGGCAACAGACGCGTCTGCATGCGATTGGACGAACCACTAAATT 311
QY 181 CCGCATTGCAAGAT-ATTGTATTATTAGTGCCTAGCTGCATACATATAAAGCCATTGAC 239
DB 312 CCGCATTGCAAGAT-ATTGTATTATTAGTGCCTAGCTGCATACATATAAAGCCATTGAC 371
QY 240 CATTACCAACATTGGTGTGCACCTC 264
DB 372 CATTACCAACATTGGTGTGCACCTC 396

RESULT 24
AAZ93077
ID AAZ93077 standard; DNA; 397 BP.
XX
AC AAZ93077;
XX
XX 04-JUL-2000 (first entry)
DT
DE Rous Sarcoma Virus promoter sequence.
XX
XX Adenovirus; vector; E1; E3; cytochrome; NADPH cytochrome reductase;
XX Rous Sarcoma virus; RSV; chemotoxicity; transfection; sensitisation;
XX prodrug; nicotinamide adenine dinucleotide phosphatase; ss.
XX
OS Rous sarcoma virus.
XX
PN WO200014256-A1.

XX
PD 16-MAR-2000.
XX
PF 03-SEP-1999; 99WO-US018834.
XX
PR 04-SEP-1998; 98US-00148275.
XX
PA (GENO-) GENOTHERAPEUTICS INC.
XX
PI Steiner MS, Lu Y;
XX
XX WPI; 2000-257001/22.
DR
XX Replication-deficient adenovirus type 5 expression vectors used for gene
PT therapy of cancer, especially prostate cancer, comprising an insertion of
PT nucleic acid encoding cytochrome p450 genes.
XX
XX Claim 8; Page 18; 110pp; English.
PS
XX Replication-deficient adenovirus type 5 expression vectors comprise an
CC adenovirus genome with a deletion in the E1 and E2 region of the genome
CC and an insertion within the region under the control of a Rous Sarcoma
CC Virus promoter can be used to induce chemotoxicity in tumour cells. Three
CC such expression vectors are described, the inserted nucleic acids in each
CC being the following: Vector (I) has an insertion of a nucleic acid
CC encoding a cytochrome 2C9 p450 and is designated AdRSV2C9 (ATCC VR-
CC 2628). Vector (II) has an insertion of a nucleic acid encoding a
CC cytochrome 3A4 p450 and is designated AdRSV3A4 (ATCC VR-2629). Vector
CC (III) has an insertion of a nucleic acid encoding a nicotinamide adenine
CC dinucleotide phosphatase (NADPH) cytochrome p450 reductase and is
CC designated AdRSVRED (ATCC VR-2630). The chemotoxicity of a tumor cell
CC can be induced by administering (I) and (III) or (II) and (III) into the
CC tumor cell (e.g. a prostate tumor cell) to selectively sensitize the cell
CC to a prodrug and then administering the prodrug which kills the cell,
CC inducing its chemotoxicity. The method uses gene-directed enzyme prodrug
CC therapy to transfer a drug susceptibility gene to the tumor which
CC activates a nontoxic prodrug intratumorally so the released drug can kill
CC the tumor cells containing the drug susceptibility gene
XX
SQ Sequence 397 BP; 108 A; 79 C; 110 G; 100 T; 0 U; 0 Other;

Query Match 94.0%; Score 248.2; DB 3; Length 397;
Best Local Similarity 98.5%; Pred. No. 6.6e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 1 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGTGCAATGCTTAACGATGAGTTAGCAACA 60
DB 132 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGTGCAATGCTTAACGATGAGTTAGCAACA 191
QY 61 TGCCTTACAGGAGAGAAAAGCAGCGTGCATGCCGATTGGTGAAGTGGTACGA 120
DB 192 TGCCTTACAGGAGAGAAAAGCAGCGTGCATGCCGATTGGTGAAGTGGTACGA 251
QY 121 TCGTGCCCTTATTAGGAGGCAACAGACGCGTCTGCATGCGATTGGACGAACCACTAAATT 180
DB 252 TCGTGCCCTTATTAGGAGGCAACAGACGCGTCTGCATGCGATTGGACGAACCACTAAATT 311
QY 181 CCGCATTGCAAGAT-ATTGTATTATTAGTGCCTAGCTGCATACATATAAAGCCATTGAC 239
DB 312 CCGCATTGCAAGAT-ATTGTATTATTAGTGCCTAGCTGCATACATATAAAGCCATTGAC 371
QY 240 CATTACCAACATTGGTGTGCACCTC 264
DB 372 CATTACCAACATTGGTGTGCACCTC 396

RESULT 25
AAQ75974/c
ID AAQ75974 standard; cDNA; 4059 BP.
XX
XX AAQ75974;
XX
DT 25-MAR-2003 (revised)

23-AUG-1995 (first entry)
 pHLA-B7 expression vector.
 expression vector; pHLA-B7; heavy human HLA-B7; bicistronic mRNA;
 light beta-2 microglobulin; class I major histocompatibility complex;
 MHC; human leukocyte antigen; HLA; covalently closed circular DNA; ds.
 Synthetic.
 Key Location/Qualifiers
 misc_feature 1..354
 /note= "pBR322 backbone contg. bacterial origin of
 replication"
 355..1170
 /tag= b
 /note= "kanamycin resistance gene open reading frame; the
 gene is taken from the transposable element Tn903"
 complement(1410..1177)
 /tag= c
 /note= "SV40 polyA signal sequence"
 complement(1412..1560)
 /tag= d
 /note= "SV40 small t intron"
 complement(1561..1794)
 /tag= e
 /note= "3' untranslated region of HLA-B7 heavy chain
 mRNA"
 complement(1795..2880)
 /tag= f
 /note= "HLA-B7 open reading frame"
 complement(2886..3415)
 /tag= g
 /note= "Rous sarcoma virus 3' LTR promoter region"
 3416..4059
 /tag= h
 /note= "pBR322 backbone"
 WO9429469-A2.
 22-DEC-1994.
 27-MAY-1994; 94WO-US006069.
 07-JUN-1993; 93US-00074344.
 (VICIA-) VICIAL INC.
 (UNMI) UNIV MICHIGAN.
 Nabel GJ, Nabel EG, Lew D, Marquet M;
 WPI; 1995-036494/05.
 New vectors for gene therapy, partic for tumours - comprising genetic
 material encoding one or more cistron(s) which express immunogenic or
 therapeutic peptide(s).
 Claim 9; Page 42-43; 50pp; English.
 This HLA-B7 antigen encoding plasmid was developed to incorporate many
 advantageous features, eg. the kanamycin resistance gene. The
 eradication of two open reading frames encoding portions of SV40 viral
 proteins lowers the risk of tumorigenicity. The vector may also operate
 as a cassette into which cistrons may be inserted and removed at will for
 the transcription and subsequent translation of peptides of interest. The
 vector is used partic. for the treatment of neoplastic disease, eg.
 melanoma, and provides enhanced gene delivery and expression in vivo.
 (Updated on 25-MAR-2003 to correct PN field.)
 Sequence 4059 BP; 975 A; 1051 C; 1033 G; 1000 T; 0 U; 0 Other;
 Query Match 94.0%; Score 248.2; DB 2; Length 4059;

Best Local Similarity 98.5%; Pred. No. 1.8e-76;
 Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 QY 1 AATGTAGCTTATTCATATCTCTCTGAGTCTTGCACATGTTAAAGATGATTAGCAACA 60
 DB 3156 AATGTAGCTTATTCATATCTCTCTGAGTCTTGCACATGTTAAAGATGATTAGCAACA 3097
 QY 61 TGCCTTTACAGAGAGAGAAAAAGCACCCTGTCATGCCGATTGGTGAAGTAAAGTGGTACGA 120
 DB 3096 TGCCTTTACAGAGAGAGAAAAAGCACCCTGTCATGCCGATTGGTGAAGTAAAGTGGTACGA 3037
 QY 121 TCGTGCCTTATTAGGAAGGCAACAGACGCGTCTGACATGATGAGATGAGACCACTAAATT 180
 DB 3036 TCGTGCCTTATTAGGAAGGCAACAGACGCGTCTGACATGATGAGATGAGACCACTAAATT 2977
 QY 181 CGCATTGCAGAGAT-ATTGCTATTAAAGTGCCTAGCTCGATACATATAAGCCATTGAC 239
 DB 2976 CGCATTGCAGAGATATTGCTATTAAAGTGCCTAGCTCGATACATATAAGCCATTGAC 2917
 QY 240 CATTACACCAATTGGTGTGCACCTC 264
 DB 2916 CATTACACCAATTGGTGTGCACCTC 2892
 RESULT 26
 AAQ62391
 ID AAQ62391 standard; DNA; 4341 BP.
 AC AAQ62391;
 DT 25-MAR-2003 (revised)
 DT 18-NOV-1994 (first entry)
 XX
 DE Vector pVAC1.
 XX
 KW Vector; pVAC1; pRC/RSV; leader sequence; termination signal;
 KW fusion protein; pSfi/Not.Tag1; pSfi leader; human; immunoglobulin; VH1;
 KW single chain; Fv; murine antibody; retroviral; envelope; plasmid;
 KW vaccine; ss.
 OS Synthetic.
 XX
 Key Location/Qualifiers
 misc_RNA complement(1..775)
 /tag= c
 /note= "Claim 9"
 606..780
 /tag= b
 /note= "Claim 8"
 606..716
 /tag= a
 /note= "Claim 7"
 WO9408008-A1.
 14-APR-1994.
 04-OCT-1993; 93WO-GB002054.
 02-OCT-1992; 92GB-00020808.
 (MEDI-) MEDICAL RES COUNCIL.
 PA HawKins RE, Russell SU, Stevenson FK, Winter GP;
 PI WPI; 1994-135575/16.
 DR
 XX Modulating immune response to a disease marker - by administering a
 PT vector which expresses the disease marker to interact with the immune
 PT system.
 XX
 PS Claim 10; Fig 7; 77pp; English.
 XX

CC This sequence represents the vector pVAC1. This vector is based on the
 CC commercially available vector pRC/RSV. Leader sequences and termination
 CC signals were introduced into the vector to allow for production of fusion
 CC proteins. The vector, pSfi/Not/Tag1, was modified to replace the pEB
 CC leader with the human immunoglobulin VH1 leader sequence that permits the
 CC encoding of an SfiI cloning site without modification of the amino acid
 CC sequence. This fragment was then cloned as an EcoRI/Blunt-HindIII
 CC fragment into NotI/Blunt- HindIII cut vector pRC/RSV to give pVAC1. The
 CC single chain Fv for an individual patient can be inserted within the VH1
 CC leader sequence. This plasmid when encoding a single chain murine
 CC antibody/retroviral fusion protein can be used as a plasmid
 CC vaccine and it induces a strong humoral response to the antibody moiety
 CC in BALB/c mice. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 4341 BP; 1032 A; 1099 C; 1091 G; 1119 T; 0 U; 0 Other;

Query Match 94.0%; Score 248.2; DB 2; Length 4341;
 Best Local Similarity 98.5%; Pred. No. 1.9e-76;
 Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAATGTTAAAGTGGTACCA 60
 DB 340 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAATGTTAAAGTGGTACCA 399
 QY 61 TGCCTTACAG 120
 DB 400 TGCCTTACAG 459
 QY 121 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGGATGGACGACCACTAAATT 180
 DB 460 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGGATGGACGACCACTAAATT 519
 QY 181 CGCATTTGCAGAGAT-ATTGTATTAAAGTGGCTAGCTCGATACATAAAGCCATTGGAC 239
 DB 520 CGCATTTGCAGAGATATTGTATTAAAGTGGCTAGCTCGATACATAAAGCCATTGGAC 579
 QY 240 CATTACACCACATTGGTGGCACCTC 264
 DB 580 CATTACACCACATTGGTGGCACCTC 604

RESULT 27
 AAS17704
 ID AAS17704 standard; DNA; 4341 BP.
 XX AAS17704;
 AC AAS17704;
 DT 12-MAR-2002 (first entry)
 DE Vector pVAC1 encoding a DNA vaccine.
 XX Cytostatic; vaccine; tetanus toxin; FrC; tumour; CTB; PCR primer; pVAC1;
 KW ds.
 XX Clostridium tetani.
 OS Homo sapiens.
 OS Synthetic.
 OS Cauliflower mosaic virus.
 XX WO200179510-A1.
 EN 25-OCT-2001.
 PD 17-APR-2001; 2001WO-GB001719.
 PF 17-APR-2000; 2000GB-00009470.
 XX (CANC-) CANCER RES VENTURES LTD.
 PA Rice J, Stevenson F;
 XX WPI; 2002-066370/09.
 DR

PT Nucleic acid construct, useful to immunize against various diseases
 PT including cancer, express the first domain of tetanus toxin FrC fused
 PT to a disease peptide antigen to provide a vaccine.

XX Disclosure; Fig 4; 71pp; English.

XX The invention relates to a nucleic acid construct for delivery into
 CC living cells in vivo, to induce an immune response to a disease peptide
 CC antigen, where the construct directs expression of a fusion protein
 CC comprising the peptide antigen and the first domain of FrC. Also included
 CC are a nucleic acid vector comprising the above construct, a host cell
 CC comprising the above construct or vector and a method of producing a
 CC nucleic acid construct for inducing an immune response. The method
 CC comprises identifying a nucleic acid sequence encoding a disease peptide
 CC antigen comprising epitopes characteristic of the disease, cloning the
 CC nucleic acid sequence, introducing the cloned nucleic acid into a vector
 CC which allows the antigen to be expressed as a fusion with a first domain
 CC FrC from tetanus toxin, and optionally isolating the construct from the
 CC vector. The construct or vector is used as a vaccine to induce an immune
 CC response, particularly to tumour antigens. The present sequence is vector
 CC pVAC1 which encodes a vaccine of the invention

XX Sequence 4341 BP; 1033 A; 1099 C; 1090 G; 1119 T; 0 U; 0 Other;

Query Match 94.0%; Score 248.2; DB 6; Length 4341;
 Best Local Similarity 98.5%; Pred. No. 1.9e-76;
 Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAATGTTAAAGTGGTACCA 60
 DB 340 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAATGTTAAAGTGGTACCA 399
 QY 61 TGCCTTACAG 120
 DB 400 TGCCTTACAG 459
 QY 121 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGGATGGACGACCACTAAATT 180
 DB 460 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGGATGGACGACCACTAAATT 519
 QY 181 CGCATTTGCAGAGAT-ATTGTATTAAAGTGGCTAGCTCGATACATAAAGCCATTGGAC 239
 DB 520 CGCATTTGCAGAGATATTGTATTAAAGTGGCTAGCTCGATACATAAAGCCATTGGAC 579
 QY 240 CATTACACCACATTGGTGGCACCTC 264
 DB 580 CATTACACCACATTGGTGGCACCTC 604

RESULT 28
 AEN83143
 ID AEN83143 standard; DNA; 4341 BP.
 XX AEN83143;
 AC AEN83143;
 DT 10-SEP-2002 (first entry)
 DE Plasmid pVAC1 complete sequence.
 XX Immune response; plant viral coat protein; pVAC1; cytostatic; virucide;
 KW cancer; B cell malignancy; ds.
 XX Synthetic.
 OS WO200240513-A2.
 PN 23-MAY-2002.
 XX 20-NOV-2001; 2001WO-GB005142.
 PF 20-NOV-2000; 2000GB-00028319.
 PR (CANC-) CANCER RES VENTURES LTD.
 XX

XX Savelyeva N, Stevenson F;
 XX WPI; 2002-500202/53.
 XX Nucleic acid construct for delivery into living cells as a vaccine,
 XX useful for treating e.g. cancer, directs the expression of a fusion
 XX protein comprising an antigen and an adjuvant sequence derived from a
 XX plant viral coat protein.
 XX Example 3; Fig 7; 84pp; English.
 XX The invention relates to a novel nucleic acid construct for inducing an
 XX immune response in vivo to an antigen, capable of directing the
 XX expression of a fusion protein that comprises an antigen and an adjuvant
 XX sequence derived from a plant viral coat protein. The construct of the
 XX invention has cytostatic and virucide activity. The nucleic acid
 XX construct is useful for inducing an immune response in a patient, for
 XX vaccinating a patient against an infectious disease caused by an antigen
 XX derived from a pathogen e.g. a virus, for treating a cancer patient or a
 XX patient with a predisposition to cancer and for treating a patient having
 XX a B cell malignancy, where the construct is encapsidated, and optionally,
 XX a second nucleic acid sequence encoding a further immunomodulatory
 XX polypeptide is administered to the patient. The construct is also useful
 XX in medical treatment, and in the preparation of a vaccine for treating or
 XX preventing a disease state associated with the antigen. The sequence
 XX shows the complete sequence of vector pVAC1
 XX Sequence 4341 BP; 1033 A; 1099 C; 1090 G; 1119 T; 0 U; 0 Other;
 XX Query Match 94.0%; Score 248.2; DB 6; Length 4341;
 XX Best Local Similarity 98.5%; Pred. No. 1.9e-76;
 XX Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 QY 1 AATGCTAGCTTATGCAATCTCTTGTAGTCTTGCACATGCTTAACGATGATTAGCAACA 60
 Db 340 AATGTAGCTTATGCAATCTCTTGTAGTCTTGCACATGCTTAACGATGATTAGCAACA 399
 QY 61 TGCTTTACAGGAGAGAAAAGACACCGTGCATGCCGATGCTGGAGTAAAGTGGTACGA 120
 Db 400 TGCTTTACAGGAGAGAAAAGACACCGTGCATGCCGATGCTGGAGTAAAGTGGTACGA 459
 QY 121 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGCATGATGGAATGGACCACTAAATT 180
 Db 450 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGCATGATGGAATGGACCACTAAATT 519
 QY 181 CCGCATTTGACAGAT-ATTGCTATTATGCTAGCTAGCTGCATACATTAACGCCATTGAC 239
 Db 520 CCGCATTTGACAGATTAATTGCTATTATGCTAGCTAGCTGCATACATTAACGCCATTGAC 579
 QY 240 CATTACACCATTTGCTGTGCACCTC 264
 Db 580 CATTACACCATTTGCTGTGCACCTC 604
 RESULT 29
 ID AAT02998
 XX AAT02998 standard; DNA; 5653 BP.
 XX AC AAT02998;
 XX 24-MAR-1996 (first entry)
 XX RSV tar Rev M10 expression plasmid pRSV:RevM10.
 XX Plasmid pRSV:RevM10; particle-mediated gene transfer; cyclic;
 XX Particle acceleration; HIV virus infection; gene therapy; ss.
 XX Synthetic.
 XX Key Location/Qualifiers
 FH misc_feature 1..36
 FT /*tag= a

FT enhancer /note= "pBR322 vector sequence"
 FT 37..610
 FT /*tag= b
 FT /note= "RSV enhancer"
 FT 611..699
 FT /*tag= c
 FT /label= tar
 FT /note= "HIV promoter tat responsive element"
 FT 700..1129
 FT /*tag= d
 FT /note= "Rev M10 open reading frame"
 FT 1243
 FT /*tag= e
 FT /note= "cattle somatotropin poly(A) site"
 FT 1993..2300
 FT /*tag= f
 FT /note= "pSVneo promoter"
 FT 2346
 FT /*tag= g
 FT /label= kanamycin resistance gene
 FT /note= "pSV2 neo Selectable marker gene"
 FT 3360
 FT /*tag= h
 FT /note= "pSV2 neo"
 FT 3459..5653
 FT /*tag= i
 FT /note= "plasmid pUC ori/amp sequence"
 XX W09529703-A1.
 XX 09-NOV-1995.
 XX 01-MAY-1995; 95WO-US005024.
 XX 29-APR-1994; 94US-00235277.
 XX (NAME/) NABEL G J.
 XX (WOFF/) WOFFENDIN C.
 XX (YANG/) YANG N.
 XX (SHEE/) SHEEHY M J.
 XX Nabel GU, Woffendin C, Yang N, Sheehy MJ;
 XX WPI; 1995-403807/51.
 XX Particle-mediated gene transfer - in T cells, monocytes, macrophage(s),
 XX dendrites or haematopoietic stem cells, partic. for treating HIV
 XX infection.
 XX Disclosure; Fig 11a-11e; 96pp; English.
 XX Expression plasmid pRSV:RevM10 contains the Rev M10 HIV protective gene
 XX (a dominant-negative inhibition gene) under the control of the Tar
 XX sequence (HIV promoter -18 to -72), i.e. gene expression is activated by
 XX Tat. The plasmid also contains the kanamycin- resistance selectable
 XX marker gene. The plasmid is used in a particle-mediated gene transfer
 XX process for Rev M10 gene expression in T-cells (preferably), monocytes,
 XX macrophages, haematopoietic stem cells or dendrites. The gold
 XX microparticle acceleration process results in stable incorporation of
 XX foreign genes in the cells. This method is used to treat HIV infection.
 XX Rev M10 transduced cells are resistant to HIV challenge. The method may
 XX be applied to the transfer of other therapeutic genes in a gene therapy
 XX process
 XX Sequence 5653 BP; 1328 A; 1428 C; 1478 G; 1419 T; 0 U; 0 Other;
 XX Query Match 94.0%; Score 248.2; DB 2; Length 5653;
 XX Best Local Similarity 98.5%; Pred. No. 2.1e-76;
 XX Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 QY 1 AATGCTAGCTTATGCAATCTCTTGTAGTCTTGCACATGCTTAACGATGATTAGCAACA 60
 Db 340 AATGTAGCTTATGCAATCTCTTGTAGTCTTGCACATGCTTAACGATGATTAGCAACA 399

QY 61 TGCTTACAGGAGAGAAAGCAACCGTGCATGCGGATTGCTGGAGTAAGTGTACGA 120
 Db 400 TGCTTACAGGAGAGAAAGCAACCGTGCATGCGGATTGCTGGAGTAAGTGTACGA 459
 QY 121 TCGTGCCTTATTAGGAGCAACAGACGCGGTCTGACATGATTGGACGAACCACTAAATT 180
 Db 460 TCGTGCCTTATTAGGAGCAACAGACGCGGTCTGACATGATTGGACGAACCACTAAATT 519
 QY 181 CCGCATTTGACAGAGAT-ATTGTATTTAAGTGCCTAGTCGATACATATAAACCCTTTTAC 239
 Db 520 CCGCATTTGACAGAGAT-ATTGTATTTAAGTGCCTAGTCGATACATATAAACCCTTTTAC 579
 QY 240 CATTCCACCACATTTGGTGTGCACCTC 264
 Db 580 CATTCCACCACATTTGGTGTGCACCTC 604
 RESULT 30
 AAT76802
 ID AAT76802 standard; DNA; 5653 BP.
 XX
 AC AAT76802;
 XX
 DT 18-NOV-1997 (first entry)
 XX
 DE RSV tar Rev m10 retroviral vector DNA sequence.
 XX
 KW inhibit; Human Immunodeficiency Virus; HIV; gene expression;
 KW transcription activation region; TAR; negative transdominant mutant;
 KW Rev M10; mutant; nuclear protein; viral regulatory protein; tat;
 KW RSV tar Rev M10 plasmid; Rous sarcoma virus; RSV; ds.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 enhancer 37..1129
 FT /*tag= b
 FT /note= "expression control sequence, contains Rous
 Sarcoma Virus enhancer and Rev M10 gene"
 FT CDS 700..1129
 FT /*tag= a
 FT /note= "Rev M10 gene"
 XX
 PN US5650306-A.
 XX
 PD 22-JUL-1997.
 XX
 PF 07-JUN-1993; 93US-00073836.
 XX
 PR 07-JUN-1993; 93US-00073836.
 XX
 PA (UNMI) UNIV MICHIGAN.
 XX
 PI Woffendin C, Liu J, Nabel GJ, Yang Z;
 XX
 DR WPI; 1997-384672/35.
 XX
 PT Recombinant nucleic acid for inhibiting HIV gene expression - comprises
 expression control sequence and transcription activation region linked to
 rev negative transdominant mutant gene.
 XX
 PS Claim 7; Fig 7; 35pp; English.
 CC
 CC Recombinant nucleic acid molecules for the improved expression of genes
 which inhibit Human Immunodeficiency Virus (HIV) gene expression are
 claimed, which comprise an expression control sequence and a
 transcription activation region (TAR) sequence, operatively linked to a
 negative transdominant mutant gene (a protective gene), where the
 negative transdominant mutant gene is a mutant of rev. Rev is an 18 kDa
 nuclear viral regulatory protein in HIV gene expression which controls
 export of viral RNA from the nucleus to the cytoplasm of infected cells.
 CC
 CC The TAR sequence which is found in the HIV genome controls the regulatory

CC activity of the tat protein. The TAR sequence is linked to the protective
 gene, and therefore controls its expression. This sequence is a preferred
 CC recombinant nucleic acid vector, designated RSV tar Rev M10 plasmid
 XX
 SQ Sequence 5653 BP; 1326 A; 1429 C; 1478 G; 1420 T; 0 U; 0 Other;
 Query Match 94.0%; Score 248.2; DB 2; Length 5653;
 Best Local Similarity 98.5%; Pred. No. 2.1e-76;
 Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 QY 1 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGGCAATGTAACGATGAGTTAGCAACA 60
 Db 340 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGGCAATGTAACGATGAGTTAGCAACA 399
 QY 61 TGCCTTACAAGGAGAGAAAGCAACCGTGCATGCGGATTGCTGGAGTAAGTGTACGA 120
 Db 400 TGCCTTACAAGGAGAGAAAGCAACCGTGCATGCGGATTGCTGGAGTAAGTGTACGA 459
 QY 121 TCGTGCCTTATTAGGAGCAACAGACGCGGTCTGACATGATTGGACGAACCACTAAATT 180
 Db 460 TCGTGCCTTATTAGGAGCAACAGACGCGGTCTGACATGATTGGACGAACCACTAAATT 519
 QY 181 CCGCATTTGACAGAGAT-ATTGTATTTAAGTGCCTAGTCGATACATATAAACCCTTTTAC 239
 Db 520 CCGCATTTGACAGAGAT-ATTGTATTTAAGTGCCTAGTCGATACATATAAACCCTTTTAC 579
 QY 240 CATTCCACCACATTTGGTGTGCACCTC 264
 Db 580 CATTCCACCACATTTGGTGTGCACCTC 604
 RESULT 31
 AAQ43814
 ID AAQ43814 standard; DNA; 5750 BP.
 XX
 AC AAQ43814;
 XX
 DT 25-MAR-2003 (revised)
 DT 20-OCT-1993 (first entry)
 XX
 DE pRLD3D4 construct.
 XX
 KW Epidermal growth factor receptor truncate protein; EGF; binding sites;
 KW adsorptive agents; mammalian cell growth abnormality; detection; growth;
 KW reproduction; signal transmission; ds.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 misc_feature 1077..1079
 FT /*tag= a
 FT /note= "codon ARA encodes Ile"
 XX
 PN US5218090-A.
 XX
 PD 08-JUN-1993.
 XX
 PF 26-OCT-1990; 90US-00604728.
 XX
 PR 12-JUN-1990; 90US-00536896.
 XX
 PA (WARN) WARNER LAMBERT CO.
 XX
 PI Connors RW;
 XX
 DR WPI; 1993-196297/24.
 DR P-ESDB; AAR38211.
 XX
 PT New epidermal growth factor receptor truncate proteins - which bind
 ligands of EGF receptor without transmitting signal for growth or
 reproduction.
 XX
 PS Disclosure; Fig 9; 42pp; English.

KW binding sites; adsorptive agents; mammalian cell growth abnormality;
 KW detection; reproduction; signal transmission; pRLD1D2D3Apal; ds.
 XX Synthetic.

XX Key Location/Qualifiers
 PH 665..2253
 FT CDS
 FT /tag= a
 FT /codon= 707-708 CG encodes Ile
 FT /note= "encodes Lp1D2D3Apal"
 FT 1939..1941
 FT /tag= b
 FT /note= "codon APA encodes Ile"

XX US5218090-A.

XX 08-JUN-1993.

XX 26-OCT-1990; 90US-00604728.

XX 12-JUN-1990; 90US-00536896.

XX (WARN) WARNER LAMBERT CO.

XX Connors RW;

XX WPI; 1993-196297/24.

XX F-PSDB; AAR38209.

XX New epidermal growth factor receptor truncate proteins - which bind
 PT ligands of EGF receptor without transmitting signal for growth or
 PT reproduction.

XX Disclosure; Fig 3; 42pp; English.

XX The sequence is that of the pRLD1D2D3 construct which encodes the
 CC epidermal growth factor (EGF) receptor truncate protein Lp1D2D3Apal.
 CC having EGF binding sites. The protein binds ligands of the EGF receptor
 CC without transmitting a signal for the growth and reproduction of a cell.
 CC It can be used as an adsorptive agent for any moieties that bind the EGF
 CC receptor as the portal of entry to a cell. It competes with the EGF
 CC thereby inhibits the action of the ligands or prevents the entry of
 CC such as in the detection of abnormalities in mammalian cell growth. It is
 CC also useful for prep. novel receptors for efficient detection of ligands
 CC and their anti-agonists or agonists. The features table indicates the
 CC discrepancies between the Lp1D2D3 protein sequence given in the
 CC specification and that which the pRLD1D2D3 DNA sequence given in the
 CC specification would encode. (Updated on 25-MAR-2003 to correct PF field.)

XX Sequence 6274 BP; 1506 A; 1610 C; 1664 G; 1493 T; 0 U; 1 Other;

Query Match 94.0%; Score 248.2; DB 2; Length 6274;
 Best Local Similarity 98.5%; Pred. No. 2.2e-76;
 Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGCTTTATGCAATACACTTTGTAGTCTTGTGCAATGCTGTAACGATGAGTTAGCAACA 60

DB 340 AATGTAGCTTTATGCAATACACTTTGTAGTCTTGTGCAATGCTGTAACGATGAGTTAGCAACA 399

QY 61 TGCCTTACAGGAGAGAAAGAACGACCGGTCTGATGCGATTTGGTGAAGTAAAGTGGTACGA 120

DB 400 TGCCTTACAGGAGAGAAAGAACGACCGGTCTGATGCGATTTGGTGAAGTAAAGTGGTACGA 459

QY 121 TCGTGCCTTTATGAGAGGAGAAAGAACGACCGGTCTGATGCGATTTGGTGAAGTAAAGTGGTACGA 180

DB 460 TCGTGCCTTTATGAGAGGAGAAAGAACGACCGGTCTGATGCGATTTGGTGAAGTAAAGTGGTACGA 519

QY 181 CGCATTGCGAGAGAT-ATTGATTATTAGTGCCTTACCTGATGATACATAATTAACGCCATTGAC 239

DB 520 CGCATTGCGAGAGAT-ATTGATTATTAGTGCCTTACCTGATGATACATAATTAACGCCATTGAC 579

QY 240 CATTACACACATTTGTGTGCACCTC 264
 DB ||||||||||||||||||||||||||||
 580 CATTACACACATTTGTGTGCACCTC 604

RESULT 34

AAA53869

ID AAA53869 standard; DNA; 6838 BP.

XX AAA53869;

XX 03-JAN-2001 (first entry)

XX Expression vector pRIG-1.

XX Vector; endogenous gene; activation; over-expression; erythropoietin;
 KW growth hormone; drug discovery; granulocyte colony stimulating factor;
 KW ds.

XX Synthetic.

XX WO2000049162-A2.

XX 24-AUG-2000.

XX 22-FEB-2000; 2000WC-US004429.

XX 19-FEB-1999; 99US-00253022.

XX 08-MAR-1999; 99US-00263814.

XX 26-MAR-1999; 99US-00276820.

XX (ATHE-) ATHERSYS INC.

XX Harrington JJ, Sherf B, Rundlett S;

XX WPI; 2000-549276/50.

XX Non-targeted activation of endogenous genes, e.g. for the production of
 PT erythropoietin, growth hormone or granulocyte-colony stimulating factor
 PT proteins and for drug discovery.

XX Example 1; Fig 14; 240pp; English.

XX New methods, vectors and cells are described for non-targeted activation
 CC and over-expression of endogenous genes. The vector constructs comprise
 CC transcriptional regulatory sequences (TRS) and unpaired splice donor
 CC sequences (USDS), preferably the vectors comprise (in sequential order) a
 CC TRS, an USDS, a rare cutting restriction site (RCRS) and a linearization
 CC site (LS) with a second TRS linked to a selectable marker (SM) lacking a
 CC polyadenylation signal. The methods, vectors and cells comprising the
 CC vectors may be used for the non-targeted activation and over-expression
 CC of endogenous genes, e.g. for the production of proteins (including
 CC erythropoietin, growth hormone or granulocyte-colony stimulating factor)
 CC and drug discovery. The advantage of these methods are that endogenous
 CC genes including those associated with human disease and development, may
 CC be activated and isolated without prior knowledge of the sequence
 CC structure, function or expression profile of the genes being known

XX Sequence 6838 BP; 1679 A; 1669 C; 1709 G; 1781 T; 0 U; 0 Other;

Query Match 94.0%; Score 248.2; DB 3; Length 6838;
 Best Local Similarity 98.5%; Pred. No. 2.3e-76;
 Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGCTTTATGCAATACACTTTGTAGTCTTGTGCAATGCTGTAACGATGAGTTAGCAACA 60

DB 1559 AATGTAGCTTTATGCAATACACTTTGTAGTCTTGTGCAATGCTGTAACGATGAGTTAGCAACA 1618

QY 61 TGCCTTACAGGAGAGAAAGAACGACCGGTCTGATGCGATTTGGTGAAGTAAAGTGGTACGA 120

DB 1619 TGCCTTACAGGAGAGAAAGAACGACCGGTCTGATGCGATTTGGTGAAGTAAAGTGGTACGA 1678

QY 121 TCGTGCCTTTATGAGAGGAGAAAGAACGACCGGTCTGATGCGATTTGGTGAAGTAAAGTGGTACGA 190

Db 1679 TCGTGCCTTATTAGGAGGCAACAGACAGGTCTGACATGGATTGCGACGAACCACTGAATT 1738
 QY 181 CGCATTCGACAGAT-ATTGTATTATTAGTCCCTAGCTGATACATAAAGCGCATTTGAC 239
 Db 1739 CGCATTCGACAGATAATTGTATTAAAGTCCCTAGCTGATACATAAAGCGCATTTGAC 1798
 QY 240 CATTCCACACATTGGTGTGCACCTC 264
 Db 1799 CATTCCACACATTGGTGTGCACCTC 1823
 RESULT 35
 AAT84562
 ID AAT84562 standard; cDNA; 8591 BP.
 AC AAT84562;
 XX
 DT 25-MAR-2003 (revised)
 DT 15-DEC-1997 (first entry)
 XX
 DE Plasmid pCLL621 encoding amyloid precursor protein APP-REP 751.
 XX
 KW Amyloid precursor protein; APP; beta-amyloid protein; BAP; substrate;
 KW muten; secretase; Alzheimer's disease; human; APP-REP 751; pCLL621; ds;
 KW cyclic.
 XX
 OS Homo; sapiens.
 OS Synthetic.
 OS Chimeric.
 XX
 FH Key Location/Qualifiers
 FT CDS 2393..3856
 FT /*tag= a
 XX
 XX US5652092-A.
 XX
 PD 29-JUL-1997.
 XX
 XX 05-JUN-1995; 95US-00462859.
 XX
 PR 01-MAY-1992; 92US-00877675.
 PR 20-SEP-1993; 93US-00123659.
 XX
 PA (AMCY) AMERICAN CYANAMID CO.
 XX
 PI Jacobsen JS, Vitek MP;
 XX
 DR WPI; 1997-392937/36.
 DR P-PSDB; AAW26394.
 XX
 XX Screening for compounds which reduce beta-amyloid protein formation -
 PT using cells which express a construct encoding a marker and an amyloid
 PT precursor muten derived from APP isoforms.
 XX
 PS Disclosure; Fig 8; 84pp; English.
 XX
 CC Plasmid pCLL621 (AAT84562), deposited in E. coli as ATCC 69406, codes
 CC for an amyloid precursor protein (APP) substrate, designated APP-REP 751
 CC (see AAW26394), that has a 276-amino acid deletion of the native APP and
 CC carries a substance P epitope marker on the N-terminal side of the beta-
 CC amyloid protein (BAP) domain. APP-REP 751 can be used in a claimed method
 CC for screening for a compound which reduces the formation of beta-amyloid
 CC protein, determined by measuring the amount of marker in a medium
 CC containing transfected cells. The method is used to detect compounds
 CC which inhibit the activity of proteolytic enzymes which cleave APP to
 CC generate BAP fragments. Such compounds can be used in the treatment of
 CC e.g. Alzheimer's disease. The deletion of a 276 amino acid portion of APP
 CC distinguishes the construct from endogenously expressed APP, and
 CC beneficially increases the resolution of APP-REP fragments resulting from
 CC the proteolytic cleavage by secretase or other amyloidogenic, BAP-
 CC generating cleavage events. (Updated on 25-MAR-2003 to correct PF field.)
 XX

SQ Sequence 8591 BP; 2225 A; 2038 C; 2247 G; 2081 T; 0 U; 0 Other;
 Query Match 94.0%; Score 248.2; DB 2; Length 8591;
 Best Local Similarity 98.5%; Pred. No. 2.5e-76;
 Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 QY 1 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGTCAACATGCTAAGATGATGATGACAA 60
 Db 4975 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGTCAACATGCTAAGATGATGACAA 5034
 QY 61 TGCCTTACAGGAGAGAAAAGCACCCGTGCATGCGCATTCGTCGAGTGGAGTGGTACGA 120
 Db 5035 TGCCTTACAGGAGAGAAAAGCACCCGTGCATGCGCATTCGTCGAGTGGAGTGGTACGA 5094
 QY 121 TCGTGCCTTATTAGGAGGCAACAGACGCGGTCTGACATGCGATTGGACGAACCACTAAAT 180
 Db 5095 TCGTGCCTTATTAGGAGGCAACAGACGCGGTCTGACATGCGATTGGACGAACCACTAAAT 5154
 QY 181 CGCATTCGACAGAT-ATTGTATTATTAGTCCCTAGCTGATACATAAAGCGCATTTGAC 239
 Db 5155 CGCATTCGACAGATAATTGTATTAAAGTCCCTAGCTGATACATAAAGCGCATTTGAC 5214
 QY 240 CATTCCACACATTGGTGTGCACCTC 264
 Db 5215 CATTCCACACATTGGTGTGCACCTC 5239
 RESULT 36
 AAT84561
 ID AAT84561 standard; cDNA; 8591 BP.
 XX
 AC AAT84561;
 XX
 DT 25-MAR-2003 (revised)
 DT 15-DEC-1997 (first entry)
 XX
 DE Plasmid pCLL602 encoding amyloid precursor protein APP-REP 751.
 XX
 KW Amyloid precursor protein; APP; beta-amyloid protein; BAP; substrate;
 KW muten; secretase; Alzheimer's disease; human; APP-REP 751; pCLL602; ds;
 KW cyclic.
 XX
 OS Homo; sapiens.
 OS Synthetic.
 OS Chimeric.
 XX
 FH Key Location/Qualifiers
 FT CDS 2393..3871
 FT /*tag= a
 XX
 XX US5652092-A.
 XX
 PD 29-JUL-1997.
 XX
 XX 05-JUN-1995; 95US-00462859.
 XX
 PR 01-MAY-1992; 92US-00877675.
 PR 20-SEP-1993; 93US-00123659.
 XX
 PA (AMCY) AMERICAN CYANAMID CO.
 XX
 PI Jacobsen JS, Vitek MP;
 XX
 DR WPI; 1997-392937/36.
 DR P-PSDB; AAW26393.
 XX
 XX Screening for compounds which reduce beta-amyloid protein formation -
 PT using cells which express a construct encoding a marker and an amyloid
 PT precursor muten derived from APP isoforms.
 XX
 PS Disclosure; Fig 7; 84pp; English.
 XX
 CC Plasmid pCLL602 (AAT84561), deposited in E. coli as ATCC 69405, codes

CC for an amyloid precursor protein (APP) substrate, designated APP-REP 751
 CC (see AAW26393), that has a 276-amino acid deletion of the native APP and
 CC carries Substance P and Met-enkephalin epitope markers placed,
 CC respectively, on the N-terminal and C-terminal sites of the beta-amyloid
 CC protein (BAP) domain. APP-REP 751 can be used in a claimed method for
 CC screening for a compound which reduces the formation of beta-amyloid
 CC protein, determined by measuring the amount of marker in a medium
 CC containing transfected cells. The method is used to detect compounds
 CC which inhibit the activity of proteolytic enzymes which cleave APP to
 CC generate BAP fragments. Such compounds can be used in the treatment of
 CC e.g. Alzheimer's disease. The deletion of a 276 amino acid portion of APP
 CC distinguishes the construct from endogenously expressed APP, and
 CC beneficially increases the resolution of APP-REP fragments resulting from
 CC the proteolytic cleavage by secretase or other amyloidogenic, BAP-
 CC generating cleavage events. (Updated on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 8591 BP; 2225 A; 2038 C; 2247 G; 2081 T; 0 U; 0 Other;

Query Match 94.0%; Score 248.2; DB 2; Length 8591;
 Best Local Similarity 98.5%; Pred. No. 2.5e-76;
 Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 QY 1 AATGTAGTCTTATGCAATACACTTGTAGTCTTGTGCAATGCTTAACGATGAGTTAGCAACA 60
 DB 4975 AATGTAGTCTTATGCAATACACTTGTAGTCTTGTGCAATGCTTAACGATGAGTTAGCAACA 5034
 QY 61 TGCCTTTACAGGAGAGAAAAGCACCCTGCGATGCGGATTTGGTGAAGTAAAGTGGTACGA 120
 DB 5035 TGCCTTTACAGGAGAGAAAAGCACCCTGCGATGCGGATTTGGTGAAGTAAAGTGGTACGA 5094
 QY 121 TCGTGCCCTTATTAGGAAGGCAACAGACGGGCTCTGACATGATTTGACACCACTAAATT 180
 DB 5095 TCGTGCCCTTATTAGGAAGGCAACAGACGGGCTCTGACATGATTTGACACCACTAAATT 5154
 QY 181 CCGCATTCGACAGAT-ATTGTATTTAAGTCTAGCTCGATACATATTAACGCCATTGAC 239
 DB 5155 CCGCATTCGACAGATTAATTGTATTAAAGTGGCTAGCTCGATACATATTAACGCCATTGAC 5214
 QY 240 CATTACCAACATTTGTCGACCTC 264
 DB 5215 CATTACCAACATTTGTCGACCTC 5239

RESULT 37
 AAT87083
 ID AAT87083 standard; cDNA; 8591 BP.
 AC AAT87083;
 XX
 DT 25-MAR-2003 (revised)
 DT 06-JAN-1998 (first entry)
 XX
 DE Plasmid pCLL602 encoding amyloid precursor protein APP-REP 751.
 XX
 KW Amyloid precursor protein; APP; beta-amyloid protein; BAP; substrate;
 KW muten; secretase; Alzheimer's disease; human; APP-REP 751; pCLL602; ds;
 XX cyclic.
 XX Homo sapiens.
 OS Synthetic.
 OS Chimeric.
 XX
 FE Key Location/Qualifiers
 CDS 2393..3871
 FT /*tag= a
 FT
 XX
 XX US5656477-A.
 XX
 PD 12-AUG-1997.
 XX
 XX 20-SEP-1993; 93US-00123659.
 XX
 XX 01-MAY-1992; 92US-00877675.

XX (AMCY) AMERICAN CYANAMID CO.
 PA Jacobeen JS, Vitek MP;
 XX
 PI WPI; 1997-414594/38.
 DR P-PSDB; AAW26509.
 DR
 XX
 PT Nucleic acid encoding amyloid precursor muten(s) - comprising reporter
 PT gene and coding sequence, for identifying compounds which modify the
 PT activity of proteolytic enzymes which cleave APP.
 PT
 XX Disclosure; Fig 7; 84pp; English.

XX Plasmid pCLL602 (AAW87083), deposited in E. coli as ATCC 69405, codes
 CC for an amyloid precursor protein (APP) substrate, designated APP-REP 751
 CC (see AAW26509), that has a 276-amino acid deletion of the native APP and
 CC carries Substance P and Met-enkephalin epitope markers placed,
 CC respectively, on the N-terminal and C-terminal sites of the beta-amyloid
 CC protein (BAP) domain. APP-REP 751 can be used in a claimed method for
 CC screening for a compound which reduces the formation of beta-amyloid
 CC protein, determined by measuring the amount of marker in a medium
 CC containing transfected cells. The method is used to detect compounds
 CC which inhibit the activity of proteolytic enzymes which cleave APP to
 CC generate BAP fragments. Such compounds can be used in the treatment of
 CC e.g. Alzheimer's disease. The deletion of a 276 amino acid portion of APP
 CC distinguishes the construct from endogenously expressed APP, and
 CC beneficially increases the resolution of APP-REP fragments resulting from
 CC the proteolytic cleavage by secretase or other amyloidogenic, BAP-
 CC generating cleavage events. (Updated on 25-MAR-2003 to correct PF field.)
 XX

SQ Sequence 8591 BP; 2225 A; 2038 C; 2247 G; 2081 T; 0 U; 0 Other;
 Query Match 94.0%; Score 248.2; DB 2; Length 8591;
 Best Local Similarity 98.5%; Pred. No. 2.5e-76;
 Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATACACTTGTAGTCTTGTGCAATGCTTAACGATGAGTTAGCAACA 60
 DB 4975 AATGTAGTCTTATGCAATACACTTGTAGTCTTGTGCAATGCTTAACGATGAGTTAGCAACA 5034
 QY 61 TGCCTTTACAGGAGAGAAAAGCACCCTGCGATGCGGATTTGGTGAAGTAAAGTGGTACGA 120
 DB 5035 TGCCTTTACAGGAGAGAAAAGCACCCTGCGATGCGGATTTGGTGAAGTAAAGTGGTACGA 5094
 QY 121 TCGTGCCCTTATTAGGAAGGCAACAGACGGGCTCTGACATGATTTGACACCACTAAATT 180
 DB 5095 TCGTGCCCTTATTAGGAAGGCAACAGACGGGCTCTGACATGATTTGACACCACTAAATT 5154
 QY 181 CCGCATTCGACAGAT-ATTGTATTTAAGTCTAGCTCGATACATATTAACGCCATTGAC 239
 DB 5155 CCGCATTCGACAGATTAATTGTATTAAAGTGGCTAGCTCGATACATATTAACGCCATTGAC 5214
 QY 240 CATTACCAACATTTGTCGACCTC 264
 DB 5215 CATTACCAACATTTGTCGACCTC 5239

RESULT 38
 AAT87084
 ID AAT87084 standard; cDNA; 8591 BP.
 AC AAT87084;
 XX
 DT 25-MAR-2003 (revised)
 DT 06-JAN-1998 (first entry)
 XX
 DE Plasmid pCLL621 encoding amyloid precursor protein APP-REP 751.
 XX
 KW Amyloid precursor protein; APP; beta-amyloid protein; BAP; substrate;
 KW muten; secretase; Alzheimer's disease; human; APP-REP 751; pCLL621; ds;
 XX cyclic.

QY 121 TCGTGCTTATTAGGAAGCAACAGACGGTCTGCATGATTGGACGAACCACTAAATT 180
DB 5095 TCGTGCTTATTAGGAAGCAACAGACGGTCTGCATGATTGGACGAACCACTAAATT 5154
QY 181 CCGCATTGACAGAT-ATTGTATTAAAGTGCTAGCTCGATACATTAAGCCATTGAC 239
DB 5155 CCGCATTGACAGAT-ATTGTATTAAAGTGCTAGCTCGATACATTAAGCCATTGAC 5214
QY 240 CATTACACCATTTGGTGTGCACCTC 264
DB 5215 CATTACACCATTTGGTGTGCACCTC 5239
RESULT 40
AAV04865
ID AAV04865 standard; DNA; 8591 BP.
XX AC AAV04865;
XX DT 01-MAY-1998 (first entry)
DE cDNA encoding amyloid precursor protein mutant APP-APP 751.
KW Beta-amyloid peptide; BAP; extracellular BAP plaque;
KW cerebrovascular deposit; Alzheimers disease; Downs syndrome;
KW amyloid precursor protein; APP; secretase; BAP aggregation;
KW abnormal proteolytic cleavage; ds.
XX OS Homo sapiens.
XX PH Key Location/Qualifiers
XX CDS 2393..3871
XX FT /*tag= a
XX PN US5703209-A.
XX PD 30-DEC-1997.
XX PF 05-JUN-1995; 95US-00464248.
XX PR 01-MAY-1992; 92US-00877675.
XX PR 20-SEP-1993; 93US-00123659.
XX PA (AMCY) AMERICAN CYANAMID CO.
XX PI Jacobsen JS, Vitek MP;
XX WPI; 1998-076482/07.
XX DR P-PSDB; AAW42978.
XX PT Amyloid precursor protein fusion polypeptides - comprising APP fragment
XX and marker, useful for research and drug screening.
XX PS Disclosure; Fig 7A-Q; 84pp; English.
XX CC The present sequence encodes an amyloid precursor protein (APP), which
CC has a deletion of 276 amino acids to within 15 amino acids of the beta-
CC amyloid peptide (BAP) domain. The protein also contains the Met-
CC enkephalin reporter epitope at the carboxy terminus. Abnormal
CC accumulation of extracellular BAP in plaques and cerebrovascular deposits
CC is characteristic in brains of individuals suffering from Alzheimers
CC disease and Downs syndrome. BAP is a poorly soluble, self-aggregating
CC protein which is derived from a larger amyloid precursor protein (APP).
CC APP is expressed as an integral membrane protein, and is cleaved by
CC secretase, between BAP 16Lys and 17Ileu. Cleavage at this site precludes
CC amyloidogenesis and results in the release of the amino-terminal APP
CC fragment. Three major isoforms of APP exist: APP-695, APP-751 and APP-
CC 770. These isoforms are derived by alternative splicing. APP-RP 751 is
CC constructed by ligating restriction fragments representing N- and C-
CC terminal APP-751 cDNA and substrate P reporter epitope sequences. APP
CC can be used as a substrate for studying abnormal proteolytic cleavage
CC which results in the release of BAP, and also to screen for drugs that

CC will inhibit such cleavage
XX SQ Sequence 8591 BP; 2225 A; 2038 C; 2247 G; 2081 T; 0 U; 0 Other;
Query Match 94.0%; Score 248.2; DB 2; Length 8591;
Best Local Similarity 98.5%; Pred. No. 2.5e-76;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 1 AATGAGTCTTATGCAATACCTCTTGTAGTCTTGGCAATGCTTAACGATGAGTTAGCAACA 60
DB 4975 AATGAGTCTTATGCAATACACCTTGTAGTCTTGGCAATGCTTAACGATGAGTTAGCAACA 5034
QY 61 TGCCTTACAGAGAGAGAAAAGACACCGTGCATGCGGATTCGTGGAAGTAAGTGTGATAGA 120
DB 5035 TGCCTTACAGAGAGAGAAAAGACACCGTGCATGCGGATTCGTGGAAGTAAGTGTGATAGA 5094
QY 121 TCGTGCTTATTAGGAAGCAACAGACGGTCTGCATGATTGGACGAACCACTAAATT 180
DB 5095 TCGTGCTTATTAGGAAGCAACAGACGGTCTGCATGATTGGACGAACCACTAAATT 5154
QY 181 CCGCATTGACAGAT-ATTGTATTAAAGTGCTAGCTCGATACATTAAGCCATTGAC 239
DB 5155 CCGCATTGACAGAT-ATTGTATTAAAGTGCTAGCTCGATACATTAAGCCATTGAC 5214
QY 240 CATTACACCATTTGGTGTGCACCTC 264
DB 5215 CATTACACCATTTGGTGTGCACCTC 5239
RESULT 41
AAV05850
ID AAV05850 standard; cDNA; 8591 BP.
XX AC AAV05850;
XX DT 01-JUN-1998 (first entry)
DE APP-REP 751 gene from pCLL621.
XX KW Amyloid precursor protein; APP; APP 751 isoform; deletion; substrate P;
XX KW epitope; Met-enkephalin; detection; secretase; beta-amyloid protein; BAP;
XX KW Alzheimer's disease; cleavage; cyclic; circular; ds.
XX OS Homo sapiens.
XX OS Synthetic.
XX PH Key Location/Qualifiers
XX CDS 2393..3856
XX FT /*tag= a
XX FT /product= "APP_REP_751"
XX PN US5693478-A.
XX PD 02-DEC-1997.
XX PF 05-JUN-1995; 95US-00464247.
XX PR 01-MAY-1992; 92US-00877675.
XX PR 20-SEP-1993; 93US-00123659.
XX PA (AMCY) AMERICAN CYANAMID CO.
XX PI Jacobsen JS, Vitek MP;
XX WPI; 1998-031744/03.
XX DR P-PSDB; AAW44745.
XX PT Amyloid precursor mutin reporter molecule assay containing antibody
XX recognised marker - used to study pathways associated with Alzheimer's
XX disease.
XX PS Disclosure; Fig 8; 84pp; English.
XX

Db 1648 CATTACACCATTTGGTGTGCACCTC 1672

RESULT 45
AAA53879
ID AAA53879 standard; DNA; 9732 BP.
XX
AC AAA53879;
XX
DT 03-JAN-2001 (first entry)
XX
DE Expression vector pRIG-TP.
XX
KW Vector; endogenous gene; activation; over-expression; erythropoietin;
KW growth hormone; drug discovery; granulocyte colony stimulating factor;
KW ds.
XX
OS Synthetic.
XX
PN WO200049162-A2.
XX
PD 24-AUG-2000.
XX
PF 22-FEB-2000; 2000WO-US004429.
XX
PR 19-FEB-1999; 99US-00253022.
PR 08-MAR-1999; 99US-00263814.
PR 26-MAR-1999; 99US-00276820.
XX
PA (ATHE-) ATHERSYS INC.
XX
PI Harrington JJ, Sherf B, Rundlett S;
XX
DR WPI; 2000-549276/50.
XX
PT Non-targeted activation of endogenous genes, e.g. for the production of
PT erythropoietin, growth hormone or granulocyte-colony stimulating factor
PT proteins and for drug discovery.
XX
PS Example 15; Fig 37; 240pp; English.
XX
CC New methods, vectors and cells are described for non-targeted activation
CC and over-expression of endogenous genes. The vector constructs comprise
CC transcriptional regulatory sequences (TRS) and unpaired splice donor
CC sequences (USDS), preferably the vectors comprise (in sequential order) a
CC TRS, an USDS, a rare cutting restriction site (RCRS) and a linearization
CC site (LS) with a second TRS linked to a selectable marker (SM) lacking a
CC polyadenylation signal. The methods, vectors and cells comprising the
CC vectors may be used for the non-targeted activation and over-expression
CC of endogenous genes, e.g. for the production of proteins (including
CC erythropoietin, growth hormone or granulocyte-colony stimulating factor)
CC and drug discovery. The advantage of these methods are that endogenous
CC genes including those associated with human disease and development, may
CC be activated and isolated without prior knowledge of the sequence
CC structure, function or expression profile of the genes being known
XX
SQ Sequence 9732 BP; 2427 A; 2512 C; 2443 G; 2348 T; 0 U; 2 Other;
Query Match 94.0%; Score 248.2; DB 3; Length 9732;
Best Local Similarity 98.5%; Pred. No. 2.7e-76;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 1 AATGTAGTCTTTATGCAATCTCTTGTAGTCTTGCACATGGTAAAGTAGGTAGCAACA 60
DB 1411 AATGTAGTCTTTATGCAATCTCTTGTAGTCTTGCACATGGTAAAGTAGGTAGCAACA 1470
QY 61 TGGCTTACAGGAGAGAAAACACCGTGCATCCGATGTGGAAGTAGGTAGCA 120
DB 1471 TGGCTTACAGGAGAGAAAACACCGTGCATCCGATGTGGAAGTAGGTAGCA 1530
QY 121 TGGTCCCTTATTAGGAGGACACAGACGGGTCTGACATGGATTGCGAACCACTAAATT 180
DB 1531 TGGTCCCTTATTAGGAGGACACAGACAGGTCTGACATGGATTGCGAACCACTGAATT 1590

QY 181 CCGCATTTGCAGAGAT-ATTGTATTTAAGTGGCTAGCTCGATACATTAACGCCATTTGAC 239
DB 1591 CCGCATTTGCAGAGATTAATTTGTTAAGTGGCTAGCTCGATACATTAACGCCATTTGAC 1650
QY 240 CATTACACCATTTGGTGTGCACCTC 264
DB 1651 CATTACACCATTTGGTGTGCACCTC 1675

RESULT 46
AAA53874
ID AAA53874 standard; DNA; 9738 BP.
XX
AC AAA53874;
XX
DT 03-JAN-2001 (first entry)
XX
DE Expression vector pRIG20.
XX
KW Vector; endogenous gene; activation; over-expression; erythropoietin;
KW growth hormone; drug discovery; granulocyte colony stimulating factor;
KW ds.
XX
OS Synthetic.
XX
PN WO200049162-A2.
XX
PD 24-AUG-2000.
XX
PF 22-FEB-2000; 2000WO-US004429.
XX
PR 19-FEB-1999; 99US-00253022.
PR 08-MAR-1999; 99US-00263814.
PR 26-MAR-1999; 99US-00276820.
XX
PA (ATHE-) ATHERSYS INC.
XX
PI Harrington JJ, Sherf B, Rundlett S;
XX
DR WPI; 2000-549276/50.
XX
PT Non-targeted activation of endogenous genes, e.g. for the production of
PT erythropoietin, growth hormone or granulocyte-colony stimulating factor
PT proteins and for drug discovery.
XX
PS Disclosure; Fig 31; 240pp; English.
XX
CC New methods, vectors and cells are described for non-targeted activation
CC and over-expression of endogenous genes. The vector constructs comprise
CC transcriptional regulatory sequences (TRS) and unpaired splice donor
CC sequences (USDS), preferably the vectors comprise (in sequential order) a
CC TRS, an USDS, a rare cutting restriction site (RCRS) and a linearization
CC site (LS) with a second TRS linked to a selectable marker (SM) lacking a
CC polyadenylation signal. The methods, vectors and cells comprising the
CC vectors may be used for the non-targeted activation and over-expression
CC of endogenous genes, e.g. for the production of proteins (including
CC erythropoietin, growth hormone or granulocyte-colony stimulating factor)
CC and drug discovery. The advantage of these methods are that endogenous
CC genes including those associated with human disease and development, may
CC be activated and isolated without prior knowledge of the sequence
CC structure, function or expression profile of the genes being known
XX
SQ Sequence 9738 BP; 2428 A; 2514 C; 2447 G; 2347 T; 0 U; 2 Other;
Query Match 94.0%; Score 248.2; DB 3; Length 9738;
Best Local Similarity 98.5%; Pred. No. 2.7e-76;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 1 AATGTAGTCTTTATGCAATCTCTTGTAGTCTTGCACATGGTAAAGTAGGTAGCAACA 60
DB 1411 AATGTAGTCTTTATGCAATCTCTTGTAGTCTTGCACATGGTAAAGTAGGTAGCAACA 1470

QY 61 TGCCTTACAGGAGAGAAAGCAACCGTGCATGCCGATTTGGTGGAAAGTAAGTGTACGA 120
 Db 1471 TGCCTTACAGGAGAGAAAGCAACCGTGCATGCCGATTTGGTGGAAAGTAAGTGTACGA 1530
 QY 121 TCGTGCCTTATTAGGAGGCAACAGACGGCTCTGCATGATTTGGACGACCACTAAATT 180
 Db 1531 TCGTGCCTTATTAGGAGGCAACAGACGGCTCTGCATGATTTGGACGACCACTAAATT 1590
 QY 181 CGCATTGCGAGAGAT-ATTGTAATTTAAGTGCCTAGCTCGATACATAAAGCGCAATTGAC 239
 Db 1591 CGCATTGCGAGAGATTAATTTAATTTAAGTGCCTAGCTCGATACATAAAGCGCAATTGAC 1650
 QY 240 CATTACACCAATTTGGTGTGCACCTC 264
 Db 1651 CATTACACCAATTTGGTGTGCACCTC 1675

RESULT 47

AAA53875
 ID AAA53875 standard; DNA; 9873 BP.

AC AAA53875;

XX 03-JAN-2001 (first entry)

DE Expression vector pRIGadi.

XX Vector; endogenous gene; activation; over-expression; erythropoietin;
 KW growth hormone; drug discovery; granulocyte colony stimulating factor;
 KW ds.

OS Synthetic.

XX WC200049162-A2.

XX 24-AUG-2000.

XX 22-FEB-2000; 2000WC-US004429.

XX 19-FEB-1999; 99US-00253022.

XX 08-MAR-1999; 99US-00263814.

XX 26-MAR-1999; 99US-00276820.

XX (ATHE-) ATHERSYS INC.

XX Harrington JJ, Sherf B, Rundlett S;

XX WPI; 2000-549276/50.

XX Non-targeted activation of endogenous genes, e.g. for the production of
 PT erythropoietin, growth hormone or granulocyte-colony stimulating factor
 PT proteins and for drug discovery.

XX Disclosure; Fig 32; 240pp; English.

XX New methods, vectors and cells are described for non-targeted activation
 CC and over-expression of endogenous genes. The vector constructs comprise
 CC transcriptional regulatory sequences (TRS) and unpaired splice donor
 CC sequences (USDS), preferably the vectors comprise (in sequential order) a
 CC TRS, an USDS, a rare cutting restriction site (RCRS) and a linearization
 CC site (LS) with a second TRS linked to a selectable marker (SM) lacking a
 CC polyadenylation signal. The methods, vectors and cells comprising the
 CC vectors may be used for the non-targeted activation and over-expression
 CC of endogenous genes, e.g. for the production of proteins (including
 CC erythropoietin, growth hormone or granulocyte-colony stimulating factor)
 CC and drug discovery. The advantage of these methods are that endogenous
 CC genes including those associated with human disease and development, may
 CC be activated and isolated without prior knowledge of the sequence
 CC structure, function or expression profile of the genes being known

XX Sequence 9873 BP; 2450 A; 2557 C; 2501 G; 2363 T; 0 U; 2 Other;

XX Query Match 94.0%; Score 248.2; DB 3; Length 9873;

Best Local Similarity 98.5%; Pred. No. 2.7e-76;
 Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 QY 1 AATGATGCTTATGCAATACTCTTTGTAGTCTTTCGCAACATGTGTAACGATGAGTTAGCAACA 60
 Db 1550 AATGATGCTTATGCAATACTCTTTGTAGTCTTTCGCAACATGTGTAACGATGAGTTAGCAACA 1609
 QY 61 TGCCTTACAGGAGAGAAAGCAACCGTGCATGCCGATTTGGTGGAAAGTAAGTGTACGA 120
 Db 1610 TGCCTTACAGGAGAGAAAGCAACCGTGCATGCCGATTTGGTGGAAAGTAAGTGTACGA 1669
 QY 121 TCGTGCCTTATTAGGAGGCAACAGACGGCTCTGCATGCCGATTTGGTGGAAAGTAAGTGTACGA 180
 Db 1670 TCGTGCCTTATTAGGAGGCAACAGACGGCTCTGCATGCCGATTTGGTGGAAAGTAAGTGTACGA 1729
 QY 181 CGCATTGCGAGAGAT-ATTGTAATTTAAGTGCCTAGCTCGATACATAAAGCGCAATTGAC 239
 Db 1730 CGCATTGCGAGAGATTAATTTAATTTAAGTGCCTAGCTCGATACATAAAGCGCAATTGAC 1789
 QY 240 CATTACACCAATTTGGTGTGCACCTC 264
 Db 1790 CATTACACCAATTTGGTGTGCACCTC 1814

RESULT 48

AAA53876

ID AAA53876 standard; DNA; 10054 BP.

AC AAA53876;

XX 03-JAN-2001 (first entry)

DE Expression vector pRIGadi.

XX Vector; endogenous gene; activation; over-expression; erythropoietin;
 KW growth hormone; drug discovery; granulocyte colony stimulating factor;
 KW ds.

OS Synthetic.

XX WC200049162-A2.

XX 24-AUG-2000.

XX 22-FEB-2000; 2000WC-US004429.

XX 19-FEB-1999; 99US-00253022.

XX 08-MAR-1999; 99US-00263814.

XX 26-MAR-1999; 99US-00276820.

XX (ATHE-) ATHERSYS INC.

XX Harrington JJ, Sherf B, Rundlett S;

XX WPI; 2000-549276/50.

XX Non-targeted activation of endogenous genes, e.g. for the production of
 PT erythropoietin, growth hormone or granulocyte-colony stimulating factor
 PT proteins and for drug discovery.

XX Disclosure; Fig 33; 240pp; English.

XX New methods, vectors and cells are described for non-targeted activation
 CC and over-expression of endogenous genes. The vector constructs comprise
 CC transcriptional regulatory sequences (TRS) and unpaired splice donor
 CC sequences (USDS), preferably the vectors comprise (in sequential order) a
 CC TRS, an USDS, a rare cutting restriction site (RCRS) and a linearization
 CC site (LS) with a second TRS linked to a selectable marker (SM) lacking a
 CC polyadenylation signal. The methods, vectors and cells comprising the
 CC vectors may be used for the non-targeted activation and over-expression
 CC of endogenous genes, e.g. for the production of proteins (including
 CC erythropoietin, growth hormone or granulocyte-colony stimulating factor)
 CC and drug discovery. The advantage of these methods are that endogenous

CC	This is the DNA sequence of expression plasmid pREP7::CTIA4-hlg that	
CC	encodes a secreted form of the Fc fragment of human IgG1 fused to murine	
CC	CTIA4. The invention provides a new DNA molecule for use in raising an	
CC	immune response to an antigen. The DNA molecule comprises: (i) a first	
CC	sequence encoding a targeting molecule (e.g. CTIA4, which acts as a	
CC	targeting molecule to antigen-presenting cells expressing B-7); (ii) a	
CC	second sequence encoding the antigen or its epitope, and (iii) optionally	
CC	a third sequence encoding a polypeptide (e.g. an immunoglobulin) which	
CC	promotes dimerization or multimerisation of the product encoded by the	
CC	DNA molecule. Also claimed are a polypeptide encoded by the DNA molecule,	
CC	and a vector including the DNA molecule. The inventors have shown that	
CC	fusion proteins consisting of antigen and cell surface receptor ligands	
CC	can deliver antigen to sites of immune induction which enhance the immune	
CC	response and possibly the efficacy of genetic vaccines. The DNA molecule	
CC	can be used in a claimed method for deviating an immune response to an	
CC	antigen in an individual. (Updated on 17-OCT-2003 to standardise OS	
CC	field)	
XX		
QQ	Sequence 11265 BP; 2717 A; 2979 C; 3002 G; 2567 T; 0 U; 0 Other;	
SS		
SS	Query Match 94.0%; Score 248.2; DB 2; Length 11265;	
SS	Best Local Similarity 98.5%; Pred. No. 2.9e-76;	
SS	Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;	
QY	1 AATGPAAGTCTTATGCAATACACTTTGTAGTCTTGTGCAACATGCTAAACGATGAGTTAGCAACA 428	
DB	369 AATGTAGTCTTATGCAATACACTTTGTAGTCTTGTGCAACATGCTAAACGATGAGTTAGCAACA 428	
QY	61 TGCCTTACAGGAGAGAAAGACACCGTGCATGCCGATTGGTGGAAAGTAAAGTGGTACGA 120	
DB	429 TGCCTTACAGGAGAGAAAGACACCGTGCATGCCGATTGGTGGAAAGTAAAGTGGTACGA 488	
QY	121 TCGTGCCTTTATTAGGAAGGCAACAGACGGGCTCTGACATGGATTGCGAAGCAACATAAATT 180	
DB	489 TCGTGCCTTTATTAGGAAGGCAACAGACAGGTCTGACATGGATTGCGAAGCAACACTGAATT 548	
QY	181 CGCATTTGCAAGAT-ATTGTAATTTAAGTGCCTAGCTCGATACATTAACGCCATTGTGAC 239	
DB	549 CGCGATTGCAAGATTAATTGTAATTAAGTGCTAGCTCGATACATTAACGCCATTGTGAC 608	
QY	240 CATTCCACCACATTTGGTGTGCACCTC 264	
DB	609 CATTCCACCACATTTGGTGTGCACCTC 633	
RESULT 50		
AAAL55269		
ID	AAAL55269 standard; DNA; 16958 BP.	
XX		
AC	AAAL55269;	
XX		
DT	10-MAY-2003 (first entry)	
DE	DNA of expression vector RC77, SEQ ID NO 3.	
XX		
XX	Vector; excisable; site-specific recombinase; enzyme; exogenous;	
XX	signalling molecule; transcription factor; cell metabolism;	
XX	differentiation stage; kinase; phosphatase; ds.	
OS	Unidentified.	
PN	WO2003002735-A2.	
XX		
PD	09-JAN-2003.	
XX		
PF	28-JUN-2002; 2002WO-CA000997.	
XX		
PR	28-JUN-2001; 2001US-0301149P.	
XX		
PA	(PHEN-) PHENOGENE THERAPEUTIQUES INC.	
XX		
PI	Lancot C, Gingras R, Gaumont M;	
XX		

PN US5589392-A.
 XX 31-DEC-1996.
 XX 29-NOV-1993; 93US-00158718.
 XX 14-JAN-1991; 91US-00640983.
 XX (STRA-) STRATAGENE.
 XX Short JM;
 XX WPI; 1997-107141/10.
 XX Nucleic acid construct for gene expression - comprising DNA sequences
 PT encoding nuclear transport signal peptide and inducible repressor.
 XX Example 2; Col 43-50; 43pp; English.
 XX DNA constructs encoding a nuclear transport signal operatively linked to
 CC a DNA sequence encoding an inducible repressor are useful as vectors for
 CC expression of exogenous genes in eukaryotic cells in vitro and in vivo,
 CC e.g. for production of transgenic animals as models for human diseases.
 CC The present sequence is that of a luciferase reporter expression vector,
 CC pRSVluc. (Updated on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 7223 BP; 1880 A; 1730 C; 1864 G; 1745 T; 0 U; 4 Other;
 Query Match 93.6%; Score 247.2; DB 2; Length 7223;
 Best Local Similarity 98.5%; Pred. No. 5.3e-76;
 Matches 260; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 QY 1 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGCACATGTAACGATGAGTACCA 60
 DB 2365 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGCACATGTAACGATGAGTACCA 2424
 QY 61 TGCTTACAGAGAGAGAAAAGCAGCGTGCATGCGGATGCTGGAGTAAGTGTGAC 120
 DB 2425 TGCTTACAGAGAGAGAAAAGCAGCGTGCATGCGGATGCTGGAGTAAGTGTGAC 2484
 QY 121 TCCTGCTTATTAGGAGGCAACAGACGCTCTGCATGATGAGTGCACGACCACTAAAT 180
 DB 2485 TCCTGCTTATTAGGAGGCAACAGACGCTCTGCATGATGAGTGCACGACCACTAAAT 2544
 QY 181 CCACATTGCAGAGAT-ATTGTAATTAAGTGCCTAGCTGCATACATAAAGCCATTGAC 239
 DB 2545 CCACATTGCAGAGAT-ATTGTAATTAAGTGCCTAGCTGCATACATAAAGCCATTGAC 2604
 QY 240 CATTCACCACTTGGTGTGCACT 263
 DB 2605 CATTCACCACTTGGTGTGCACT 2628
 RESULT 53
 AAT71261
 ID AAT71261 standard; DNA; 565 BP.
 AC AAT71261;
 XX
 XX 30-MAR-1998 (first entry)
 XX Rous sarcoma virus v-src gene.
 XX Cognate transgene; v-src gene; lymphoma; cellular immunogen; cancer;
 KW self-determinant immunoreactivity; cancer vaccination; breast carcinoma;
 KW colon carcinoma; immunotherapy; proto-oncogene; rous sarcoma virus; ss.
 XX Rous sarcoma virus.
 OS
 XX W09725860-A1.
 PN 24-JUL-1997.
 XX

PF 13-JAN-1997; 97WO-US000582.
 XX 19-JAN-1996; 96US-0010262P.
 XX (UYAL-) UNIV ALLEGHENY HEALTH SCI.
 XX Halpern MS, England JM;
 XX WPI; 1997-384993/35.
 XX Proto-oncogene immunogen - used in vaccine for the prevention and
 PT treatment of cancer.
 XX Disclosure; Page 69; 81pp; English.
 PS This sequence represents the Rous sarcoma virus v-src cognate transgene
 CC (CTG). Deletion of amino acids 430-433 of the encoded protein renders the
 CC CTG non-transforming. This sequence can be used in the cellular immunogen
 CC of the invention. The cellular immunogen of the invention is for
 CC immunising against the product of a target proto-oncogene, over-
 CC expression of which is associated with cancer, comprises host cells
 CC transfected with a construct containing at least one transgene related to
 CC the proto-oncogene and driven by a strong promoter. The product of the
 CC transgene induces immunoreactivity to host self-determinants on the
 CC product of proto-oncogene. The cellular immunogens are used for
 CC protective vaccination against cancer (e.g. carcinoma of breast or colon,
 CC or various lymphomas) and for immunotherapy of cancer. Use of the
 CC immunogen eliminates the need to isolate immunogenic, HLA host-matched
 CC peptides. The method is not based on immune recognition of a determinant
 CC defined by a cancer-specific mutation and generates a systemic (anti-
 CC metastatic) response
 XX
 SQ Sequence 565 BP; 148 A; 114 C; 162 G; 141 T; 0 U; 0 Other;
 Query Match 92.7%; Score 244.8; DB 2; Length 565;
 Best Local Similarity 97.4%; Pred. No. 1.2e-75;
 Matches 261; Conservative 0; Mismatches 2; Indels 5; Gaps 1;
 QY 1 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGCACATG----GTAACGATGAGTAC 55
 DB 233 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGCACATGCTTATGTACGATGAGTAC 292
 QY 56 CAACATGCGCTTACAGGAGAGAAAAAGCAGCGTGCATGCCGATTCGTGTGAAAGTAAAGTGG 115
 DB 293 CAACATGCGCTTACAGGAGAGAAAAAGCAGCGTGCATGCCGATTCGTGTGAAAGTAAAGTGG 352
 QY 116 TAGCATCGTCCCTTTTAGAAGGCAACAGCGGTCTGCATGATGAGTGTGACGACCACT 175
 DB 353 TAGCATCGTCCCTTTTAGAAGGCAACAGCGGTCTGCATGATGAGTGTGACGACCACT 412
 QY 176 AAATTCGCAATTGCAGAGATATTGTAATTAAGTGCCTAGCTGCATACATAAAGCCATT 235
 DB 413 GAATTCGCAATTGCAGAGATATTGTAATTAAGTGCCTAGCTGCATACATAAAGCCATT 472
 QY 236 TGACCATTCACCACTTGGTGTGCACT 263
 DB 473 TGACCATTCACCACTTGGTGTGCACT 500
 RESULT 54
 AAZ60824
 ID AAZ60824 standard; DNA; 565 BP.
 XX AAZ60824;
 XX 16-MAY-2000 (first entry)
 XX Nucleotide sequence of a cognate transgene of v-src.
 XX Cognate transgene; CTG; tumorigenic; cellular immunogen; immunisation;
 KW proto-oncogene; malignancy; allogenic cell; vaccine; cancer; ss.
 XX Rat sarcoma virus.
 OS

XX WO200004927-A1.
 PN 03-FEB-2000.
 PD 08-JUL-1999; 99WO-US015594.
 PF 24-JUL-1998; 98US-0093965P.
 PR (UVAL-) UNIV ALLEGHNEY HEALTH SCI.
 PA (HALP/) HALPERN M S.
 PA (ENGL/) ENGLAND J M.
 XX Halpern MS, England JM;
 PI WPI; 2000-182543/16.
 DR Cellular immunogens comprising allogenic donor cells transfected with a
 PT construct comprising a proto-oncogene cognate, useful as cancer vaccines.
 PT Disclosure; Page 75-76; 77pp; English.
 PS The present sequence represents a cognate transgene (CTG) which is
 CC rendered non-tumorigenic by deletion of amino acids 9-155. The CTG is
 CC used in the course of the invention. The specification describes a
 CC cellular immunogen for immunizing a host against the effects of the
 CC product of a target proto-oncogene which is associated with a
 CC malignancy. The cellular immunogen comprises allogenic cells transfected
 CC with transgene construct comprising a transgene cognate to target proto-
 CC oncogene and a strong promoter. The cellular immunogen is useful for
 CC vaccinating a host against cancer by inserting the transgene construct
 CC into the body of the host for the expression of the transgene. The method
 CC of the invention is designed to target mutation-driven non-self
 CC determinants. The cellular immunogens induce reactivity for self-
 CC determinants in the over expressed product of tumour associated and over
 CC expressed proto-oncogenes
 XX SQ Sequence 565 BP; 148 A; 114 C; 162 G; 141 T; 0 U; 0 Other;
 Query Match 92.7%; Score 244.8; DB 3; Length 565;
 Best Local Similarity 97.4%; Pred. No. 1.2e-75;
 Matches 261; Conservative 0; Mismatches 2; Indels 5; Gaps 1;
 Qy 1 AATGTAGTCTTATGCAATATCTTTGTAGTCTTGTGCAATG-----GTAACGATGAGTTAG 55
 Db 233 AATGTAGTCTTATGCAATATCTTTGTAGTCTTGTGCAATGCTTATGTAACGATGAGTTAG 292
 Qy 56 CAACATGCTTACAGAGGAGAAAGACACCGTCATGCCGATGGTGGAGTAAGGTGG 115
 Db 293 CAACATGCTTACAGAGGAGAAAGACACCGTCATGCCGATGGTGGAGTAAGGTGG 352
 Qy 116 TACGATCGTCCCTTATTAGGAAGCAACAGACGGGTCTGACATGATTTGGACGACCAT 175
 Db 353 TACGATCGTCCCTTATTAGGAAGCAACAGACGGGTCTGACATGATTTGGACGACCAT 412
 Qy 176 AATTCGGATTCGACAGATTTGTTATTTAAGTCCCTAGCTCGATACAAATTAACGCCATT 235
 Db 413 GAATTCGGATTCGACAGATTTGTTATTTAAGTCCCTAGCTCGATACAAATTAACGCCATT 472
 Qy 236 TGACCATTCACACATGTTGTCACCT 263
 Db 473 TGACCATTCACACATGTTGTCACCT 500
 RESULT 55
 AAD28311
 ID AAD28311 standard; DNA; 5130 BP.
 AC AAD28311;
 XX 22-APR-2002 (first entry)
 DT LSRNL vector.

XX Regulatory element; vector; erythropoietin; growth hormone; insulin;
 KW immunoglobulin; bone morphogenetic protein; interferon; interleukin;
 KW superoxide dismutase; T-cell receptor; surface membrane protein; MoMuLV;
 KW viral antigen; transport protein; addressin; regulatory protein; MoMuLV;
 KW moloney murine leukemia virus; chimeric; hepatitis B virus; ds.
 XX Hepatitis B virus.
 OS Moloney murine leukemia virus.
 OS Unidentified.
 OS Chimeric.
 XX Key Location/Qualifiers
 FT LTR 1..589 /tag= a /note= "MoMuLV 5' LTR"
 FT misc_feature 659..897 /tag= b /note= "Retroviral packaging region"
 FT misc_feature 1034..1714 /tag= c /note= "Hepatitis B surface antigen"
 FT promoter 2279..2595 /tag= d /note= "RSV promoter"
 FT misc_feature 2951..3745 /tag= e /note= "Neomycin phosphotransferase gene"
 FT LTR 4537..5130 /tag= f /note= "MoMuLV 3' LTR"
 XX WO200202783-A2.
 PD 10-JAN-2002.
 XX 29-JUN-2001; 2001WO-US020714.
 XX 03-JUL-2000; 2000US-0215851P.
 XX (GALA-) GALA DESIGN INC.
 XX Bleck GT;
 XX WPI; 2002-154749/20.
 XX Novel regulatory elements including nucleic acid encoding hybrid alpha-
 PT lactalbumin promoter or mutant RNA export element, for expressing one or
 PT more proteins e.g. antibodies, pharmaceutical proteins in host cells.
 XX Example 1; Fig 12; 151pp; English.
 XX The invention relates to novel regulatory elements and vectors for the
 CC expression of one or more proteins in a host cell. The invention further
 CC provides methods of indirectly detecting the expression of a protein of
 CC interest, comprising providing the host cell transfected with a vector
 CC encoding a polyclonal sequence comprising a signal protein and a
 CC desired protein operably linked by an internal ribosome entry site
 CC (IRES), and culturing the host cell under suitable conditions so that the
 CC signal protein and the desired protein is produced, where the presence of
 CC elements and vectors of the invention are useful for the expression of
 CC proteins of interest in a host cell. They are useful for producing an
 CC immunoglobulin (Ig), preferably secretory Ig. They are useful in the
 CC expression of one or more proteins such as erythropoietin, growth
 CC hormone, insulin, immunoglobulins, protein C, cytokines and their
 CC receptors, hormones, Von Willebrands factor, lung surfactant, serum
 CC albumins, DNase, vascular endothelial growth factor, receptors for
 CC hormones or growth factors, rheumatoid factors, nerve growth factors, CD
 CC proteins, osteoinductive factors, immunotoxins, bone morphogenetic
 CC protein, interferons, colony stimulating factors, interleukins,
 CC superoxide dismutase, T-cell receptors, surface membrane proteins, viral
 CC antigens, transport proteins, addressins, regulatory proteins,

CC antibodies, chimeric proteins and their fragments. The vectors are
 CC particularly useful for expressing G protein coupled receptors and other
 CC transmembrane proteins. The retroviral vectors are useful for expressing
 CC proteins in mammalian tissue culture host cells, including rat fibroblast
 CC cells, bovine kidney cells and human kidney cells. The present sequence
 CC is LSRNL vector used in the invention. The vector comprises the following
 CC elements: moloney murine leukemia virus (MoMuLV) 5' LTR, MoMuLV viral
 CC packaging signal, hepatitis B surface antigen; RSV promoter; neomycin
 CC phosphotransferase gene and 3' MoMuLV LTR

SQ Sequence 5130 BP; 1187 A; 1335 C; 1332 G; 1276 T; 0 U; 0 Other;

Query Match 87.9%; Score 232; DB 6; Length 5130;
 Best Local Similarity 97.0%; Pred. No. 1e-70;
 Matches 258; Conservative 0; Mismatches 5; Indels 3; Gaps 2;

QY 1 AATGTAGTCTTATGCAATACCTTGTAGTCTTGGCAATGCTTAACGATGAGTTAGCAACA 60
 DB 2325 AATGTAGTCTTATGCAATACCTTGTAGTCTTGGCAATGCTTAACGATGAGTTAGCAACA 2384
 QY 61 TGCCTTACAGGAGAGAAAAGACACCGCTGCATGCCGATTGGTGGAGTAAGGTGCTACGA 120
 DB 2385 TGCCTTACAGGAGAGAAAAGACACCGCTGCATGCCGATTGGTGGAGTAAGGTGCTACGA 2444
 QY 121 TCGTGCCCTTATTAGGAGGCAACAGACGGGTCTGACATGATGGAGCAACCACTAAATT 180
 DB 2445 TCGTGCCCTTATTAGGAGGCAACAGACGGGTCTGACATGATGGAGCAACCACTAAATT 2504
 QY 181 CCGCATTTGACAGAGAT-ATTGATTTAAGTGCTAGCTCGATACATTAACGCCA--TTTG 237
 DB 2505 CCGCATTTGACAGAGATTTGATTTAAGTGCTAGCTCGATACATTAACGCCA--TTTG 2564
 QY 238 ACCATTACACCATTTGGTGGCACT 263
 DB 2565 ACCATTACACCATTTGGTGGCACT 2590

RESULT 56

AA028272

ID AAD28272 standard; DNA; 7170 BP.

XX AC AAD28272;

XX DT 22-APR-2002 (first entry)

XX DE LSRNL vector.

XX KW LSRNL vector; pharmaceutical; industrial; diagnostic; screening; MoMuLV;
 XX KW moloney murine leukemia virus; chimeric; hepatitis B virus; ds.
 XX OS Hepatitis B virus.
 XX OS Moloney murine leukemia virus.
 XX OS Unidentified.
 XX OS Chimeric.

XX PH Key Location/Qualifiers

XX LTR 1..589

XX /*tag= a

XX /*note= "MoMuLV 5' LTR"

XX misc_feature 659..857

XX /*tag= b

XX /*note= "retroviral packaging region"

XX misc_feature 1034..1714

XX /*tag= c

XX /*note= "Hepatitis B surface antigen"

XX promoter 2279..2595

XX /*tag= d

XX /*note= "RSV promoter"

XX misc_feature 2951..3745

XX /*tag= e

XX /*note= "Neomycin phosphotransferase gene"

XX LTR 4537..5130

XX /*tag= f

FT /note= "MoMuLV 3' LTR"

XX W0200202738-A2.

XX PD 10-JAN-2002.

XX PF 29-JUN-2001; 2001WO-US020710.

XX PR 03-JUL-2000; 2000US-0215925P.

XX PA (GALA-) GALA DESIGN INC.

XX PI Bremel RD, Millier LU, Black GT, York D;

XX DR WPI; 2002-154737/20.

XX PS Example 1; Fig 12; 191pp; English.

CC The invention relates to a host cell comprising a genome having at least
 CC two integrated integrating vectors. The integrating vectors comprise at
 CC least one exogenous gene operably linked to a promoter. The host cell is
 CC useful for producing a desired protein and for comparing protein
 CC functions. The host cells comprises a reporter gene which is from gene
 CC fluorescent protein, luciferase, beta-galactosidase and beta-lactamase,
 CC and the assaying step further comprises detecting a signal from the
 CC reporter gene. The desired protein includes proteins for pharmaceutical,
 CC industrial, diagnostic and other purposes. The host cells is useful for
 CC indirectly detecting the expression of a desired protein, comprising
 CC providing the host cell transfected with a vector encoding a
 CC polycistronic sequence comprising a signal protein and a desired protein
 CC operably linked by an internal ribosome entry site (IRES), and culturing
 CC the host cell under suitable conditions so that the signal protein and
 CC the desired protein is produced, where the presence of signal protein
 CC indicates the presence of desired protein. The present sequence is LSRNL
 CC vector used in the invention. The vector comprises the following
 CC elements: moloney murine leukemia virus (MoMuLV) 5' LTR, MoMuLV viral
 CC packaging signal, hepatitis B surface antigen; RSV promoter; neomycin
 CC phosphotransferase gene and 3' MoMuLV LTR

SQ Sequence 7170 BP; 1688 A; 1891 C; 1841 G; 1750 T; 0 U; 0 Other;

Query Match 87.9%; Score 232; DB 6; Length 7170;
 Best Local Similarity 97.0%; Pred. No. 1.2e-70;
 Matches 258; Conservative 0; Mismatches 5; Indels 3; Gaps 2;

QY 1 AATGTAGTCTTATGCAATACCTTGTAGTCTTGGCAATGCTTAACGATGAGTTAGCAACA 60
 DB 4365 AATGTAGTCTTATGCAATACCTTGTAGTCTTGGCAATGCTTAACGATGAGTTAGCAACA 4424
 QY 61 TGCCTTACAGGAGAGAAAAGACACCGCTGCATGCCGATTGGTGGAGTAAGGTGCTACGA 120
 DB 4425 TGCCTTACAGGAGAGAAAAGACACCGCTGCATGCCGATTGGTGGAGTAAGGTGCTACGA 4484
 QY 121 TCGTGCCCTTATTAGGAGGCAACAGACGGGTCTGACATGATGGAGCAACCACTAAATT 180
 DB 4485 TCGTGCCCTTATTAGGAGGCAACAGACGGGTCTGACATGATGGAGCAACCACTAAATT 4544
 QY 181 CCGCATTTGACAGAGAT-ATTGATTTAAGTGCTAGCTCGATACATTAACGCCA--TTTG 237
 DB 4545 CCGCATTTGACAGAGATTTGATTTAAGTGCTAGCTCGATACATTAACGCCA--TTTG 4604
 QY 238 ACCATTACACCATTTGGTGGCACT 263
 DB 4605 ACCATTACACCATTTGGTGGCACT 4630

RESULT 57

ACD27899

ID ACD27899 standard; DNA; 10460 BP.

Db		 284 TGACCATTCACCACATTGGTGTGCACCTC 312
RESULT 59		
AAQ06311		
ID	AAQ06311 standard; DNA; 3276 BP.	
XX	XX	
AC	AAQ06311;	
XX	XX	
DT	25-MAR-2003 (revised)	
DT	29-JAN-1991 (first entry)	
XX	XX	
DE	Sequence of plasmid p238BGL.	
KX	IFN-gamma receptor; autoimmune disease; multiple sclerosis;	
KW	hypersensitivity; ds.	
XX	XX	
OS	Homo sapiens.	
XX	XX	
FH	Key Location/Qualifiers	
FT	CDS 243..426	
FT	/tag= b	
FT	Sig-peptide 243..405	
FT	/tag= c	
FT	/label= S.P.1	
FT	LTR 279..242	
FT	/tag= a	
FT	polyA_signal 585...590	
FT	/tag= d	
XX	XX	
FN	EP993502-A.	
PD	24-OCT-1990.	
PF	11-APR-1990; 90EP-00106992.	
PR	19-APR-1989; 89EP-00810295.	
XX	(HOFF) HOFFMANN-LA ROCHE AG.	
PA	Fountoulak M, Garotta G, Stuber D;	
PI	WPL; 1990-322042/43.	
XX	P-PSDB; AAR07066.	
DR	XX	
PT	Soluble interferon-gamma receptors - for treating auto-immune diseases,	
PT	chronic inflammations, etc.	
XX	Disclosure; Fig 5l; 174pp; English.	
PS	XX	
CC	IFN-gamma is a therapeutically active agent in the treatment of	
CC	autoimmune disease, allograft transplant rejections, multiple sclerosis,	
CC	chronic inflammations and delayed hypersensitivity. It is also useful in	
CC	identifying IFN-gamma agonists and antagonists. See also AAQ06301.	
CC	(Updated on 25-MAR-2003 to correct PR field.)	
XX	XX	
SQ	Sequence 3276 BP; 814 A; 794 C; 914 G; 754 T; 0 U; 0 Other;	
	Query Match 80.7%; Score 213; DB 2; Length 3276;	
	Best Local Similarity 92.2%; Pred. No. 4.2e-64;	
	Matches 248; Conservative 0; Mismatches 15; Indels 6; Gaps 2	
QY	1 AATGTAAGTTTATCGAATACTCTTGTAAGTTCGAACATG-----GTACAGATGAGTAG 55	
Db	45 AATGTAGCCTTTATGCAATACTCTTGTAAGTTCGAACATG-----GTACAGATGAGTAG 104	
QY	56 CAACATGCTTACAAGGAGAGAAAAGCACCGTGCAATGCCGATTGCTGAAGTAAGGTGG 115	
Db	105 CACATGCTTACAAGGAGAGAAAAGCACCGTGCAATGCCGATTGCTGAAGTAAGGTGG 164	
QY	116 TAGCATCGTCCTTTATTAGGAAGGCACACAGACGGGCTTCGACATGGATTGGACGAACCAT 175	

Db 105 CACATGCGCTTACAGAGGAGAAAAGCACCGCTGCGATGCCGATGGTGGAGTAAGGTGG 164
 QY 116 TACGATCGTGCTTATTAGAGAGGCAACAGACGGGTCTGCATGATGGAGCAACCACT 175
 Db 165 TA-GATCGTGCGCTTATTAGAGAGGCAACAGACGGGTCTGCATGATGGAGCAACCACT 223
 QY 176 AAATTCGGCATTCGACAGAGATATTGTTTAAAGTGCCTAGCTCGATACAAATAAAGCGCAATT 235
 Db 224 GAATTCGCATTGCAGAGAGATATTGTTTAAAGTGCCTAGCTCGATACAAATAAAGCGCAATT 283
 QY 236 TGACCAATTACCAATTCGGTGCACCTC 264
 Db 284 TGACCAATTCACCAATTCGGTGCACCTC 312

RESULT 61

AAQ06313
 ID AAQ06313 standard; DNA; 3427 BP.

XX AC AAQ06313;

XX 25-MAR-2003 (revised)
 DT 29-JAN-1991 (first entry)

XX Sequence of plasmid p267BGL.

XX IFN-gamma receptor; autoimmune disease; multiple sclerosis;
 KW hypersensitivity; ds.

XX Homo sapiens.

XX Key Location/Qualifiers
 FH 279..492
 FT LTR /*tag= a
 FT CDS 493..585
 FT /*tag= b
 FT Sig-peptide 493..564
 FT /*tag= c
 FT polyA_signal /label= S.P.2
 FT 736..741
 FT /*tag= d

XX EF393502-A.

XX 24-OCT-1990.

XX 11-APR-1990; 90EP-00106992.

XX 19-APR-1989; 89EP-00810295.

XX (HOFF) HOFFMANN-LA ROCHE AG.

XX Fountoulak M, Garotta G, Stuber D;

XX WPI; 1990-322042/43.

XX P-PSDB; AAR07067.

XX Soluble interferon-gamma receptors - for treating auto-immune diseases,
 XX chronic inflammations, etc.

XX Disclosure; Fig 59; 174pp; English.

XX IFN-gamma is a therapeutically active agent in the treatment of
 CC autoimmune disease, allograft transplant rejections, multiple sclerosis,
 CC chronic inflammations and delayed hypersensitivity. It is also useful in
 CC identifying IFN-gamma agonists and antagonists. See also AAQ06301.
 CC (Updated on 25-MAR-2003 to correct PR field.)

XX Query Match 80.7%; Score 213; DB 2; Length 3427;
 XX Best Local Similarity 92.2%; Pred. No. 4.3e-64;
 XX Matches 248; Conservative 0; Mismatches 15; Indels 6; Gaps 2;

QY 1 AATGAGTCTTATGCAATACCTCTTGTAGTCTTTGCACATG-----CTAACGATGAGTTAG 55
 Db 45 AATGAGTCTTATGCAATACCTCTTGTAGTCTTTGCACATGCTTATGTAACGATGAGTTAG 104
 QY 56 CAACATGCGCTTACAAGGAGAGAAAAAGCACCGTCGATGCCGATTTGGTGAAGTAAGGTGG 115
 Db 105 CAACATGCGCTTACAAGGAGAGAAAAAGCACCGTCGATGCCGATTTGGTGAAGTAAGGTGG 164
 QY 116 TACGATCGTGCTTATTAGAGAGGCAACAGACGGGTCTGCATGATGGAGCAACCACT 175
 Db 165 TA-GATCGTGCGCTTATTAGAGAGGCAACAGACGGGTCTGCATGATGGAGCAACCACT 223
 QY 176 AAATTCGGCATTCGACAGAGATATTGTTTAAAGTGCCTAGCTCGATACAAATAAAGCGCAATT 235
 Db 224 GAATTCGCATTGCAGAGAGATATTGTTTAAAGTGCCTAGCTCGATACAAATAAAGCGCAATT 283
 QY 236 TGACCAATTCACCAATTCGGTGCACCTC 264
 Db 284 TGACCAATTCACCAATTCGGTGCACCTC 312

RESULT 62

AAQ06312
 ID AAQ06312 standard; DNA; 3979 BP.

XX AC AAQ06312;

XX 25-MAR-2003 (revised)
 DT 29-JAN-1991 (first entry)

XX Sequence of plasmid p264BGL.

XX IFN-gamma receptor; autoimmune disease; multiple sclerosis;
 KW hypersensitivity; ds.

XX Homo sapiens.

XX Key Location/Qualifiers
 FH 243..426
 FT CDS /*tag= b
 FT Sig-peptide 243..405
 FT /*tag= c
 FT /label= S.P.1
 FT LTR 279..242
 FT /*tag= a
 FT polyA_signal 1288..1292
 FT /*tag= d

XX EF393502-A.

XX 24-OCT-1990.

XX 11-APR-1990; 90EP-00106992.

XX 19-APR-1989; 89EP-00810295.

XX (HOFF) HOFFMANN-LA ROCHE AG.

XX Fountoulak M, Garotta G, Stuber D;

XX WPI; 1990-322042/43.

XX P-PSDB; AAR07066.

XX Soluble interferon-gamma receptors - for treating auto-immune diseases,
 XX chronic inflammations, etc.

XX Disclosure; Fig 55; 174pp; English.

XX IFN-gamma is a therapeutically active agent in the treatment of
 CC autoimmune disease, allograft transplant rejections, multiple sclerosis,
 CC chronic inflammations and delayed hypersensitivity. It is also useful in
 CC identifying IFN-gamma agonists and antagonists. See also AAQ06301.

Example 13; Fig 13A-C; 56pp; Japanese.

RESULT 66	
AAZ27850	
ID	AAZ27850 standard; cDNA; 11282 BP.
XX	
AC	AAZ27850;
XX	
XX	
DT	23-DEC-1999 (first entry)
XX	
XX	Complete cDNA sequence of pCYTts.
XX	
KW	Gene expression system; cis-acting element; gene therapy;
KW	temperature-sensitive RNA-dependent RNA polymerase;
KW	inducible alphaviral gene expression system; pCYTts;
KW	hormone-based gene control system; tetracycline gene control system; ss.
XX	
OS	Synthetic.
XX	
PN	W09950432-K1.
XX	
XX	
PD	07-OCT-1999.
XX	
PF	25-MAR-1999; 99MO-IB000523.
XX	
PR	27-MAR-1998; 98US-0079562P.
XX	
PA	(CYTO-) CYTOS BIOTECHNOLOGY AG.
PA	(RENN/) RENNER W A.
PA	(NIEB/) NIEBA L.
PA	(BOOR/) BOORSMA M.
XX	
PI	Renner WA. Nieba L. Boorsma M.

XX DR WPI; 1999-591327/50.
 XX PT A new system to regulate gene expression in eukaryotic cells.
 XX PS Claim 15; Fig 3; 99pp; English.
 XX CC This sequence represents the complete cDNA sequence for the vector
 CC pCvYts. The invention relates to a DNA molecule comprising a
 CC polynucleotide (I) encoding an RNA molecule. The encoded RNA comprises:
 CC (a) at least one cis-acting element; (b) an open reading frame (ORF1)
 CC encoding a non-cyclophatic, temperature-sensitive RNA-dependent RNA
 CC polymerase; and (c) a second sequence that is: (i) a protein-encoding ORF
 CC (ORF2) that is in a translatable format after RNA-dependent RNA
 CC replication event(s); (ii) a sequence complementary to the ORF2; or (iii)
 CC a sequence encoding an untranslated RNA molecule. The pCvYts sequence is
 CC an example of the DNA molecule, and is an inducible alphavirus gene
 CC expression system. The invention is used in gene therapy and recombinant
 CC technology to regulate expression of introduced genes. The invention does
 CC not have the problems of toxicity and/or high basal level expression
 CC associated with prior art tetracycline-based and hormone-based gene
 CC control systems
 XX CC
 XX SQ Sequence 11282 BP; 3152 A; 2821 C; 2767 G; 2542 T; 0 U; 0 Other;
 Query Match 77.7%; Score 205.2; DB 2; Length 11282;
 Best Local Similarity 98.6%; Pred. No. 4e-61;
 Matches 207; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 ATGAGTCTTATGCAATACCTCTTGTAGCTTTCGCAACATGTTAGAGTACCAACAT 61
 Db 664 ATCCAGTCTTATGCAATACCTCTTGTAGCTTTCGCAACATGTTAGAGTACCAACAT 723
 QY 62 GCCTTACAG 121
 Db 724 GCCTTACAG 783
 QY 122 CGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGAGTGGACGACCACTAAATTC 181
 Db 784 CGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGAGTGGACGACCACTAAATTC 843
 QY 182 CGCATTCGACAGATATTGTATTATTAAGTCCC 211
 Db 844 CGCATTCGACAGATATTGTATTATTAAGTCCC 873
 RESULT 67
 AAD04741
 ID AAD04741 standard; cDNA; 11282 BP.
 AC AAD04741;
 XX 17-JUL-2001 (first entry)
 XX Alphaviral vector pCvYts cDNA.
 XX pCvYts; alphaviral vector; vaccine; therapy; cancer; antiparasitic;
 KW antimalarial; anticancer; anti-HIV; antiviral; infectious disease;
 KW Human immunodeficiency virus; HIV; influenza; passive immunisation;
 KW carcinoma; liver; skin; stomach; ovarian tumour; ss.
 XX Rous sarcoma virus.
 OS Alphavirus.
 OS Unidentified.
 OS Chimeric.
 XX WO200130989-A2.
 PN 03-MAY-2001.
 XX 26-OCT-2000; 2000WO-1B001557.
 XX 27-OCT-1999; 99US-016796P.

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA (RENN/) RENNER W A.
 PA (NIEB/) NIEBA L.
 XX Renner WA, Nieba L;
 XX WPI; 2001-308631/32.
 XX Preparing alphaviral vectors with mutations in a selected gene, for use
 PT as vaccines, particularly against pathogens that mutate rapidly,
 PT comprises replicating in the presence of a nucleoside analog.
 XX Claim 6; Fig 3; 103pp; English.
 XX The present invention relates to a method for preparing viral vectors
 CC which comprises inserting a gene of interest into an alphaviral vector
 CC such as pCvYts, pinRep5 and replicating the vector in the presence of
 CC alphaviral replicase and nucleoside analogues (5'azacytidine (AZT), FU-
 CC 5' fluorouridine) to produce a modified gene of interest. The replication
 CC is repeated until the modified gene in 90 % of the vector population
 CC contain a mutation in the modified gene which is 90-99 % identical with
 CC the gene of interest. The vector populations are used in vaccines for
 CC treatment or prevention of a wide variety of infectious diseases (viral
 CC or parasitic, e.g. human immuno deficiency virus (HIV), influenza,
 CC Trypanosoma or Plasmodium) and cancers such as liver carcinoma, stomach
 CC carcinoma, skin carcinoma and ovarian tumours. Vaccines containing the
 CC mutant populations will therefore be effective against viral escape
 CC mutants. Mutagenesis in a eukaryotic cell ensures that expressed proteins
 CC are correctly glycosylated. Antisera raised against the vaccines can be
 CC used for passive immunisation. The present cDNA sequence is an alphaviral
 CC vector pCvYts. The vector contains Rous Sarcoma Virus promoter, cis-
 CC acting sequence elements, non-structural proteins 1-4, gene of interest,
 CC alphavirus subgenomic promoter, ampicillin resistance marker for
 CC selection and a CoIE1 sequence for bacterial amplification
 XX SQ Sequence 11282 BP; 3152 A; 2821 C; 2767 G; 2542 T; 0 U; 0 Other;
 Query Match 77.7%; Score 205.2; DB 4; Length 11282;
 Best Local Similarity 98.6%; Pred. No. 4e-61;
 Matches 207; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 ATGAGTCTTATGCAATACCTCTTGTAGCTTTCGCAACATGTTAGAGTACCAACAT 61
 Db 664 ATCCAGTCTTATGCAATACCTCTTGTAGCTTTCGCAACATGTTAGAGTACCAACAT 723
 QY 62 GCCTTACAG 121
 Db 724 GCCTTACAG 783
 QY 122 CGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGAGTGGACGACCACTAAATTC 181
 Db 784 CGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGAGTGGACGACCACTAAATTC 843
 QY 182 CGCATTCGACAGATATTGTATTATTAAGTCCC 211
 Db 844 CGCATTCGACAGATATTGTATTATTAAGTCCC 873
 RESULT 68
 AAF84024
 ID AAF84024 standard; cDNA; 11282 BP.
 XX AAF84024;
 XX 22-AUG-2001 (first entry)
 DT Complete cDNA sequence of plasmid pCvYt.
 XX pCvYt; cellular; taxol; gene therapy; RNA replication; endogenous gene;
 KW ss.
 XX Synthetic.

XX PN WO200142442-A2.
 XX PD 14-JUN-2001.
 XX PF 08-DEC-2000; 2000WO-IB001841.
 XX PR 10-DEC-1999; 99US-0169988P.
 XX PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 XX PI Hennecke F, Renner WA;
 XX DR WPI; 2001-381672/40.
 XX PT Modifying endogenous target gene expression in eukaryotic cell for
 PT performing gene therapy, involves inserting exogenous polynucleotides in
 PT gene to produce recombinant eukaryotic host cell and culturing the cell.
 XX PS Disclosure; Fig 8A-D; 131pp; English.
 XX CC The invention relates to a method of modifying expression characteristics
 CC of an endogenous target gene within a genome of a eukaryotic cell or
 CC producing a polypeptide encoded by the target gene of a eukaryotic cell.
 CC The method involves inserting exogenous polynucleotides in 5' and 3'
 CC regions flanking the coding region of target gene to produce a
 CC recombinant eukaryotic host cell, and culturing the cell. The method is
 CC useful for producing cells which exhibit increased expression of
 CC endogenous genes which lead to the production of additional products, and
 CC for amplifying endogenous genes involved in the production of cellular
 CC products such as taxol. The method is also useful for producing the
 CC biological products, and their derivatives, and for regulating the
 CC activity of target genes by modifying the expression of regulatory
 CC proteins involved in the regulation of the target genes. The method or a
 CC DNA vector system is useful for performing gene therapy on an individual
 CC (e.g., domesticated animal or human). The present sequence represents the
 CC complete cDNA sequence of a vector pCYTs, a DNA vector system for
 CC modifying the expression characteristics of an endogenous target gene
 CC within the genome of a eukaryotic cell comprising a 5' targeting
 CC construct and a 3' targeting construct, where the 5' and 3' targeting
 CC construct encode genetic elements required for RNA replication
 XX SQ Sequence 11282 BP; 3152 A; 2821 C; 2767 G; 2542 T; 0 U; 0 Other;
 Query Match 77.7%; Score 205.2; DB 5; Length 11282;
 Best Local Similarity 98.6%; Pred. No. 4e-61;
 Matches 207; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 ATGTAGCTTATGCACTCTTTGAGTCTTGCAACATGTTAAGTGTAGTACAT 61
 Db 654 ATCCAGTCTTATGCACTCTTTGAGTCTTGCAACATGTTAAGTGTAGTACAT 723
 QY 62 GCCTTACAGGAGAGAAAGACCGTGCATGCCGATTTGGTGAAGTGTAGTACAT 121
 Db 724 GCCTTACAGGAGAGAGAAAGACCGTGCATGCCGATTTGGTGAAGTGTAGTACAT 783
 QY 122 CGTGCCTTTATTAGGAGGCAACAGACGGGTCTTGACATGGATTGGACCACTAAATTC 181
 Db 784 CGTGCCTTTATTAGGAGGCAACAGACGGGTCTTGACATGGATTGGACCACTAAATTC 843
 QY 182 CGCATTTGCAGAGATATTTGATTTAAGTGC 211
 Db 844 CGCATTTGCAGAGATATTTGATTTAAGTGC 873
 RESULT 69
 ABK10062
 ID ABK10062 standard; DNA; 5283 BP.
 XX AC ABK10062;
 XX XX
 DT 21-MAY-2002 (first entry)
 XX XX

DE Expression vector construct pVGI.1 containing VEGF-2 insert.
 XX Human; vascular endothelial growth factor 2; VEGF-2; ds; pVGI.1;
 KW chronic limb ischaemia; myocardial ischaemia; autoimmune disorder; pHE4a;
 KW allergic reaction; organ rejection; inflammatory condition; arrhythmia;
 KW hyperproliferative disorder; viral infection; bacterial infection;
 KW fungal infection; parasitic infection; cardiovascular disorder; embolism;
 KW heart valve disease; aneurysm; arterial occlusive disorder; gene therapy.
 XX OS Synthetic.
 XX PN WO200211769-A1.
 XX PD 14-FEB-2002.
 XX PF 03-AUG-2001; 2001WO-US024658.
 XX PR 04-AUG-2000; 2000US-0223276P.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PI Coleman TA;
 XX DR WPI; 2002-217153/27.
 XX PT Isolated nucleic acid having expression vector construct with vascular
 PT endothelial growth factor-2 insert, useful for treating chronic limb
 PT ischaemia or myocardial ischaemia, autoimmune disorders and allergic
 PT conditions.
 XX FS Disclosure; Fig 31; 241pp; English.
 XX CC The invention relates to an isolated nucleic acid comprising pVGI.1
 CC expression vector construct containing the vascular endothelial growth
 CC factor 2 (VEGF-2) insert. The nucleic acid is useful for producing a host
 CC cell by transducing, transforming or transfecting a host cell with the
 CC DNA and for treating a patient having chronic limb ischaemia or
 CC myocardial ischaemia, or a disease or disorder selected from autoimmune
 CC disorders (e.g. rheumatoid arthritis, dermatitis), allergic reactions or
 CC conditions (e.g. asthma), organ rejection, inflammatory conditions (e.g.
 CC Crohn's disease), hyperproliferative disorders (e.g. Gaucher's disease),
 CC diseases due to viral, bacterial, fungal or parasitic infection,
 CC cardiovascular disorders (e.g. cardiomyopathy), arrhythmia, heart valve
 CC diseases, aneurysms, arterial occlusive disorders and embolism. This
 CC sequence represents the pVGI.1 expression vector containing the VEGF-2
 CC insert
 XX SQ Sequence 5283 BP; 1244 A; 1422 C; 1417 G; 1200 T; 0 U; 0 Other;
 Query Match 71.1%; Score 187.6; DB 6; Length 5283;
 Best Local Similarity 91.5%; Pred. No. 4.6e-55;
 Matches 214; Conservative 0; Mismatches 9; Indels 11; Gaps 1;
 QY 41 GTACGATGAGTTAGCAACATGCTTACAGGAGAGAAAAGCAGCGTGCATGCCGATTG 100
 Db 252 GTACGATGAGTTAGCAACATGCTTACAGGAGAGAAAAGCAGCGTGCATGCCGATTG 311
 QY 101 GTGGAAGTAAAG-----GTGGTACGATCGTCTTTATTAGGAAGGCAACAGACGG 149
 Db 312 GTGGGAGTAAAGTGTATGATCGTGTATGATCGTCTTTATTAGGAAGGCAACAGACGG 371
 QY 150 GTCTGACATGAGTTGGAGCAACCACTAAATTCGCGATTCGAGAGATATTTATTAAAGTG 209
 Db 372 GTCTTAACAGGATTGGAGCAACCACTGAATTCGCGATTCGAGAGATATTTATTAAAGTG 431
 QY 210 CCTAGCTCGATACATAAAGCCATTTGACCATTCACCATTTGGTGTGCACCT 263
 Db 432 CCCAGCTCGATACATAAAGCCATTTGACCATTCACCATTTGGTGTGCACCT 485
 RESULT 70
 AAD53272
 ID AAD53272 standard; DNA; 4993 BP.

XX AC AAD53272;
 XX DT 28-MAY-2003 (first entry)
 XX DE MESV2/EGFP/RSV retroviral vector DNA.
 XX KW Retroviral vector; congenital disease; cancer; Parkinson's disease;
 XX KW Alzheimer's disease; gene therapy; retroviral DNA; ds.
 XX OS Retrovirus.
 XX PN WO200294989-A2.
 XX PD 28-NOV-2002.
 XX PF 17-MAY-2002; 2002WO-US015816.
 XX PR 18-MAY-2001; 2001US-0292201P.
 XX PR 30-NOV-2001; 2001US-0334972P.
 XX PA (SCRI) SCRIPPS RES INST.
 XX PI Edelman GM, Owens G;
 XX DR WPI; 2003-140366/13.
 XX PT New retroviral vector plasmid for introducing expressible polynucleotides
 PT into cells, comprises a retrovirus long terminal repeat having U5, R and
 PT U3 regions, a constitutive transport element, and a cloning site.
 XX PS Claim 18; Col 95-97; 61pp; English.
 XX CC The invention relates to novel retroviral vector plasmids for introducing
 CC expressible polynucleotides into cells. The vectors comprise a retrovirus
 CC long terminal repeat (LTR) having U5, R and U3 regions, a constitutive
 CC transport element (CRE) and a cloning site. The retroviral vector plasmid
 CC is useful in introducing an expressible polynucleotide into a cell such
 CC as a neural stem cell and in treating or ameliorating a pathologic
 CC condition in a subject such as a congenital diseases, cancer, Parkinson's
 CC disease or Alzheimer's disease. The plasmid may also be used to produce
 CC retroviral vectors useful for delivering genes into eukaryotic cells in
 CC culture and in living organisms. Sequences of the invention are also
 CC useful in gene therapy. The present sequence is MESV2/EGFP/RSV retroviral
 CC vector DNA
 XX SQ Sequence 4993 BP; 1206 A; 1328 C; 1303 G; 1156 T; 0 U; 0 Other;
 Query Match 66.0%; Score 174.2; DB 7; Length 4993;
 Best Local Similarity 98.3%; Pred. No. 2.4e-50;
 Matches 176; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 AATGTAGCTTATGCATCACTCTTGTAGTCTTGCACATGGTAACGATGATTAGCA 60
 Db 1908 AATGTAGCTTATGCATCACTCTTGTAGTCTTGCACATGGTAACGATGATTAGCA 1967
 QY 61 TGCCTTACAGGAGAGAAAAGCAGCGGTGATGCGCATGCGCAATGGTGAAGTAAAGTGGTACGA 120
 Db 1968 TGCCTTACAGGAGAGAAAAGCAGCGGTGATGCGCATGCGCAATGGTGAAGTAAAGTGGTACGA 2027
 QY 121 TCGTGCCTTATTAGAGGCAACAGACGCGGTCTGACATGGATTGGACGACACCACTAAAT 179
 Db 2028 TCGTGCCTTATTAGAGGCAACAGACGCGGTCTGACATGGATTGGACGACACCACTAGAT 2086
 RESULT 71
 AAD53270
 ID AAD53270 standard; DNA; 5643 BP.
 XX AC AAD53270;
 XX DT 28-MAY-2003 (first entry)
 XX

DE MESV2/ACTE/IRESEGF retroviral vector DNA.
 XX KW Retroviral vector; congenital disease; cancer; Parkinson's disease;
 XX KW Alzheimer's disease; gene therapy; retroviral DNA; ds.
 XX OS Retrovirus.
 XX PN WO200294989-A2.
 XX PD 28-NOV-2002.
 XX PF 17-MAY-2002; 2002WO-US015816.
 XX PR 18-MAY-2001; 2001US-0292201P.
 XX PR 30-NOV-2001; 2001US-0334972P.
 XX PA (SCRI) SCRIPPS RES INST.
 XX PI Edelman GM, Owens G;
 XX DR WPI; 2003-140366/13.
 XX PT New retroviral vector plasmid for introducing expressible polynucleotides
 PT into cells, comprises a retrovirus long terminal repeat having U5, R and
 PT U3 regions, a constitutive transport element, and a cloning site.
 XX PS Claim 18; Col 98-91; 61pp; English.
 XX CC The invention relates to novel retroviral vector plasmids for introducing
 CC expressible polynucleotides into cells. The vectors comprise a retrovirus
 CC long terminal repeat (LTR) having U5, R and U3 regions, a constitutive
 CC transport element (CRE) and a cloning site. The retroviral vector plasmid
 CC is useful in introducing an expressible polynucleotide into a cell such
 CC as a neural stem cell and in treating or ameliorating a pathologic
 CC condition in a subject such as a congenital diseases, cancer, Parkinson's
 CC disease or Alzheimer's disease. The plasmid may also be used to produce
 CC retroviral vectors useful for delivering genes into eukaryotic cells in
 CC culture and in living organisms. Sequences of the invention are also
 CC useful in gene therapy. The present sequence is MESV2/ACTE/IRESEGF
 CC retroviral vector DNA
 XX SQ Sequence 5643 BP; 1356 A; 1505 C; 1472 G; 1310 T; 0 U; 0 Other;
 Query Match 66.0%; Score 174.2; DB 7; Length 5643;
 Best Local Similarity 98.3%; Pred. No. 2.5e-50;
 Matches 176; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 AATGTAGCTTATGCATCACTCTTGTAGTCTTGCACATGGTAACGATGATTAGCA 60
 Db 2558 AATGTAGCTTATGCATCACTCTTGTAGTCTTGCACATGGTAACGATGATTAGCA 2617
 QY 61 TGCCTTACAGGAGAGAAAAGCAGCGGTGATGCGCATGCGCAATGGTGAAGTAAAGTGGTACGA 120
 Db 2618 TGCCTTACAGGAGAGAAAAGCAGCGGTGATGCGCATGCGCAATGGTGAAGTAAAGTGGTACGA 2677
 QY 121 TCGTGCCTTATTAGAGGCAACAGACGCGGTCTGACATGGATTGGACGACCACTAAAT 179
 Db 2678 TCGTGCCTTATTAGAGGCAACAGACGCGGTCTGACATGGATTGGACGACCACTAGAT 2736
 RESULT 72
 AAD53271
 ID AAD53271 standard; DNA; 5643 BP.
 XX AC AAD53271;
 XX DT 28-MAY-2003 (first entry)
 XX DE MESV2/IRESEGF/RSV retroviral vector DNA.
 XX KW Retroviral vector; congenital disease; cancer; Parkinson's disease;
 XX KW Alzheimer's disease; gene therapy; retroviral DNA; ds.
 XX

OS Retrovirus.
 XX WO200294989-A2.
 XX
 XX 28-NOV-2002.
 XX
 XX 17-MAY-2002; 2002WO-US015816.
 XX
 XX 18-MAY-2001; 2001US-0292201P.
 PR 30-NOV-2001; 2001US-0334972P.
 XX (SCRI) SCRIPPS RES INST.
 XX Edelman GM, Owens G;
 XX WPI; 2003-140366/13.
 XX
 XX New retroviral vector plasmid for introducing expressible polynucleotides
 PT into cells, comprises a retrovirus long terminal repeat having U5, R and
 PT U3 regions, a constitutive transport element, and a cloning site.
 PT
 XX
 XX Claim 18; Col 91-94; 61pp; English.
 XX
 XX The invention relates to novel retroviral vector plasmids for introducing
 CC expressible polynucleotides into cells. The vectors comprise a retrovirus
 CC long terminal repeat (LTR) having U5, R and U3 regions, a constitutive
 CC transport element (CRE) and a cloning site. The retroviral vector plasmid
 CC is useful in introducing an expressible polynucleotide into a cell such
 CC as a neural stem cell and in treating or ameliorating a pathologic
 CC condition in a subject such as a congenital diseases, cancer, Parkinson's
 CC disease or Alzheimer's disease. The plasmid may also be used to produce
 CC retroviral vectors useful for delivering genes into eukaryotic cells in
 CC culture and in living organisms. Sequences of the invention are also
 CC useful in gene therapy. The present sequence is MESV2/IRESEGFP/RSV
 CC retroviral vector DNA
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 XX Sequence 5643 BP; 1356 A; 1506 C; 1472 G; 1309 T; 0 U; 0 Other;
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 Best Local Similarity 98.3%; Pred. No. 2.5e-50;
 Matches 176; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 AATGTAGTCTTATGCAATACACTTTGTAGTCTTGTGCAATGTTGCAATGTTAGTACCA 60
 DB 2558 AATGTAGTCTTATGCAATACACTTTGTAGTCTTGTGCAATGTTGCAATGTTAGTACCA 2617
 QY 61 TGCCTTACAGGAGAGAAAAGCACCGTGCATGCCGATTTGGTGGAGTAAAGTGTACGA 120
 DB 2618 TGCCTTACAGGAGAGAAAAGCACCGTGCATGCCGATTTGGTGGAGTAAAGTGTACGA 2677
 QY 121 TCGTGCCTTATTAGGAGGCAACAGACCGGCTCTGACATGATTTGACCACTAAAT 179
 DB 2678 TCGTGCCTTATTAGGAGGCAACAGACAGGCTCTGACATGATTTGACCACTAAAT 2736
 RESULT 73
 AAD14296
 ID AAD14296 standard; DNA; 6250 BP.
 XX
 XX AAD14296;
 XX
 XX 06-NOV-2001 (first entry)
 XX
 XX MESVR/EGFP/ECFP/RSVPro(ori) vector.
 XX
 XX Transcriptional regulatory element; translational regulatory element;
 KW gene expression; diagnostic application; therapeutic application; MESVR;
 KW retrovirus vector; enhanced green fluorescent protein; EGFP; IRES;
 KW internal ribosome entry sequence; ori; origin of replication; SV40; ECFP;
 KW enhanced cyan fluorescent protein; ds.
 XX
 XX Murine embryonic stem cell virus.
 OS Rous sarcoma virus.

OS Rhesus macaque polyoma virus.
 OS Synthetic.
 OS Chimeric.
 XX WO200155371-A1.
 XX
 XX 02-AUG-2001.
 XX
 XX 26-JAN-2001; 2001WO-US002733.
 XX
 XX 28-JAN-2000; 2000US-0178816P.
 PR 02-MAR-2000; 2000US-0186496P.
 PR 30-MAY-2000; 2000US-0207804P.
 PR 07-SEP-2000; 2000US-0230852P.
 PR 07-SEP-2000; 2000US-0230956P.
 PR 12-JAN-2001; 2001US-0261312P.
 XX
 XX (SCRI) SCRIPPS RES INST.
 XX
 XX Mauro VP, Edelman GM, Chappell GM, Jones FS, Owens G, Meech R;
 PI WPI; 2001-483242/52.
 XX
 XX Identifying oligonucleotides with transcriptional/translational
 PT regulatory activity in eukaryotic cells by integrating an oligonucleotide
 PT into cell genome and detecting a change in expression of expressible
 PT polynucleotides.
 XX
 XX Claim 103; Page 156-160; 172pp; English.
 XX
 XX The present invention relates to a method for the identification of an
 CC oligonucleotide with transcriptional/translational regulatory activity in
 CC a eukaryotic cell. The method involves integrating an oligonucleotide
 CC into the genome of a eukaryotic cell so that it is linked to an
 CC expressible polynucleotide or contacting the eukaryotic cell with library
 CC of vectors, obtained by cloning a library of oligonucleotide into
 CC multiple copies of expression vectors comprising polynucleotide, and
 CC detecting changes in expression of the polynucleotide. The method is
 CC useful for identifying an oligonucleotide having transcriptional or
 CC translational activity in a eukaryotic cell. It is also useful for
 CC identifying synthetic transcriptional or translational regulatory
 CC elements. The transcriptional or translational regulatory elements are
 CC useful in a variety of gene expression configurations for regulating
 CC control of expression, and in expression vectors for controlling gene
 CC expressions in diagnostic and therapeutic applications. The present
 CC sequence is MESVR/EGFP/ECFP/RSVPro(ori) vector based on Murine embryonic
 CC stem cell virus (MESV) retrovirus. The vector comprises reporter genes
 CC encoding enhanced green fluorescent protein (EGFP) and enhanced cyan
 CC fluorescent protein (ECFP). The upstream long terminal repeat (LTR)
 CC region of the retrovirus was modified to contain Rous sarcoma virus (RSV)
 CC enhancer elements. The downstream LTR region was modified to contain a
 CC multiple cloning site for the insertion of exogenous sequences that
 CC regulate transcriptional activity and the endogenous viral core promoter
 CC was replaced with a strong basal promoter. The vector also contains a
 CC simian virus 40 (SV40) origin of replication (ori) and is useful for
 CC identifying synthetic internal ribosome entry sequence (IRES) elements
 XX
 XX Sequence 6250 BP; 1474 A; 1764 C; 1611 G; 1401 T; 0 U; 0 Other;
 SQ
 Query Match 66.0%; Score 174.2; DB 4; Length 6250;
 Best Local Similarity 98.3%; Pred. No. 2.6e-50;
 Matches 176; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 AATGTAGTCTTATGCAATACACTTTGTAGTCTTGTGCAATGTTGCAATGTTAGTACCA 60
 DB 3165 AATGTAGTCTTATGCAATACACTTTGTAGTCTTGTGCAATGTTGCAATGTTAGTACCA 3224
 QY 61 TGCCTTACAGGAGAGAAAAGCACCGTGCATGCCGATTTGGTGGAGTAAAGTGTACGA 120
 DB 3225 TGCCTTACAGGAGAGAAAAGCACCGTGCATGCCGATTTGGTGGAGTAAAGTGTACGA 3284
 QY 121 TCGTGCCTTATTAGGAGGCAACAGACCGGCTCTGACATGATTTGACCACTAAAT 179

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GenCore version 5.1.6

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 Sercore version 3.1.6

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Run on: March 11, 2004, 08:11:32 ; Search time 48.7624 Seconds

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Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query %			DB	ID	Description
	Score	Match	Length			
1	261.4	99.0	11627	4	US-09-470-981-1	Sequence 1, Appli
2	257.6	97.6	4365	5	US-08-564-313-1	Sequence 1, Appli
3	257.6	97.6	4365	5	FCI-US94-06069-1	Sequence 1, Appli
C 4	248.2	94.0	4059	2	US-08-564-313-2	Sequence 2, Appli
C 5	248.2	94.0	4059	5	FCI-US94-06069-2	Sequence 2, Appli
6	248.2	94.0	5653	3	US-08-073-836-3	Sequence 3, Appli
7	248.2	94.0	5653	1	US-08-235-277-1	Sequence 1, Appli
8	248.2	94.0	6836	4	US-09-479-122-18	Sequence 18, Appl
9	248.2	94.0	6836	4	US-09-479-122-18	Sequence 18, Appl
10	248.2	94.0	6836	4	US-09-484-997-18	Sequence 18, Appl
11	248.2	94.0	6836	4	US-09-481-355-18	Sequence 18, Appl
12	248.2	94.0	6836	4	US-09-481-282-18	Sequence 18, Appl
13	248.2	94.0	6836	4	US-09-435-659A-18	Sequence 18, Appl
14	248.2	94.0	6836	4	US-09-484-996-18	Sequence 18, Appl
15	248.2	94.0	8591	1	US-09-479-123-18	Sequence 18, Appl
16	248.2	94.0	8591	1	US-08-462-859A-6	Sequence 6, Appli
17	248.2	94.0	8591	1	US-08-462-859A-8	Sequence 8, Appli
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19	248.2	94.0	8591	1	US-08-123-659A-8	Sequence 8, Appli
20	248.2	94.0	8591	1	US-08-464-447A-6	Sequence 6, Appli
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22	248.2	94.0	8591	1	US-08-464-248A-6	Sequence 6, Appli
23	248.2	94.0	9737	4	US-09-479-122-22	Sequence 22, Appl
24	248.2	94.0	9737	4	US-09-479-122-22	Sequence 22, Appl
25	248.2	94.0	9737	4	US-09-479-122-28	Sequence 28, Appl
26	248.2	94.0	9737	4	US-09-484-997-22	Sequence 22, Appl
27	248.2	94.0	9737	4	US-09-484-997-23	Sequence 23, Appl

ALIGNMENTS

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RESULT 1
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; Patent No. 6685938
; GENERAL INFORMATION:
; APPLICANT: CHERESH, David A.
; APPLICANT: ELICEIRI, Brian
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR MODULATION OF
; TITLE OF INVENTION: ANGIOGENESIS AND VASCULAR PERMEABILITY USING SRC OR
; TITLE OF INVENTION: YES TYROSINE KINASES
; FILE REFERENCE: TSRI 651.2
; CURRENT APPLICATION NUMBER: US/09/470,881
; CURRENT FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: PCT/US99/11780
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,220
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 11627
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: RCASBP (A) based
; OTHER INFORMATION: on avian sarcoma virus
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; OTHER INFORMATION: pBR322 sequences
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; NAME/KEY: misc feature
; LOCATION: (1)..(21)
; OTHER INFORMATION: R
; NAME/KEY: misc feature
; LOCATION: (22)..(101)
; OTHER INFORMATION: U5
; NAME/KEY: misc feature
; LOCATION: (102)..(119)
; NAME/KEY: LTR
; LOCATION: (7166)..(7494)
; OTHER INFORMATION: downstream
; NAME/KEY: misc feature
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; OTHER INFORMATION: U3
; NAME/KEY: misc feature
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; NAME/KEY: misc feature
; LOCATION: (7415)..(7494)
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; OTHER INFORMATION: PPT
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; LOCATION: (388)..(391)
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; OTHER INFORMATION: gag p27
; NAME/KEY: gene
; LOCATION: (1843)..(2108)
; OTHER INFORMATION: gag p12
; NAME/KEY: gene
; LOCATION: (2109)..(2480)
; OTHER INFORMATION: gag p15
; NAME/KEY: misc signal
; LOCATION: (2481)..(2483)
; OTHER INFORMATION: gag stop
; NAME/KEY: gene
; LOCATION: (2501)..(4216)
; OTHER INFORMATION: pol RT
; NAME/KEY: gene
; LOCATION: (4217)..(5185)
; OTHER INFORMATION: pol IN
; NAME/KEY: misc signal
; LOCATION: (5186)..(5188)
; OTHER INFORMATION: pol stop
; NAME/KEY: gene
; LOCATION: (5244)..(6263)
; OTHER INFORMATION: env gp85
; NAME/KEY: gene
; LOCATION: (6264)..(6878)
; OTHER INFORMATION: env gp37
; NAME/KEY: misc signal
; LOCATION: (6879)..(6881)
; OTHER INFORMATION: env stop
; NAME/KEY: misc feature
; LOCATION: (7027)
; OTHER INFORMATION: Clai site/ the Clai site in gag is methylated in
; OTHER INFORMATION: Dam+ strains and does not cut
US-09-470-881-1

Query Match 99.0%; Score 261.4; DB 4; Length 11627;
Best Local Similarity 99.6%; Pred. No. 4.6e-82;
Matches 262; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGTCTTATGCAATACTCTTGTAGTCTTGTGCAACATGTAACCATGAGTTAGCAACA 60
Db 7166 AATGAGTCTTATGCAATACTCTTGTAGTCTTGTGCAACATGTAACCATGAGTTAGCAACA 7225

QY 61 TGCCTTACAGGAGACAAAAGCACCGTCATGCCGATTTGGTGAAGTAAGTGTACGA 120
Db 7226 TGCCTTACAGGAGACAAAAGCACCGTCATGCCGATTTGGTGAAGTAAGTGTACGA 7285

QY 121 TCGTGCCCTTATTAGGAAGGCAACAGACGGGTCTTGACATGATTCGACGACCACTAAATT 180
Db 7286 TCGTGCCCTTATTAGGAAGGCAACAGACGGGTCTTGACATGATTCGACGACCACTAAATT 7345

QY 181 CCGCATTCGACAGATATTGTATTAACTAGTCCCTAGCTGCATACATATAAGCCATTGGAC 240
Db 7346 CCGCATTCGACAGATATTGTATTAACTAGTCCCTAGCTGCATACATATAAGCCATTGGAC 7405

QY 241 ATTCCACCACATTGCTGTGCACCT 263
Db 7406 ATTCCACCACATTGCTGTGCACCT 7428

RESULT 2
US-08-564-313-1
; Sequence 1, Application US/08564313
; Patent No. 5910488

```

```

GENERAL INFORMATION:
APPLICANT: Nabel, Elizabeth
APPLICANT: Nabel, Gary
APPLICANT: Lew, Denise
APPLICANT: Marquet, Magda
TITLE OF INVENTION: PLASMIDS SUITABLE FOR GENE THERAPY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson and Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/564,313
FILING DATE: 01-DEC-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/074,344
FILING DATE: 07-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Israel, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: VICAL.033CP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
TELEFAX: 619-235-0176
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4965 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
IMMEDIATE SOURCE:
CLONE: HLA-B7 and Beta-2
US-08-564-313-1

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Query Match          97.6%; Score 257.6; DB 2; Length 4965;
Best Local Similarity 98.5%; Pred. No. 6.9e-81;
Matches 260; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AATGTAGCTTTATGCAATCTCTTGTAGTCTTGTGCAACATGCTAAGAGTGTAGCAACA 60
DB 260 AATGTAGCTTTATGCAATCTCTTGTAGTCTTGTGCAACATGCTAAGAGTGTAGCAACA 319
QY 61 TGCCTTACAGGAGAGAGAAAAGCAACCGTGCATGCCGATTGGTGGAAAGTAAGTGTACGA 120
DB 320 TGCCTTACAGGAGAGAGAAAAGCAACCGTGCATGCCGATTGGTGGAAAGTAAGTGTACGA 379
QY 121 TCGTGCCTTTATTAGAGAGCAACAGACGGGCTGACATGATGATGAGCAACCACTAAAT 180
DB 380 TCGTGCCTTTATTAGAGAGCAACAGACGGGCTGACATGATGATGAGCAACCACTAAAT 439
QY 181 CCGCATTTGCAGAGATATTGTATTAAAGTCCTAGCTGATACATAAATACGCCATTGACC 240
DB 440 CCGCATTTGCAGAGATATTGTATTAAAGTCCTAGCTGATACATAAATACGCCATTGACC 499
QY 241 ATTCACACATTTGGTGTGCACCTC 264
DB 500 ATTCACACATTTGGTGTGCACCTC 523

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RESULT 3
PCT-US94-06069-1
Sequence 1, Application PC/TUS9406069
GENERAL INFORMATION:
APPLICANT: Vical Incorporated
APPLICANT: Regents of the University of Michigan
APPLICANT: Nabel, Elizabeth
APPLICANT: Nabel, Gary
APPLICANT: Lew, Denise
APPLICANT: Marquet, Magda
TITLE OF INVENTION: PLASMIDS SUITABLE FOR GENE THERAPY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson and Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06069
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/074,344
FILING DATE: 07-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Israel, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: VICAL.033VPC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
TELEFAX: 619-235-0176
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4965 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
STRAIN: HLA-B7 and Beta-2
PCT-US94-06069-1

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Query Match          97.6%; Score 257.6; DB 5; Length 4965;
Best Local Similarity 98.5%; Pred. No. 6.9e-81;
Matches 260; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AATGTAGCTTTATGCAATCTCTTGTAGTCTTGTGCAACATGCTAAGAGTGTAGCAACA 60
DB 260 AATGTAGCTTTATGCAATCTCTTGTAGTCTTGTGCAACATGCTAAGAGTGTAGCAACA 319
QY 61 TGCCTTACAGGAGAGAGAAAAGCAACCGTGCATGCCGATTGGTGGAAAGTAAGTGTACGA 120
DB 320 TGCCTTACAGGAGAGAGAAAAGCAACCGTGCATGCCGATTGGTGGAAAGTAAGTGTACGA 379
QY 121 TCGTGCCTTTATTAGAGAGCAACAGACGGGCTGACATGATGATGAGCAACCACTAAAT 180
DB 380 TCGTGCCTTTATTAGAGAGCAACAGACGGGCTGACATGATGATGAGCAACCACTAAAT 439
QY 181 CCGCATTTGCAGAGATATTGTATTAAAGTCCTAGCTGATACATAAATACGCCATTGACC 240
DB 440 CCGCATTTGCAGAGATATTGTATTAAAGTCCTAGCTGATACATAAATACGCCATTGACC 499

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QY 241 ATTACACACATTGGTGTGCACCTC 264
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Db 500 ATTACACACATTGGTGTGCACCTC 523
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RESULT 4
US-08-564-313-2/c
; Sequence 2, Application US/08564313
; Patent No. 5910488
; GENERAL INFORMATION:
; APPLICANT: Nabel, Elizabeth
; APPLICANT: Nabel, Gary
; APPLICANT: Lew, Denise
; APPLICANT: Marquet, Magda
; TITLE OF INVENTION: PLASMIDS SUITABLE FOR GENE THERAPY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fast-SEQ Version 1.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/564,313
; FILING DATE: 01-DEC-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/074,344
; FILING DATE: 07-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Israel, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: VICAL.033CP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 619-235-0176
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4059 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; IMMEDIATE SOURCE:
; CLONE: HLA-B7
US-08-564-313-2

Query Match 94.0%; Score 248.2; DB 2; Length 4059;
Best Local Similarity 98.5%; Pred. No. 1.3e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 1 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAACATGGTAACGATGAGTTAGCAACA 60
Db 3156 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAACATGGTAACGATGAGTTAGCAACA 3097
QY 61 TGCCTTACAGGAGAGAAAAGCACCCTGTCATGCCGATGGTGAAGTGGTGTAGCA 120
Db 3096 TGCCTTACAGGAGAGAAAAGCACCCTGTCATGCCGATGGTGAAGTGGTGTAGCA 3037
QY 121 TCGTGCCTTATTAGGAGGCAACAGACCGGCTCTGACATGATTGGACCAACCACTAAATT 180
Db 3036 TCGTGCCTTATTAGGAGGCAACAGACAGGCTCTGACATGATTGGACCAACCACTGAATT 2977

QY 181 CGCATTGCAGAGAT-ATTGTATTTAAGTCCCTAGCTGATACATAATAACGCCATTTCAC 239
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Db 2976 CGCATTGCAGAGATATTGTATTTAAGTCCCTAGCTGATACATAATAACGCCATTTCAC 2917
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QY 240 CATTCCACACATTGGTGTGCACCTC 264
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Db 2916 CATTCCACACATTGGTGTGCACCTC 2892
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RESULT 5
PCT-US94-06069-2/c
; Sequence 2, Application PC/TUS9406069
; GENERAL INFORMATION:
; APPLICANT: Vical Incorporated
; APPLICANT: Regents of the University of Michigan
; APPLICANT: Nabel, Elizabeth
; APPLICANT: Nabel, Gary
; APPLICANT: Lew, Denise
; APPLICANT: Marquet, Magda
; TITLE OF INVENTION: PLASMIDS SUITABLE FOR GENE THERAPY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fast-SEQ Version 1.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06069
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/074,344
; FILING DATE: 07-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Israel, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: VICAL.033VPC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 619-235-0176
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4059 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; STRAIN: HLA-B7
PCT-US94-06069-2

Query Match 94.0%; Score 248.2; DB 5; Length 4059;
Best Local Similarity 98.5%; Pred. No. 1.3e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 1 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAACATGGTAACGATGAGTTAGCAACA 60
Db 3156 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAACATGGTAACGATGAGTTAGCAACA 3097
QY 61 TGCCTTACAGGAGAGAAAAGCACCCTGTCATGCCGATGGTGAAGTGGTGTAGCA 120
Db 3096 TGCCTTACAGGAGAGAAAAGCACCCTGTCATGCCGATGGTGAAGTGGTGTAGCA 3037

QY 121 TCGTGCCCTTATTAGGAGGCAACAGACGGCTGTCACATGATTGACGAAACCACTAAATT 180
Db 3036 TCGTGCCCTTATTAGGAGGCAACAGACAGGCTGTCACATGATTGACGAAACCACTAAATT 2977
QY 181 CCGCATTCGAGAGAT-ATTGTATTAAAGTGGCTAGCTCGATACATAATAAACCCCAATTGAC 239
Db 2976 CCGCATTCGAGAGAT-ATTGTATTAAAGTGGCTAGCTCGATACATAATAAACCCCAATTGAC 2917
QY 240 CATTACCAACATGGTGGACCTC 264
Db 2916 CATTACCAACATGGTGGACCTC 2892
RESULT 6
US-08-073-836-3
; Sequence 3, Application US/08073836
; Patent No. 5650306
; GENERAL INFORMATION:
; APPLICANT: Nabel, Gary J.
; APPLICANT: Yang, Zhi-yong
; APPLICANT: Liu, Jinsong
; TITLE OF INVENTION: RECOMBINANT NUCLEIC ACIDS FOR INHIBITING
; TITLE OF INVENTION: HIV GENE EXPRESSION
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL AND FLORES
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States of America
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/073,836
; FILING DATE: 07-JUN-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UM 9646
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5653 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-073-836-3
Query Match 94.0%; Score 248.2; DB 1; Length 5653;
Best Local Similarity 98.5%; Pred. No. 1.5e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 1 AATGTAGCTCTTATGCAATACCTCTTGTAGTCTTGCAACATGTTGACGATGAGTTAGCAACA 60
Db 340 AATGTAGCTCTTATGCAATACCTCTTGTAGTCTTGCAACATGTTGACGATGAGTTAGCAACA 399
QY 61 TGCCTTACAGGAGAGAGAAAGCACCGTCATGCCGATTTGGTGAAGTAAGGTGTTACGA 120
Db 400 TGCCTTACAGGAGAGAGAGAAAGCACCGTCATGCCGATTTGGTGAAGTAAGGTGTTACGA 459
QY 121 TCGTGCCCTTATTAGGAGGCAACAGACGGGCTGTCACATGATTGACGAAACCACTAAATT 180
Db 460 TCGTGCCCTTATTAGGAGGCAACAGACAGGCTGTCACATGATTGACGAAACCACTAAATT 519
QY 181 CCGCATTCGAGAGAT-ATTGTATTAAAGTGGCTAGCTCGATACATAATAAACCCCAATTGAC 239

Db 520 CCGCATTCGAGAGAT-ATTGTATTAAAGTGGCTAGCTCGATACATAATAAACCCCAATTGAC 579
QY 240 CATTACCAACATGGTGGACCTC 264
Db 580 CATTACCAACATGGTGGACCTC 604
RESULT 7
US-08-235-277-1
; Sequence 1, Application US/08235277
; Patent No. 5733543
; GENERAL INFORMATION:
; APPLICANT: NABEL, GARY J
; APPLICANT: WOFFENDIN, CLIVE
; APPLICANT: YANG, MIN-SUN
; APPLICANT: SHEEHY, MICHAEL J
; TITLE OF INVENTION: INTRODUCTION OF HIV-PROTECTIVE GENES
; TITLE OF INVENTION: INTO CELLS BY PARTICLE-MEDIATED GENE TRANSFER
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/235,277
; FILING DATE: 29-APR-1994
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5733543man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 6042-008-68
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5653 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: Other nucleic acid
US-08-235-277-1
Query Match 94.0%; Score 248.2; DB 1; Length 5653;
Best Local Similarity 98.5%; Pred. No. 1.5e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 1 AATGTAGCTCTTATGCAATACCTCTTGTAGTCTTGCAACATGTTGACGATGAGTTAGCAACA 60
Db 340 AATGTAGCTCTTATGCAATACCTCTTGTAGTCTTGCAACATGTTGACGATGAGTTAGCAACA 399
QY 61 TGCCTTACAGGAGAGAGAAAGCACCGTCATGCCGATTTGGTGAAGTAAGGTGTTACGA 120
Db 400 TGCCTTACAGGAGAGAGAGAAAGCACCGTCATGCCGATTTGGTGAAGTAAGGTGTTACGA 459
QY 121 TCGTGCCCTTATTAGGAGGCAACAGACGGGCTGTCACATGATTGACGAAACCACTAAATT 180
Db 460 TCGTGCCCTTATTAGGAGGCAACAGACAGGCTGTCACATGATTGACGAAACCACTAAATT 519
QY 181 CCGCATTCGAGAGAT-ATTGTATTAAAGTGGCTAGCTCGATACATAATAAACCCCAATTGAC 239
Db 520 CCGCATTCGAGAGAT-ATTGTATTAAAGTGGCTAGCTCGATACATAATAAACCCCAATTGAC 579

QY 240 CATTCCACCAATGGTGTGCACCTC 264
Db 580 CATTCCACCAATGGTGTGCACCTC 604

RESULT 8

US-09-479-122-18
; Sequence 18, Application US/09479122
; Patent No. 6410266
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; TITLE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003C
; CURRENT FILING DATE: 2000-01-07
; PRIOR FILING DATE: 2000-01-07
; PRIOR FILING DATE: 1999-03-26
; PRIOR FILING DATE: 1999-03-26
; PRIOR FILING DATE: 1998-09-24
; PRIOR FILING DATE: 1998-09-24
; PRIOR FILING DATE: 1997-09-26
; PRIOR FILING DATE: 1997-09-26
; PRIOR FILING DATE: 1999-03-08
; PRIOR FILING DATE: 1999-03-08
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 6836
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-479-122-18

Query Match 94.0%; Score 248.2; DB 4; Length 6836;
Best Local Similarity 98.5%; Pred. No. 1.7e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 1 AATGTAGTCTTATGCAATACTCTTGTAGTCTTGGCAACATGGTAACGATGAGTTAGCAACA 60
Db 1558 AATGTAGTCTTATGCAATACTCTTGTAGTCTTGGCAACATGGTAACGATGAGTTAGCAACA 1617
QY 61 TGCCTTACAGGAGAGAAAAGACCGGTCTGACATGGATTGGACGAAACCACTAAATT 180
Db 1618 TGCCTTACAGGAGAGAAAAGACCGGTCTGACATGGATTGGACGAAACCACTAAATT 1677
QY 121 TCGTGCCCTTATTAGGAAGGCAACAGACCGGTCTGACATGGATTGGACGAAACCACTAAATT 180
Db 1678 TCGTGCCCTTATTAGGAAGGCAACAGACCGGTCTGACATGGATTGGACGAAACCACTAAATT 1737
QY 181 CGCATTCGACAGAT-ATTGTATTATTAAGTGCCTAGCTCGATACATAATAAACGCCATTGAC 239
Db 1738 CGCATTCGACAGATAAATTGTATTATTAAGTGCCTAGCTCGATACATAATAAACGCCATTGAC 1797
QY 240 CATTCCACCAATGGTGTGCACCTC 264
Db 1798 CATTCCACCAATGGTGTGCACCTC 1822

RESULT 9

US-09-484-997-18
; Sequence 18, Application US/09484997
; Patent No. 6524818
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; TITLE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003J

; CURRENT APPLICATION NUMBER: US/09/484,997
; CURRENT FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 6836
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-484-997-18

Query Match 94.0%; Score 248.2; DB 4; Length 6836;
Best Local Similarity 98.5%; Pred. No. 1.7e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 1 AATGTAGTCTTATGCAATACTCTTGTAGTCTTGGCAACATGGTAACGATGAGTTAGCAACA 60
Db 1558 AATGTAGTCTTATGCAATACTCTTGTAGTCTTGGCAACATGGTAACGATGAGTTAGCAACA 1617
QY 61 TGCCTTACAGGAGAGAAAAGACCGGTCTGACATGGATTGGTGAAGTAAGTGTGTACGA 120
Db 1618 TGCCTTACAGGAGAGAAAAGACCGGTCTGACATGGATTGGTGAAGTAAGTGTGTACGA 1677
QY 121 TCGTGCCCTTATTAGGAAGGCAACAGACCGGTCTGACATGGATTGGACGAAACCACTAAATT 180
Db 1678 TCGTGCCCTTATTAGGAAGGCAACAGACCGGTCTGACATGGATTGGACGAAACCACTAAATT 1737
QY 181 CGCATTCGACAGAT-ATTGTATTATTAAGTGCCTAGCTCGATACATAATAAACGCCATTGAC 239
Db 1738 CGCATTCGACAGATAAATTGTATTATTAAGTGCCTAGCTCGATACATAATAAACGCCATTGAC 1797
QY 240 CATTCCACCAATGGTGTGCACCTC 264
Db 1798 CATTCCACCAATGGTGTGCACCTC 1822

RESULT 10

US-09-481-355-18
; Sequence 18, Application US/09481355
; Patent No. 6524824
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; TITLE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003F
; CURRENT APPLICATION NUMBER: US/09/481,355
; CURRENT FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 6836
; TYPE: DNA


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; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003H
; CURRENT APPLICATION NUMBER: US/09/484,996
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1998-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 6836
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-484-996-18

Query Match          94.0%; Score 248.2; DB 4; Length 6836;
Best Local Similarity 98.5%; Pred. No. 1.7e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATACACTCTTGTAGTCTTGCACATGTAACGATGAGTTAGCAACA 60
DB 1558 AATGTAGTCTTATGCAATACACTCTTGTAGTCTTGCACATGTAACGATGAGTTAGCAACA 1617
QY 61 TGCCTTACAGGAGAGAGAAAAGCACCCTGTCATGCGGATTTGGTGAAGTAAGTGGTACGA 120
DB 1618 TGCCTTACAGGAGAGAGAAAAGCACCCTGTCATGCGGATTTGGTGAAGTAAGTGGTACGA 1677
QY 121 TCGTGCCTTATTAGAAGGCAACAGACGGGTCTGACATGATTTGGACGACCACTAAATT 180
DB 1678 TCGTGCCTTATTAGAAGGCAACAGACGGGTCTGACATGATTTGGACGACCACTAAATT 1737
QY 181 CGCATTCGACAGAT-ATTGTATTAAAGTGCCTAGCTCGATACATAATAACGCCATTTGAC 239
DB 1738 CGCATTCGACAGATTAATTGATTAAAGTGCCTAGCTCGATACATAATAACGCCATTTGAC 1797
QY 240 CATTCCACCACATTTGGTGACCTC 264
DB 1798 CATTCCACCACATTTGGTGACCTC 1822

RESULT 14
US-09-479-123-18
; Sequence 18, Application US/09479123
; Patent No. 6670185
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERP, BRUCE
; APPLICANT: KUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003B
; CURRENT APPLICATION NUMBER: US/09/479,123
; CURRENT FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 6836
```

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-479-123-18

Query Match          94.0%; Score 248.2; DB 4; Length 6836;
Best Local Similarity 98.5%; Pred. No. 1.7e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATACACTCTTGTAGTCTTGCACATGTAACGATGAGTTAGCAACA 60
DB 1558 AATGTAGTCTTATGCAATACACTCTTGTAGTCTTGCACATGTAACGATGAGTTAGCAACA 1617
QY 61 TGCCTTACAGGAGAGAGAAAAGCACCCTGTCATGCGGATTTGGTGAAGTAAGTGGTACGA 120
DB 1618 TGCCTTACAGGAGAGAGAAAAGCACCCTGTCATGCGGATTTGGTGAAGTAAGTGGTACGA 1677
QY 121 TCGTGCCTTATTAGAAGGCAACAGACGGGTCTGACATGATTTGGACGACCACTAAATT 180
DB 1678 TCGTGCCTTATTAGAAGGCAACAGACGGGTCTGACATGATTTGGACGACCACTAAATT 1737
QY 181 CGCATTCGACAGAT-ATTGTATTAAAGTGCCTAGCTCGATACATAATAACGCCATTTGAC 239
DB 1738 CGCATTCGACAGATTAATTGATTAAAGTGCCTAGCTCGATACATAATAACGCCATTTGAC 1797
QY 240 CATTCCACCACATTTGGTGACCTC 264
DB 1798 CATTCCACCACATTTGGTGACCTC 1822

RESULT 15
US-08-462-859A-6
; Sequence 6, Application US/08462859A
; Patent No. 5652092
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vittek, W. P.
; TITLE OF INVENTION: No. 5652092el Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSER: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,859A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 31,844-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201)831-3246
; TELEFAX: (201)831-3305
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8591 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2393..3868
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US-08-462-859A-6

Query Match 94.0%; Score 248.2; DB 1; Length 8591;
Best Local Similarity 98.5%; Pred. No. 1.8e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGAGTCTTATGCAATACCTTTGTAGTCTTGGCAATGTAACGATGAGTTAGCAACA 60
DB 4975 AATGAGTCTTATGCAATACCTTTGTAGTCTTGGCAATGTAACGATGAGTTAGCAACA 5034
QY 61 TGCCTTACAGAGGAGAGAAAAGACACCGTGCATGCGGATTTGGTGAAGTAAGTGTGACGA 120
DB 5035 TGCCTTACAGAGGAGAGAAAAGACACCGTGCATGCGGATTTGGTGAAGTAAGTGTGACGA 5094
QY 121 TCGTGCCTTATTAGGAGGACACAGACGCGTCTGACATGGATTTGGACGACCACTAAATT 180
DB 5095 TCGTGCCTTATTAGGAGGACACAGACGCGTCTGACATGGATTTGGACGACCACTAAATT 5154
QY 181 CGCATTTGCAGAGAT-ATTGTAATTTAAGTGCCTAGCTCGATACAAATAAAGCCATTGAC 239
DB 5155 CGCATTTGCAGAGAT-ATTGTAATTTAAGTGCCTAGCTCGATACAAATAAAGCCATTGAC 5214
QY 240 CATTCAACCACTTGTGTGCACCTC 264
DB 5215 CATTCAACCACTTGTGTGCACCTC 5239

RESULT 16

US-08-462-859A-8
; Sequence 8, Application US/08462859A
; Patent No. 5652092

GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vitek, M. P.
; TITLE OF INVENTION: No. 5652092el Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 07470-8426

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,859A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 31,844-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201)831-3246
; TELEFAX: (201)831-3305
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8591 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2393...3853

US-08-462-859A-8
Query Match 94.0%; Score 248.2; DB 1; Length 8591;
Best Local Similarity 98.5%; Pred. No. 1.8e-77;

Query Match

94.0%; Score 248.2; DB 1; Length 8591;
Best Local Similarity 98.5%; Pred. No. 1.8e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGAGTCTTATGCAATACCTTTGTAGTCTTGGCAATGTAACGATGAGTTAGCAACA 60
DB 4975 AATGAGTCTTATGCAATACCTTTGTAGTCTTGGCAATGTAACGATGAGTTAGCAACA 5034
QY 61 TGCCTTACAGAGGAGAGAAAAGACACCGTGCATGCGGATTTGGTGAAGTAAGTGTGACGA 120
DB 5035 TGCCTTACAGAGGAGAGAAAAGACACCGTGCATGCGGATTTGGTGAAGTAAGTGTGACGA 5094
QY 121 TCGTGCCTTATTAGGAGGACACAGACGCGTCTGACATGGATTTGGACGACCACTAAATT 180
DB 5095 TCGTGCCTTATTAGGAGGACACAGACGCGTCTGACATGGATTTGGACGACCACTAAATT 5154
QY 181 CGCATTTGCAGAGAT-ATTGTAATTTAAGTGCCTAGCTCGATACAAATAAAGCCATTGAC 239
DB 5155 CGCATTTGCAGAGAT-ATTGTAATTTAAGTGCCTAGCTCGATACAAATAAAGCCATTGAC 5214
QY 240 CATTCAACCACTTGTGTGCACCTC 264
DB 5215 CATTCAACCACTTGTGTGCACCTC 5239

RESULT 17

US-08-123-659A-6
; Sequence 6, Application US/08123659A
; Patent No. 5656477

GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vitek, M. P.
; TITLE OF INVENTION: No. 5656477el Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Anne Rosenblum
; STREET: 163 Delaware Avenue, Suite 212
; CITY: Delmar
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 12054

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/123,659A
; FILING DATE: 20-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rosenblum, Anne M.
; REGISTRATION NUMBER: 30,419
; REFERENCE/DOCKET NUMBER: 31,844-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (518)475-0611
; TELEFAX: (518)475-0619
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8591 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2393...3868

US-08-123-659A-6
Query Match 94.0%; Score 248.2; DB 1; Length 8591;
Best Local Similarity 98.5%; Pred. No. 1.8e-77;

Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 QY 1 AATGTAGCTTATGCAATACCTTGTAGTCTTGCACATGTTAGGTTAGCAACA 60
 Db 4975 AATGTAGCTTATGCAATACCTTGTAGTCTTGCACATGTTAGGTTAGCAACA 5034
 QY 61 TGCCTTACAGGAGAGAAAAGCACCGTGCATGCGCATGCGTGGAAAGTAAGTGGTACGA 120
 Db 5035 TGCCTTACAGGAGAGAAAAGCACCGTGCATGCGCATGCGTGGAAAGTAAGTGGTACGA 5094
 QY 121 TCGTCCCTTATTAGGAAGCAACAGACGCGGTCTGCATGAGTGGAGCAACCACTGAATT 180
 Db 5095 TCGTCCCTTATTAGGAAGCAACAGACGCGGTCTGCATGAGTGGAGCAACCACTGAATT 5154
 QY 181 CGCATTGCGAGAGAT-ATTGTATTAAAGTCCCTAGCTGCATGATCAATAAAGCGCATTTGAC 239
 Db 5155 CGCATTGCGAGATTAATTGTATTAAAGTCCCTAGCTGCATGATCAATAAAGCGCATTTGAC 5214
 QY 240 CATTCACCAATGTTGGTGCACCTC 264
 Db 5215 CATTCACCAATGTTGGTGCACCTC 5239

RESULT 18
 US-08-123-659A-8
 ; Sequence 8, Application US/08123659A
 ; Patent No. 5656477
 ; GENERAL INFORMATION:
 ; APPLICANT: Jacobsen, J. S.
 ; APPLICANT: Vitek, M. P.
 ; TITLE OF INVENTION: No. 5656477el Amyloid Precursor and Method of
 ; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
 ; TITLE OF INVENTION: of B-Amyloid Peptide
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Anne Rosenblum
 ; STREET: 163 Delaware Avenue, Suite 212
 ; CITY: Delmar
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 12054
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/123,659A
 ; FILING DATE: 20-SEP-1993
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Rosenblum, Anne M.
 ; REGISTRATION NUMBER: 30,419
 ; REFERENCE/DOCKET NUMBER: 31,844-01
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (518)475-0611
 ; TELEFAX: (518)475-0619
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 8591 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: circular
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 2393..3853
 ; US-08-123-659A-8

Query Match 94.0%; Score 248.2; DB 1; Length 8591;
 Best Local Similarity 98.5%; Pred. No. 1.8e-77;
 Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGCTTATGCAATACCTTGTAGTCTTGCACATGTTAGGTTAGCAACA 60
 Db 4975 AATGTAGCTTATGCAATACCTTGTAGTCTTGCACATGTTAGGTTAGCAACA 5034
 QY 61 TGCCTTACAGGAGAGAAAAGCACCGTGCATGCGCATGCGTGGAAAGTAAGTGGTACGA 120
 Db 5035 TGCCTTACAGGAGAGAAAAGCACCGTGCATGCGCATGCGTGGAAAGTAAGTGGTACGA 5094
 QY 121 TCGTCCCTTATTAGGAAGCAACAGACGCGGTCTGCATGAGTGGAGCAACCACTGAATT 180
 Db 5095 TCGTCCCTTATTAGGAAGCAACAGACGCGGTCTGCATGAGTGGAGCAACCACTGAATT 5154
 QY 181 CGCATTGCGAGAGAT-ATTGTATTAAAGTCCCTAGCTGCATGATCAATAAAGCGCATTTGAC 239
 Db 5155 CGCATTGCGAGATTAATTGTATTAAAGTCCCTAGCTGCATGATCAATAAAGCGCATTTGAC 5214
 QY 240 CATTCACCAATGTTGGTGCACCTC 264
 Db 5215 CATTCACCAATGTTGGTGCACCTC 5239

RESULT 19
 US-08-464-247A-6
 ; Sequence 6, Application US/08464247A
 ; Patent No. 5693478
 ; GENERAL INFORMATION:
 ; APPLICANT: Jacobsen, J. S.
 ; APPLICANT: Vitek, M. P.
 ; TITLE OF INVENTION: No. 5693478el Amyloid Precursor and Method of
 ; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
 ; TITLE OF INVENTION: of B-Amyloid Peptide
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: American Cyanamid Company
 ; STREET: One Campus Drive
 ; CITY: Parsippany
 ; STATE: New Jersey
 ; COUNTRY: United States
 ; ZIP: 07054
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/464,247A
 ; FILING DATE: 05-JUN-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Barnhard, Elizabeth M.
 ; REGISTRATION NUMBER: 31,088
 ; REFERENCE/DOCKET NUMBER: 31,844-03
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 201-683-2158
 ; TELEFAX: 201-683-4117
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 8591 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: circular
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 2393..3868
 ; US-08-464-247A-6

Query Match 94.0%; Score 248.2; DB 1; Length 8591;
 Best Local Similarity 98.5%; Pred. No. 1.8e-77;
 Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 QY 1 AATGTAGCTTATGCAATACCTTGTAGTCTTGCACATGTTAGGTTAGCAACA 60

Db 5035 TGCCTTACAGGAGAGAAAAGCACCGTGCATGCCGATGCTGGAGTAAGGTGGTACGA 5094
Qy 121 TCGTGCCTTATTAGAGAGGCAACAGACGGGCTCTGACATGATTTGGACGACCACTAAATT 180
Db 5095 TCGTGCCTTATTAGAGAGGCAACAGACAGGCTCTGACATGATTTGGACGACCACTAAATT 5154
Qy 181 CCGCATTCGAGAGAT-ATTGTATTAAAGTGGCTAGCTCGATACATAAAGCCATTGGAC 239
Db 5155 CCGCATTCGAGAGATATTGTATTAAAGTGGCTAGCTCGATACATAAAGCCATTGGAC 5214
Qy 240 CATTCACCAACATTGGTGTGCACCTC 264
Db 5215 CATTCACCAACATTGGTGTGCACCTC 5239
RESULT 22
US-08-464-248A-8
; Sequence 8, Application US/08464248A
; Patent No. 5703209
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vitek, W. P.
; TITLE OF INVENTION: No. 5703209el Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,248A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 31,844-02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201)831-3246
; TELEFAX: (201)831-3305
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8591 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2393...3853
US-08-464-248A-8
Query Match 94.0%; Score 248.2; DB 1; Length 8591;
Best Local Similarity 98.5%; Pred. No. 1.8e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
Qy 1 AATGTAGCTTTATGCAATACCTCTTGTAGTCTTGGCAATCGTAAACGATCAGTTAGCAACA 60
Db 4975 AATGTAGCTTTATGCAATACCTCTTGTAGTCTTGGCAATCGTAAACGATCAGTTAGCAACA 5034
Qy 61 TGCCTTACAGGAGAGAAAAGCACCGTGCATGCCGATGCTGGAGTAAGGTGGTACGA 120
Db 5035 TGCCTTACAGGAGAGAAAAGCACCGTGCATGCCGATGCTGGAGTAAGGTGGTACGA 5094

Qy 121 TCGTGCCTTATTAGAGAGGCAACAGACGGGCTCTGACATGATTTGGACGACCACTAAATT 180
Db 5095 TCGTGCCTTATTAGAGAGGCAACAGACAGGCTCTGACATGATTTGGACGACCACTAAATT 5154
Qy 181 CCGCATTCGAGAGAT-ATTGTATTAAAGTGGCTAGCTCGATACATAAAGCCATTGGAC 239
Db 5155 CCGCATTCGAGAGATAATTGTATTAAAGTGGCTAGCTCGATACATAAAGCCATTGGAC 5214
Qy 240 CATTCACCAACATTGGTGTGCACCTC 264
Db 5215 CATTCACCAACATTGGTGTGCACCTC 5239
RESULT 23
US-09-479-122-22
; Sequence 22, Application US/09479122
; Patent No. 6410266
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERE, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; TITLE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003C
; CURRENT APPLICATION NUMBER: US/09/479,122
; CURRENT FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-479-122-22
Query Match 94.0%; Score 248.2; DB 4; Length 9737;
Best Local Similarity 98.5%; Pred. No. 1.9e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
Qy 1 AATGTAGCTTTATGCAATACCTCTTGTAGTCTTGGCAATCGTAAACGATCAGTTAGCAACA 60
Db 1411 AATGTAGCTTTATGCAATACCTCTTGTAGTCTTGGCAATCGTAAACGATCAGTTAGCAACA 1470
Qy 61 TGCCTTACAGGAGAGAAAAGCACCGTGCATGCCGATGCTGGAGTAAGGTGGTACGA 120
Db 1471 TGCCTTACAGGAGAGAAAAGCACCGTGCATGCCGATGCTGGAGTAAGGTGGTACGA 1530
Qy 121 TCGTGCCTTATTAGAGAGGCAACAGACGGGCTCTGACATGATTTGGACGACCACTAAATT 180
Db 1531 TCGTGCCTTATTAGAGAGGCAACAGACAGGCTCTGACATGATTTGGACGACCACTAAATT 1590
Qy 181 CCGCATTCGAGAGAT-ATTGTATTAAAGTGGCTAGCTCGATACATAAAGCCATTGGAC 239
Db 1591 CCGCATTCGAGAGATAATTGTATTAAAGTGGCTAGCTCGATACATAAAGCCATTGGAC 1650
Qy 240 CATTCACCAACATTGGTGTGCACCTC 264

Db 1651 CATTACACCATGGTGTGCACCTC 1675

RESULT 24

US-09-479-122-23
; Sequence 23, Application US/09479122
; Patent No. 6410266
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003C
; CURRENT APPLICATION NUMBER: US/09/479,122
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-479-122-23

Query Match 94.0%; Score 248.2; DB 4; Length 9737;

Best Local Similarity 98.5%; Pred. No. 1.9e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1 AATGTAGTCTTATGCAATACCTTTGTAGTCTTTGCAACATGTAAGTACGATGAGTTAGCAACA 60
Db 1411 AATGTAGTCTTATGCAATACCTTTGTAGTCTTTGCAACATGTAAGTACGATGAGTTAGCAACA 1470
Qy 61 TGCCTTACAGGAGAGAAAAGACCGCTGCATGCCGATTTGGTGAAGTAAAGTGGTACGA 120
Db 1471 TGCCTTACAGGAGAGAAAAGACCGCTGCATGCCGATTTGGTGAAGTAAAGTGGTACGA 1530
Qy 121 TCGTGCCTTATTAGGAGGCAACAGCGGCTGACATGATGATGAGTGGACCAACCACTAAATT 180
Db 1531 TCGTGCCTTATTAGGAGGCAACAGCGGCTGACATGATGATGAGTGGACCAACCACTAAATT 1590
Qy 181 CCGCATTCGAGAGAT-ATTGTTATTAAAGTGCCTAGCTCGATACATAAATACGCCATTGAC 239
Db 1591 CCGCATTCGAGAGAT-ATTGTTATTAAAGTGCCTAGCTCGATACATAAATACGCCATTGAC 1650
Qy 240 CATTACACCATGGTGTGCACCTC 264
Db 1651 CATTACACCATGGTGTGCACCTC 1675

RESULT 25

US-09-479-122-28
; Sequence 28, Application US/09479122
; Patent No. 6410266
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE

; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003C
; CURRENT APPLICATION NUMBER: US/09/479,122
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-479-122-28

Query Match 94.0%; Score 248.2; DB 4; Length 9737;
Best Local Similarity 98.5%; Pred. No. 1.9e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
Qy 1 AATGTAGTCTTATGCAATACCTTTGTAGTCTTTGCAACATGTAAGTACGATGAGTTAGCAACA 60
Db 1411 AATGTAGTCTTATGCAATACCTTTGTAGTCTTTGCAACATGTAAGTACGATGAGTTAGCAACA 1470
Qy 61 TGCCTTACAGGAGAGAAAAGACCGCTGCATGCCGATTTGGTGAAGTAAAGTGGTACGA 120
Db 1471 TGCCTTACAGGAGAGAAAAGACCGCTGCATGCCGATTTGGTGAAGTAAAGTGGTACGA 1530
Qy 121 TCGTGCCTTATTAGGAGGCAACAGCGGCTGACATGATGATGAGTGGACCAACCACTAAATT 180
Db 1531 TCGTGCCTTATTAGGAGGCAACAGCGGCTGACATGATGATGAGTGGACCAACCACTAAATT 1590
Qy 181 CCGCATTCGAGAGAT-ATTGTTATTAAAGTGCCTAGCTCGATACATAAATACGCCATTGAC 239
Db 1591 CCGCATTCGAGAGAT-ATTGTTATTAAAGTGCCTAGCTCGATACATAAATACGCCATTGAC 1650
Qy 240 CATTACACCATGGTGTGCACCTC 264
Db 1651 CATTACACCATGGTGTGCACCTC 1675

RESULT 26

US-09-484-997-22
; Sequence 22, Application US/09484997
; Patent No. 6524818
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003C
; CURRENT APPLICATION NUMBER: US/09/484,997
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24


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; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
; US-09-484-997-22

Query Match          94.0%; Score 248.2; DB 4; Length 9737;
Best Local Similarity 98.5%; Pred. No. 1.9e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGTGCAACATGTTACGATGAGTTAGCAACA 60
Db 1411 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGTGCAACATGTTACGATGAGTTAGCAACA 1470

Qy 61 TGCCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
Db 1471 TGCCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1530

Qy 121 TCGTGCCTTTATTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
Db 1471 TCGTGCCTTTATTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1590

Qy 181 CGCATTTGCAGAGAT-ATTGTATTATTAAGTGCCTGATGATGATGATGATGATGATGATGATG 239
Db 1591 CGCATTTGCAGAGAT-ATTGTATTATTAAGTGCCTGATGATGATGATGATGATGATGATGATG 1650

Qy 240 CATTACACCATTTGGTGTGCACCTC 264
Db 1651 CATTACACCATTTGGTGTGCACCTC 1675

RESULT 27
US-09-484-997-23
; Sequence 23, Application US/09484997
; Patent No. 6524818
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; TITLE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003J
; CURRENT APPLICATION NUMBER: US/09/484,997
; CURRENT FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
; US-09-484-997-23

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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
; US-09-484-997-23

Query Match          94.0%; Score 248.2; DB 4; Length 9737;
Best Local Similarity 98.5%; Pred. No. 1.9e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGTGCAACATGTTACGATGAGTTAGCAACA 60
Db 1411 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGTGCAACATGTTACGATGAGTTAGCAACA 1470

Qy 61 TGCCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
Db 1471 TGCCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1530

Qy 121 TCGTGCCTTTATTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
Db 1531 TCGTGCCTTTATTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1590

Qy 181 CGCATTTGCAGAGAT-ATTGTATTATTAAGTGCCTGATGATGATGATGATGATGATGATGATG 239
Db 1591 CGCATTTGCAGAGAT-ATTGTATTATTAAGTGCCTGATGATGATGATGATGATGATGATGATG 1650

Qy 240 CATTACACCATTTGGTGTGCACCTC 264
Db 1651 CATTACACCATTTGGTGTGCACCTC 1675

RESULT 28
US-09-484-997-28
; Sequence 28, Application US/09484997
; Patent No. 6524818
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; TITLE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003J
; CURRENT APPLICATION NUMBER: US/09/484,997
; CURRENT FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
; US-09-484-997-28

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Query Match 94.0%; Score 248.2; DB 4; Length 9737;
Best Local Similarity 98.5%; Pred. No. 1.9e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1 AATGTAGTCTTATGCAATACACTCTTTAGTCTTTGCAACATGGTAACGATGAGTTAGCAACA 60
Db 1411 AATGTAGTCTTATGCAATACACTCTTTAGTCTTTGCAACATGGTAACGATGAGTTAGCAACA 1470

Qy 61 TGCCTTACAGAGAGAGAAAGACACCGTCTGCATGCGATTTGGTGAAGTAAGTGTGACGA 120
Db 1471 TGCCTTACAGAGAGAGAAAGACACCGTCTGCATGCGATTTGGTGAAGTAAGTGTGACGA 1530

Qy 121 TCGTGCCCTTATTAGGAGAGAAAGACACCGTCTGCATGCGATTTGGTGAAGTAAGTGTGAC 180
Db 1531 TCGTGCCCTTATTAGGAGAGAAAGACACCGTCTGCATGCGATTTGGTGAAGTAAGTGTGAC 1590

Qy 240 CATTCACCACTTGGTGTGCACCTC 264
Db 1651 CATTCACCACTTGGTGTGCACCTC 1675

RESULT 29
US-09-481-355-22
; Sequence 22, Application US/09481355
; Patent No. 6524824
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003F
; CURRENT APPLICATION NUMBER: US/09/481,355
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-481-355-22

Query Match 94.0%; Score 248.2; DB 4; Length 9737;
Best Local Similarity 98.5%; Pred. No. 1.9e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1 AATGTAGTCTTATGCAATACACTCTTTAGTCTTTGCAACATGGTAACGATGAGTTAGCAACA 60
Db 1411 AATGTAGTCTTATGCAATACACTCTTTAGTCTTTGCAACATGGTAACGATGAGTTAGCAACA 1470

Qy 61 TGCCTTACAGAGAGAGAAAGACACCGTCTGCATGCGATTTGGTGAAGTAAGTGTGACGA 120

Db 1471 TGCCTTACAGAGAGAGAAAGACACCGTCTGCATGCGATTTGGTGAAGTAAGTGTGACGA 1530

Qy 121 TCGTGCCCTTATTAGGAGAGAAAGACACCGTCTGCATGCGATTTGGTGAAGTAAGTGTGAC 180
Db 1531 TCGTGCCCTTATTAGGAGAGAAAGACACCGTCTGCATGCGATTTGGTGAAGTAAGTGTGAC 1590

Qy 181 CGCATTTGCAGAGAT-ATTGTATTATTAGTGCCTAGCTCGATACATAATAAAGCCATTGAC 239
Db 1591 CGCATTTGCAGAGATATTGTATTATTAGTGCCTAGCTCGATACATAATAAAGCCATTGAC 1650

Qy 240 CATTCACCACTTGGTGTGCACCTC 264
Db 1651 CATTCACCACTTGGTGTGCACCTC 1675

RESULT 30
US-09-481-355-23
; Sequence 23, Application US/09481355
; Patent No. 6524824
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003F
; CURRENT APPLICATION NUMBER: US/09/481,355
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-481-355-23

Query Match 94.0%; Score 248.2; DB 4; Length 9737;
Best Local Similarity 98.5%; Pred. No. 1.9e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1 AATGTAGTCTTATGCAATACACTCTTTAGTCTTTGCAACATGGTAACGATGAGTTAGCAACA 60
Db 1411 AATGTAGTCTTATGCAATACACTCTTTAGTCTTTGCAACATGGTAACGATGAGTTAGCAACA 1470

Qy 61 TGCCTTACAGAGAGAGAAAGACACCGTCTGCATGCGATTTGGTGAAGTAAGTGTGACGA 120
Db 1471 TGCCTTACAGAGAGAGAAAGACACCGTCTGCATGCGATTTGGTGAAGTAAGTGTGACGA 1530

Qy 121 TCGTGCCCTTATTAGGAGAGAAAGACACCGTCTGCATGCGATTTGGTGAAGTAAGTGTGAC 180
Db 1531 TCGTGCCCTTATTAGGAGAGAAAGACACCGTCTGCATGCGATTTGGTGAAGTAAGTGTGAC 1590

Qy 181 CGCATTTGCAGAGAT-ATTGTATTATTAGTGCCTAGCTCGATACATAATAAAGCCATTGAC 239
Db 1591 CGCATTTGCAGAGATATTGTATTATTAGTGCCTAGCTCGATACATAATAAAGCCATTGAC 1650

;	ORGANISM:	Homo sapiens	
;	FEATURE:		
;	NAME/KEY:	modified_base	
;	LOCATION:	(8347)	
;	OTHER INFORMATION:	a, c, t, g, other or unknown	
;	FEATURE:		
;	NAME/KEY:	modified_base	
;	LOCATION:	(8499)	
;	OTHER INFORMATION:	a, c, t, g, other or unknown	
US-09-481-282-28			
Query Match	94.0%;	Score 248.2;	DB 4; Length 9737;
Best Local Similarity	98.5%;	Pred. No. 1.9e-77;	
Matches 261;	Conservative 0;	Mismatches 3;	Indels 1; Gaps 1;
QY	1	AATGTAGTCTTATGCAATACCTCTTTGTAGTCTTTGCAACATGTTAAAGATGATGATGACAA	60
Db	1411	AATGTAGTCTTATGCAATACCTTTGTAGTCTTTGCAACATGTTAAAGATGATGATGACAA	1470
QY	61	TGCCTTACAGGAGAGAAAGACCGTGCATGCGATTGGTGGAAAGTAAGTGGTACGA	120
Db	1471	TGCCTTACAGGAGAGAAAGACCGTGCATGCGATTGGTGGAAAGTAAGTGGTGGTACGA	1530
QY	121	TGTGCTCTTATTAGGAAGCAACAGACGGGCTTGACATGATTTGCACGAACCACTAAAT	180
Db	1531	TGTGCTCTTATTAGGAAGCAACAGACGGGCTTGACATGATTTGCACGAACCACTAAAT	1590
QY	181	CGCATTTGCAGAGAT-ATTGTTATTTAAGTGCCTAGCTCGATNCAATTAAGCCCATTTGAC	239
Db	1591	CGCATTTGCAGAGATTAATTTGTTATTTAAGTGCCTAGCTCGATNCAATTAAGCCCATTTGAC	1650
QY	240	CATTCAACCACTTTGGTGTGCACCTC	264
Db	1651	CATTCAACCACTTTGGTGTGCACCTC	1675
RESULT 35			
US-09-455-659A-22			
;	Sequence 22,	Application US/09455659A	
;	Patent No. 6602686		
;	GENERAL INFORMATION:		
;	APPLICANT:	HARRINGTON, JOHN J.	
;	APPLICANT:	SHERF, BRUCE	
;	APPLICANT:	RUNDLETT, STEPHEN	
;	TITLE OF INVENTION:	COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF	
;	TITLE OF INVENTION:	ENDOGENOUS GENES	
;	FILE REFERENCE:	0221-0003A	
;	CURRENT APPLICATION NUMBER:	US/09/455,659A	
;	CURRENT FILING DATE:	1999-12-07	
;	PRIOR APPLICATION NUMBER:	09/276,820	
;	PRIOR FILING DATE:	1999-03-26	
;	PRIOR APPLICATION NUMBER:	09/263,814	
;	PRIOR FILING DATE:	1999-03-08	
;	PRIOR APPLICATION NUMBER:	09/253,022	
;	PRIOR FILING DATE:	1999-02-19	
;	PRIOR APPLICATION NUMBER:	09/159,643	
;	PRIOR FILING DATE:	1998-09-24	
;	PRIOR APPLICATION NUMBER:	08/941,223	
;	PRIOR FILING DATE:	1997-09-26	
;	NUMBER OF SEQ ID NOS:	33	
;	SOFTWARE:	PatentIn Ver. 2.1	
;	SEQ ID NO 22		
;	LENGTH:	9737	
;	TYPE:	DNA	
;	ORGANISM:	Homo sapiens	
;	FEATURE:		
;	NAME/KEY:	modified_base	
;	LOCATION:	(8347)	
;	OTHER INFORMATION:	a, c, t, g, other or unknown	
;	FEATURE:		
;	NAME/KEY:	modified_base	
;	LOCATION:	(8499)	
;	OTHER INFORMATION:	a, c, t, g, other or unknown	

RESULT 39

FILE REFERENCE: 0221-0003H

; FILE REFERENCE

D^b 1651 CATTCAACCATTTGGTGTGCACCTC 1675

QY 240 CATTACACATTGGTGTGCACCTC 264

; FILE REFERENCE

; FILE REFERENCE

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; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-479-123-22

Query Match          94.0%; Score 248.2; DB 4; Length 9737;
Best Local Similarity 98.5%; Pred. No. 1.9e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY      1  AATGTAGCTCTTATGCAATCACTCTTGTAGTCTTGCACATGGTAACGATGAGTTAGCAACA 60
          |||
Db      1411 AATGTAGCTCTTATGCAATCACTCTTGTAGTCTTGCACATGGTAACGATGAGTTAGCAACA 1470
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QY      61  TGCCTTCAAGGAGAGAAAGACCGTGTCATGCCGATGTTGCGAAGTAAAGTGTGTAACA 120
          |||

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QY	121	TCGTGCGCTTTATGAGAAGCGCAACAGACGGGTCTGCATGATTCGACGACCACTAATTT	180
Db	1531	TCGTGCGCTTTATGAGAAGCGCAACAGACGGTCTGCATGATTCGACGACCACTGATTT	1590
QY	181	CGCATTGCGAGAGAT-ATTGTATTAAATGCGCTAGCTGCATACATAAAGCCGCAATTCAC	239
Db	1591	CGCATTGCGAGAGATAATTGTATTAAATGCGCTAGCTGCATACATAAAGCCGCAATTCAC	1650
QY	240	CATTCCACCAATTCGTTGCGACCTC	264
Db	1651	CATTCCACCAATTCGTTGCGACCTC	1675

RESULT 42

US-09-479-123-23

; Sequence 23, Application US/09479123

; Patent No. 6670185

; GENERAL INFORMATION:

; APPLICANT: HARRINGTON, JOHN J.

; APPLICANT: SHERF, BRUCE

; APPLICANT: RUNDLETT, STEPHEN

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF

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/ CURRENT APPLICATION NUMBER: US/09/479,123
/
/ CURRENT FILING DATE: 2000-01-07
/
/ PRIOR APPLICATION NUMBER: 09/263,814
/
/ PRIOR FILING DATE: 1999-03-08
/
/ PRIOR APPLICATION NUMBER: 09/253,022
/
/ PRIOR FILING DATE: 1999-02-19
/
/ PRIOR APPLICATION NUMBER: 09/159,643
/
/ PRIOR FILING DATE: 1998-09-24
/
/ PRIOR APPLICATION NUMBER: 08/941,223
/
/ PRIOR FILING DATE: 1997-09-26
/
/ NUMBER OF SEQ ID NOS: 33
/
/ SOFTWARE: Patent In Ver. 2.1
/
/ SEQ ID NO 23
/
/ LENGTH: 9737
/
/ TYPE: DNA
/
/ ORGANISM: Homo sapiens
/
/ FEATURE:
/
/ NAME/KEY: modified_base
/
/ LOCATION: (8347)
/
/ OTHER INFORMATION: a, c, t, g, other or unknown
/
/ FEATURE:
/

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Qy 181 CCGATTGCGAGAGAT-ATTGTAATTAAGTGCCTAGCTCGATACATAAAGCCGCAATTTGAC 239
Db 1725 CCGATTGCGAGAGAT-ATTGTAATTAAGTGCCTAGCTCGATACATAAAGCCGCAATTTGAC 1784
Qy 240 CATTCCACCATTTGGTGTGCACCTC 264
Db 1785 CATTCCACCATTTGGTGTGCACCTC 1809

RESULT 45

US-09-484-997-24
; Sequence 24, Application US/09484997
; Patent No. 6524818
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003J
; CURRENT APPLICATION NUMBER: US/09/484,997
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 9871
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8481)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8633)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-484-997-24

Query Match 94.0%; Score 248.2; DB 4; Length 9871;
Best Local Similarity 98.5%; Pred. No. 2e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGTGCAACATGTAACGATGAGTTAGCAACA 60
Db 1545 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGTGCAACATGTAACGATGAGTTAGCAACA 1604
Qy 61 TGCCTTACAGGAGAGAAAAGCACCCTGATGCCGATTTGGTGAAGTAAAGTGTGACGA 120
Db 1605 TGCCTTACAGGAGAGAAAAGCACCCTGATGCCGATTTGGTGAAGTAAAGTGTGACGA 1664
Qy 121 TCGTCCCTTTATAGGAAGCAACAGACAGCGGTCTGACATGGATTGGAGCAACCACTAAATT 180
Db 1665 TCGTCCCTTTATAGGAAGCAACAGACAGCGGTCTGACATGGATTGGAGCAACCACTAAATT 1724
Qy 181 CCGATTGCGAGAGAT-ATTGTAATTAAGTGCCTAGCTCGATACATAAAGCCGCAATTTGAC 239
Db 1725 CCGATTGCGAGAGAT-ATTGTAATTAAGTGCCTAGCTCGATACATAAAGCCGCAATTTGAC 1784

Qy 240 CATTCCACCATTTGGTGTGCACCTC 264

Db 1785 CATTCCACCATTTGGTGTGCACCTC 1809

RESULT 46

US-09-481-355-24
; Sequence 24, Application US/09481355
; Patent No. 6524824
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003F
; CURRENT APPLICATION NUMBER: US/09/481,355
; CURRENT FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 9871
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8481)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8633)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-481-355-24

Query Match 94.0%; Score 248.2; DB 4; Length 9871;
Best Local Similarity 98.5%; Pred. No. 2e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGTGCAACATGTAACGATGAGTTAGCAACA 60
Db 1545 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGTGCAACATGTAACGATGAGTTAGCAACA 1604
Qy 61 TGCCTTACAGGAGAGAAAAGCACCCTGATGCCGATTTGGTGAAGTAAAGTGTGACGA 120
Db 1605 TGCCTTACAGGAGAGAAAAGCACCCTGATGCCGATTTGGTGAAGTAAAGTGTGACGA 1664
Qy 121 TCGTCCCTTTATAGGAAGCAACAGACAGCGGTCTGACATGGATTGGAGCAACCACTAAATT 180
Db 1665 TCGTCCCTTTATAGGAAGCAACAGACAGCGGTCTGACATGGATTGGAGCAACCACTAAATT 1724
Qy 181 CCGATTGCGAGAGAT-ATTGTAATTAAGTGCCTAGCTCGATACATAAAGCCGCAATTTGAC 239
Db 1725 CCGATTGCGAGAGAT-ATTGTAATTAAGTGCCTAGCTCGATACATAAAGCCGCAATTTGAC 1784
Qy 240 CATTCCACCATTTGGTGTGCACCTC 264
Db 1785 CATTCCACCATTTGGTGTGCACCTC 1809

RESULT 47

US-09-481-282-24
; Sequence 24, Application US/09481282
; Patent No. 6541221
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003US
US-09-481-282-24

; PRIOR FILING DATE: 1997-09-26
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 24
 ; LENGTH: 9871
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: modified_base
 ; LOCATION: (8481)
 ; OTHER INFORMATION: a, c, t, g, other or unknown
 ; FEATURE:
 ; NAME/KEY: modified_base
 ; LOCATION: (8633)
 ; OTHER INFORMATION: a, c, t, g, other or unknown
 US-09-455-659A-24
 Query Match 94.0%; Score 248.2; DB 4; Length 9871;
 Best local Similarity 98.5%; Pred. No. 2e-77; 3; Indels 1; Gaps 1;
 Matches 261; Conservative 0; Mismatches 0; Mismatches 1; Gaps 1;
 Qy 1 AATGTAGTCTTATGCAATACACTTTGTAGTCTTTGCAACATGCTAAACATGAGTTAGCAACA 60
 Db 1545 AATGTAGTCTTATGCAATACACTTTGTAGTCTTTGCAACATGCTAAACATGAGTTAGCAACA 1604
 Qy 61 TGCCTTTACAAGAGAGAAAGAACACCGTGCATGCGGATTTCGTGGAAGTAAAGTGGTACGA 120
 Db 1605 TGCCTTTACAAGAGAGAAAGAACACCGTGCATGCGGATTTCGTGGAAGTAAAGTGGTACGA 1664
 Qy 121 TGTGCGCTTTATTAGGAAGGCAACAGACGGGTCTGCATGATGTGACAGCAACCACTTAATT 180
 Db 1665 TGTGCGCTTTATTAGGAAGGCAACAGACGGGTCTGCATGATGTGACAGCAACCACTTAATT 1724
 Qy 181 CGGCATTCGACGAT-ATTGTATTTAAGTGGCTAGCTCGATACATAAAGCCATTTCAC 239
 Db 1725 CGGCATTCGACGATATTGTATTTAAGTGGCTAGCTCGATACATAAAGCCATTTCAC 1784
 Qy 240 CATTCACCACATTGTTGTGCACCTC 264
 Db 1785 CATTCACCACATTGTTGTGCACCTC 1809
 RESULT 49
 US-09-484-396-24
 ; Sequence 24, Application US/03484996
 ; Patent No. 6623958
 ; GENERAL INFORMATION:
 ; APPLICANT: SHERRIF, BRUCE
 ; APPLICANT: HARRINGTON, JOHN J.
 ; APPLICANT: RUNDLETT, STEPHEN
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
 ; TITLE OF INVENTION: ENDOGENOUS GENES
 ; FILE REFERENCE: 0221-0003H
 ; CURRENT APPLICATION NUMBER: US/09/484,996
 ; CURRENT FILING DATE: 2000-01-18
 ; PRIOR APPLICATION NUMBER: 09/276,820
 ; PRIOR FILING DATE: 1999-03-26
 ; PRIOR APPLICATION NUMBER: 09/263,814
 ; PRIOR FILING DATE: 1998-03-08
 ; PRIOR APPLICATION NUMBER: 09/253,022
 ; PRIOR FILING DATE: 1999-02-19
 ; PRIOR APPLICATION NUMBER: 09/159,643
 ; PRIOR FILING DATE: 1998-09-24
 ; PRIOR APPLICATION NUMBER: 08/941,223
 ; PRIOR FILING DATE: 1997-09-26
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 24
 ; LENGTH: 9871
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: modified_base

LOCATION: (8481)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8633)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-484-996-24

Query Match 94.0%; Score 248.2; DB 4; Length 9871;
Best Local Similarity 98.5%; Pred. No. 2e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 1 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGTGCAACATGTAACGATGAGTTAGCAACA 60
Db |||||
1545 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGTGCAACATGTAACGATGAGTTAGCAACA 1604
QY |||||
61 TGCCTTACAAGGAGAGAAAAGCAACCGTGCATGCCGATTTGGTGAAGTAAGTGGTACGA 120
Db |||||
1605 TGCCTTACAAGGAGAGAAAAGCAACCGTGCATGCCGATTTGGTGAAGTAAGTGGTACGA 1664
QY |||||
121 TCGTGCCTTATTAGGAAGCAACACCGTGCATGCCGATTTGGTGAAGTAAGTGGTACGA 180
Db |||||
1665 TCGTGCCTTATTAGGAAGCAACACCGTGCATGCCGATTTGGTGAAGTAAGTGGTACGA 1724
QY |||||
181 CGCATTCGACAGAT-ATTGTAATTTAAAGTCCCTAGCTCGATACATAAAGCCCAATTTGAC 239
Db |||||
1725 CGCATTCGACAGAT-ATTGTAATTTAAAGTCCCTAGCTCGATACATAAAGCCCAATTTGAC 1784
QY |||||
240 CATTCACCAATTTGGTGGCACCTC 264
Db |||||
1785 CATTCACCAATTTGGTGGCACCTC 1809

RESULT 50
US-09-479-123-24
; Sequence 24, Application US/09479123
; Patent No. 6670185
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003B
; CURRENT APPLICATION NUMBER: US/09/479,123
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 9871
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8481)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8633)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-479-123-24

Query Match 94.0%; Score 248.2; DB 4; Length 9871;
Best Local Similarity 98.5%; Pred. No. 2e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGTGCAACATGTAACGATGAGTTAGCAACA 60
Db |||||
1545 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGTGCAACATGTAACGATGAGTTAGCAACA 1604
QY |||||
61 TGCCTTACAAGGAGAGAAAAGCAACCGTGCATGCCGATTTGGTGAAGTAAGTGGTACGA 120
Db |||||
1605 TGCCTTACAAGGAGAGAAAAGCAACCGTGCATGCCGATTTGGTGAAGTAAGTGGTACGA 1664
QY |||||
121 TCGTGCCTTATTAGGAAGCAACACCGTGCATGCCGATTTGGTGAAGTAAGTGGTACGA 180
Db |||||
1665 TCGTGCCTTATTAGGAAGCAACACCGTGCATGCCGATTTGGTGAAGTAAGTGGTACGA 1724
QY |||||
181 CGCATTCGACAGAT-ATTGTAATTTAAAGTCCCTAGCTCGATACATAAAGCCCAATTTGAC 239
Db |||||
1725 CGCATTCGACAGAT-ATTGTAATTTAAAGTCCCTAGCTCGATACATAAAGCCCAATTTGAC 1784
QY |||||
240 CATTCACCAATTTGGTGGCACCTC 264
Db |||||
1785 CATTCACCAATTTGGTGGCACCTC 1809

RESULT 51
US-09-479-122-25
; Sequence 25, Application US/09479122
; Patent No. 6410266
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003C
; CURRENT APPLICATION NUMBER: US/09/479,122
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 10060
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8670)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8822)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-479-122-25

Query Match 94.0%; Score 248.2; DB 4; Length 10060;
Best Local Similarity 98.5%; Pred. No. 2e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGTGCAACATGTAACGATGAGTTAGCAACA 60
Db |||||
1734 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGTGCAACATGTAACGATGAGTTAGCAACA 1793
QY |||||
61 TGCCTTACAAGGAGAGAAAAGCAACCGTGCATGCCGATTTGGTGAAGTAAGTGGTACGA 120
Db |||||
1794 TGCCTTACAAGGAGAGAAAAGCAACCGTGCATGCCGATTTGGTGAAGTAAGTGGTACGA 1853
QY |||||
121 TCGTGCCTTATTAGGAAGCAACACCGTGCATGCCGATTTGGTGAAGTAAGTGGTACGA 180

Ds 1854 TCGTGCCTTATTAGGAGGCAACAGACAGGCTGTGACATGGATTGGACGAAACCACTGAATT 1913
Qy 181 CGCATTCGACAGAT-ATTGTATTAAAGTCCCTAGCTCGATACAAATAAAGCCATTGAC 239
Ds 1914 CGCATTCGACAGATTAATTGATTAAAGTCCCTAGCTCGATACAAATAAAGCCATTGAC 1973
Qy 240 CATTACCAATTTGGTGGACCTC 264
Ds 1974 CATTACCAATTTGGTGGACCTC 1998

RESULT 52
US-09-484-997-25
; Sequence 25, Application US/09484997
; Patent No. 6524818
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003J
; CURRENT APPLICATION NUMBER: US/09/484,997
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 10060
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8670)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8822)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-484-997-25

Query Match 94.0%; Score 248.2; DB 4; Length 10060;
Best Local Similarity 98.5%; Pred. No. 2e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
Qy 1 AATGTAGCTTTATGCAATACCTTTGTAGTCTTGCAACATGGTAACGATGAGTTAGCAACA 60
Ds 1734 AATGTAGCTTTATGCAATACCTTTGTAGTCTTGCAACATGGTAACGATGAGTTAGCAACA 1793
Qy 61 TGCCTTACAGGAGAGAAAGACCGCTGATGCCGATTCGTAAGTAAGTGGTACGA 120
Ds 1794 TGCCTTACAGGAGAGAAAGACCGCTGATGCCGATTCGTAAGTAAGTGGTACGA 1853
Qy 121 TCGTGCCTTATTAGGAGGCAACAGACAGGCTGTGACATGGATTGGACGAAACCACTAAATT 180
Ds 1854 TCGTGCCTTATTAGGAGGCAACAGACAGGCTGTGACATGGATTGGACGAAACCACTAAATT 1913
Qy 181 CGCATTCGACAGAT-ATTGTATTAAAGTCCCTAGCTCGATACAAATAAAGCCATTGAC 239
Ds 1914 CGCATTCGACAGATTAATTGATTAAAGTCCCTAGCTCGATACAAATAAAGCCATTGAC 1973
Qy 240 CATTACCAATTTGGTGGACCTC 264
Ds 1974 CATTACCAATTTGGTGGACCTC 1998

RESULT 54
US-09-481-282-25
; Sequence 25, Application US/09481282
; Patent No. 6541221
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF

;	PRIOR FILING DATE: 1998-09-24	
;	PRIOR APPLICATION NUMBER: 08/941,223	
;	PRIOR FILING DATE: 1997-09-26	
;	NUMBER OF SEQ ID NOS: 33	
;	SOFTWARE: PatentIn Ver. 2.1	
;	SEQ ID NO 25	
;	LENGTH: 10060	
;	TYPE: DNA	
;	ORGANISM: Homo sapiens	
;	FEATURE:	
;	NAME/KEY: modified_base	
;	LOCATION: (8670)	
;	OTHER INFORMATION: a, c, t, g, other or unknown	
;	FEATURE:	
;	NAME/KEY: modified_base	
;	LOCATION: (8822)	
;	OTHER INFORMATION: a, c, t, g, other or unknown	
;	US-09-455-659A-25	
	Query Match	94.0%; Score 248.2; DB 4; Length 10060;
	Best Local Similarity	98.5%; Pred. NO. 2e-77;
	Matches 261; Conservative	0; Mismatches 3; Indels 1; Gaps 1;
QY	1	ATGTGATCTTATGCAATACACTCTTGTAGTCTTGCAACATGGGTAAACGATGAGTTAGCAACA 60
Db	1734	AATGTAGTCTTATGCAATACACTCTTGTAGTCTTGCAACATGGGTAAACGATGAGTTAGCAACA 1793
QY	61	TGCCTTACAAGGAGAGAAAGACACCGTGCATGCCGATTGGTGGAGGTAAAGGTGGTACGA 120
Db	1794	TGCCTTACAAGGAGAGAAAGACACCGTGCATGCCGATTGGTGGAGGTAAAGGTGGTACGA 1853
QY	121	TGTTGCCCTTATTAGGAGGCAACAGACGGGTCTGCATGGATTTGACGACGACCACTAAATT 180
Db	1854	TGTTGCCCTTATTAGGAGGCAACAGACGGGTCTGCATGGATTTGACGACGACCACTAAATT 1913
QY	181	CGCATTTGCAGAGAT-ATTGTATTTAAGTGCTAGCTCGATCAATAAAGCCCAATTGCAC 239
Db	1914	CGCATTTGCAGAGATATTGTATTTAAGTGGCTAGCTCGATCAATAAAGCCCAATTGCAC 1973
QY	240	CATTCAACCACTGGTGTGCACCTC 264
Db	1974	CATTCAACCACTGGTGTGCACCTC 1998
RESULT 56		
US-09-484-996-25		
;	Sequence 25, Application US/09484996	
;	Patent No. 6623958	
;	GENERAL INFORMATION:	
;	APPLICANT: HARRINGTON, JOHN J.	
;	APPLICANT: SHERP, BRUCE	
;	APPLICANT: RUNDLETT, STEPHEN	
;	TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF	
;	TITLE OF INVENTION: ENDOGENOUS GENES	
;	FILE REFERENCE: 0221-0003H	
;	CURRENT APPLICATION NUMBER: US/09/484,996	
;	CURRENT FILING DATE: 2000-01-18	
;	PRIOR APPLICATION NUMBER: 09/276,820	
;	PRIOR FILING DATE: 1999-03-26	
;	PRIOR APPLICATION NUMBER: 09/263,814	
;	PRIOR FILING DATE: 1998-03-08	
;	PRIOR APPLICATION NUMBER: 09/253,022	
;	PRIOR FILING DATE: 1999-02-19	
;	PRIOR APPLICATION NUMBER: 09/159,643	
;	PRIOR FILING DATE: 1998-09-24	
;	PRIOR APPLICATION NUMBER: 08/941,223	
;	PRIOR FILING DATE: 1997-09-26	
;	NUMBER OF SEQ ID NOS: 33	
;	SOFTWARE: PatentIn Ver. 2.1	
;	SEQ ID NO 25	
;	LENGTH: 10060	
;	TYPE: DNA	
;	ORGANISM: Homo sapiens	

```
;
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8670)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8822)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-484-996-25

Query Match          94.0%; Score 248.2; DB 4; Length 10060;
Best Local Similarity 98.5%; Pred. No. 2e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATACCTTGTAGTCTTGCACATGTAAGTGTAGTACCA 60
Db 1734 AATGTAGTCTTATGCAATACCTTGTAGTCTTGCACATGTAAGTGTAGTACCA 1793
QY 61 TGCCTTACAGGAGAGAAAAGCAGCCGTCATGCCGATTTGGTGAAGTAAAGTGTACGA 120
Db 1794 TGCCTTACAGGAGAGAAAAGCAGCCGTCATGCCGATTTGGTGAAGTAAAGTGTACGA 1853
QY 121 TCGTGCCCTTATTAGGAAGCAACAGACAGCGGTCTGACATGATTTGGACGAACCACTAAAT 180
Db 1794 TGCCTTACAGGAGAGAAAAGCAGCCGTCATGCCGATTTGGTGAAGTAAAGTGTACGA 1853
QY 1854 TCGTGCCCTTATTAGGAAGCAACAGACAGCGGTCTGACATGATTTGGACGAACCACTAAAT 1913
QY 181 CGCATTTGCAGAGAT-ATTGTATTATTAAGTGCCTAGCTCGATGATTTGGACGAACCACTAAAT 239
Db 1914 CGCATTTGCAGAGATTAATTGTATTATTAAGTGCCTAGCTCGATGATTTGGAC 1973
QY 240 CATTCCACACATTTGGTGTGCACCTC 264
Db 1974 CATTCCACACATTTGGTGTGCACCTC 1998
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RESULT 57
US-09-479-123-25
; Sequence 25, Application US/09479123
; Patent No. 6670185
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003B
; CURRENT APPLICATION NUMBER: US/09/479,123
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 10060
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8670)
; OTHER INFORMATION: a, c, t, g, other or unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8822)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-479-123-25

Query Match          94.0%; Score 248.2; DB 4; Length 10060;
Best Local Similarity 98.5%; Pred. No. 2e-77;
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Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATACCTTGTAGTCTTGCACATGTAAGTGTAGTACCA 60
Db 1734 AATGTAGTCTTATGCAATACCTTGTAGTCTTGCACATGTAAGTGTAGTACCA 1793
QY 61 TGCCTTACAGGAGAGAAAAGCAGCCGTCATGCCGATTTGGTGAAGTAAAGTGTACGA 120
Db 1794 TGCCTTACAGGAGAGAAAAGCAGCCGTCATGCCGATTTGGTGAAGTAAAGTGTACGA 1853
QY 121 TCGTGCCCTTATTAGGAAGCAACAGACAGCGGTCTGACATGATTTGGACGAACCACTAAAT 180
Db 1854 TCGTGCCCTTATTAGGAAGCAACAGACAGCGGTCTGACATGATTTGGACGAACCACTAAAT 1913
QY 181 CGCATTTGCAGAGAT-ATTGTATTATTAAGTGCCTAGCTCGATGATTTGGACGAACCACTAAAT 239
Db 1914 CGCATTTGCAGAGATTAATTGTATTATTAAGTGCCTAGCTCGATGATTTGGAC 1973
QY 240 CATTCCACACATTTGGTGTGCACCTC 264
Db 1974 CATTCCACACATTTGGTGTGCACCTC 1998

RESULT 58
US-09-167-322-13
; Sequence 13, Application US/09167322
; Patent No. 6365151
; GENERAL INFORMATION:
; APPLICANT: Allegheny University of the Health
; Sciences, Halpern, Michael S.
; England, James M.
; TITLE OF INVENTION: CANCER VACCINE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.
; STREET: Suite 1800, Two Penn Center Plaza
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/167,322
; FILING DATE: 07-Oct-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/00582
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 7933-33 PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; INFORMATION FOR SEQ ID NO: 13:
; LENGTH: 565 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-167-322-13
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Query Match          92.7%; Score 244.8; DB 4; Length 565;
Best Local Similarity 97.4%; Pred. No. 8.8e-77;
Matches 261; Conservative 0; Mismatches 2; Indels 5; Gaps 1;

QY 1 AATGTAGTCTTATGCAATACCTTGTAGTCTTGCACATG-----GTAAGTGTAGTAC 55
```

Db 233 ATGTAGCTTTATGCAATCTCTTGTAGTCTTGCACATGCTTATGACGATGAGTTAG 292
QY 56 CAACATGCTTACAGGAGAGAGAAAGACCGTGCATGCCGATTTGGTGGAGATAGGTGG 115
Db 293 CAACATGCTTACAGGAGAGAGAAAGACCGTGCATGCCGATTTGGTGGAGATAGGTGG 352
QY 116 TACGATGCTGCTTTATTAGGAGGCAACAGACGGGTCTGCATGGATTGGACGACCACT 175
Db 353 TACGATGCTGCTTTATTAGGAGGCAACAGACGGGTCTGCATGGATTGGACGACCACT 412
QY 176 AAATTTCGCGATTCGACGATATTTGTTAAAGTGCCTAGCTCGCATACAAATAAGCCCAT 235
Db 413 GAATTCGCGATTCGACGATATTTGTTAAAGTGCCTAGCTCGCATACAAATAAGCCCAT 472
QY 236 TGACCATTCACCATGTTGGTGCACCT 263
Db 473 TGACCATTCACCATGTTGGTGCACCT 500

RESULT 59

US-08-972-218-2
; Sequence 2, Application US/08972218
; Patent No. 6197502

GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Oxburger, Georg H.
; APPLICANT: Koller, Daniel
; APPLICANT: Bailey, James E.

; TITLE OF INVENTION: EXPRESSION CLONING PROCESSES FOR THE
; TITLE OF INVENTION: DISCOVERY, CHARACTERIZATION AND ISOLATION OF GENES
; TITLE OF INVENTION: ENCODING POLYPEPTIDES WITH A PREDETERMINED PROPERTY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of The Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/972,218
; FILING DATE: 14-NOV-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; FILING DATE:

ATTORNEY/AGENT INFORMATION:
; NAME: Abrams, Samuel
; REGISTRATION NUMBER: 30,605
; REFERENCE/DOCKET NUMBER: 008359-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5656
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9521 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-972-218-2

Query Match 77.7%; Score 205.2; DB 3; Length 9521;
Best Local Similarity 98.6%; Pred. No. 3e-62;
Matches 207; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 AUGTAGCTTTATGCAATCTCTTGTAGTCTTGCACATGCTTATGACGATGAGTTAGCAACAT 61

Db 664 ATCCAGTCTTTATGCAATCTCTTGTAGTCTTGCACATGCTTATGACGATGAGTTAGCAACAT 723
QY 62 GCCTTACAGGAGAGAGAAAGACCGTGCATGCCGATTTGGTGGAGATAGGTGGTACCAT 121
Db 724 GCCTTACAGGAGAGAGAAAGACCGTGCATGCCGATTTGGTGGAGATAGGTGGTACCAT 783
QY 122 CGTGCTTTATTAGGAGGCAACAGACGGGTCTGCATGGATTGGACGACCACTAAATTC 181
Db 784 CGTGCTTTATTAGGAGGCAACAGACGGGTCTGCATGGATTGGACGACCACTAAATTC 843
QY 182 CGCATTCGACGATATTTGTTAAAGTGCC 211
Db 844 CGCATTCGACGATATTTGTTAAAGTGCC 873

RESULT 60

US-09-193-707-2
; Sequence 2, Application US/09193707
; Patent No. 6524792

GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Oxburger, Georg H.
; APPLICANT: Koller, Daniel
; APPLICANT: Bailey, James E.

; TITLE OF INVENTION: EXPRESSION CLONING PROCESSES FOR THE DISCOVERY,
; TITLE OF INVENTION: CHARACTERIZATION AND ISOLATION OF GENES ENCODING POLYPEPTIDES WITH
; TITLE OF INVENTION: A PREDETERMINED PROPERTY
; FILE REFERENCE: 8358-0005-999
; CURRENT APPLICATION NUMBER: US/09/193,707
; CURRENT FILING DATE: 1998-11-17
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 9521
; TYPE: DNA
; ORGANISM: Alphavirus, Sindbis Virus
US-09-193-707-2

Query Match 77.7%; Score 205.2; DB 4; Length 9521;
Best Local Similarity 98.6%; Pred. No. 3e-62;
Matches 207; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 AUGTAGCTTTATGCAATCTCTTGTAGTCTTGCACATGCTTATGACGATGAGTTAGCAACAT 61
Db 664 ATCCAGTCTTTATGCAATCTCTTGTAGTCTTGCACATGCTTATGACGATGAGTTAGCAACAT 723
QY 62 GCCTTACAGGAGAGAGAAAGACCGTGCATGCCGATTTGGTGGAGATAGGTGGTACCAT 121
Db 724 GCCTTACAGGAGAGAGAAAGACCGTGCATGCCGATTTGGTGGAGATAGGTGGTACCAT 783
QY 122 CGTGCTTTATTAGGAGGCAACAGACGGGTCTGCATGGATTGGACGACCACTAAATTC 181
Db 784 CGTGCTTTATTAGGAGGCAACAGACGGGTCTGCATGGATTGGACGACCACTAAATTC 843
QY 182 CGCATTCGACGATATTTGTTAAAGTGCC 211
Db 844 CGCATTCGACGATATTTGTTAAAGTGCC 873

RESULT 61

US-09-733-042-1
; Sequence 1, Application US/09733042
; Patent No. 6576443

GENERAL INFORMATION:
; APPLICANT: Hennecke, Frank
; APPLICANT: Renner, Wolfgang A.

; TITLE OF INVENTION: Replicon Based Activation of Endogenous Genes
; FILE REFERENCE: 1700.0100001
; CURRENT APPLICATION NUMBER: US/09/733,042
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/169,988
; PRIOR FILING DATE: 1999-12-10

NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 11282
; TYPE: DNA
; ORGANISM: pCytts
US-09-733-042-1

Query Match 77.7%; Score 205.2; DB 4; Length 11282;
Best Local Similarity 98.6%; Pred. No. 3.2e-62;
Matches 207; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ATGTAGTCTTATGCAATCTCTTGTAGTCTTCCACATGCTTAACGATGATGATGATGAT 61
DB 664 ATCCAGTCTTATGCAATCTCTTGTAGTCTTCCACATGCTTAACGATGATGATGATGAT 723
QY 62 GCCTTACAGGAGAGAAAGCCGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 121
DB 724 GCCTTACAGGAGAGAAAGCCGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 783
QY 122 CGTCCCTTATTAGGAGGCAACAGACGGGTCTGATGATGATGATGATGATGATGATGAT 181
DB 784 CGTCCCTTATTAGGAGGCAACAGACGGGTCTGATGATGATGATGATGATGATGATGAT 843
QY 182 CGATTCGAGATATTTATTTAAGTGCC 211
DB 844 CGCATTCGAGATATTTATTTAAGTGCC 873

RESULT 62
US-08-470-299-2
; Sequence 2, Application US/08470299
; Patent No. 5783181
; GENERAL INFORMATION:
; APPLICANT: Browne, Michael J.
; APPLICANT: Murphy, Kay E.
; APPLICANT: Chapman, Conrad G.
; APPLICANT: Clinkenbeard, Helen E.
; APPLICANT: Young, Peter R.
; APPLICANT: Shatzman, Allan R.
; TITLE OF INVENTION: No. 5783181el Compounds
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road, P.O. Box 1539
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/470,299
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P31005C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5024
; TELEFAX: 610-270-5090
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6926 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
US-08-470-299-2

Query Match 29.2%; Score 77; DB 1; Length 6926;
Best Local Similarity 98.9%; Pred. No. 5.1e-17;
Matches 88; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 177 AATCCCGCATTCGAGAGAT-ATTGTATTAAAGTCTAGCTCGATACATAAAAGCCATT 235
DB 683 AATCCCGCATTCGAGAGATAATTGTATTAAAGTCTAGCTCGATACATAAAAGCCATT 742

QY 236 TGACCATTCACACATTTGGTGTGCACCTC 264
DB 743 TGACCATTCACACATTTGGTGTGCACCTC 771

RESULT 63
US-09-299-141-5
; Sequence 5, Application US/09299141
; Patent No. 6461606
; GENERAL INFORMATION:
; APPLICANT: FLOTTE, TERENCE R.
; APPLICANT: SONG, SIHONG
; APPLICANT: BYRNE, BARRY J.
; APPLICANT: MORGAN, MICHAEL
; TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
; FILE REFERENCE: 4300.011800
; CURRENT APPLICATION NUMBER: US/09/299,141
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: 60/083,025
; EARLIER FILING DATE: 1998-04-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 7492
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: p43C-AT-IN
US-09-299-141-5

Query Match 29.2%; Score 77; DB 4; Length 7492;
Best Local Similarity 98.9%; Pred. No. 5.3e-17;
Matches 88; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 177 AATCCCGCATTCGAGAGAT-ATTGTATTAAAGTCTAGCTCGATACATAAAAGCCATT 235
DB 1 AATCCCGCATTCGAGAGATAATTGTATTAAAGTCTAGCTCGATACATAAAAGCCATT 60

QY 236 TGACCATTCACACATTTGGTGTGCACCTC 264
DB 61 TGACCATTCACACATTTGGTGTGCACCTC 89

RESULT 64
US-08-989-394-10
; Sequence 10, Application US/08989394
; Patent No. 5994136
; GENERAL INFORMATION:
; APPLICANT: Naldini, Luigi
; APPLICANT: Dull, Thomas
; APPLICANT: Parson, Deborah A.
; APPLICANT: Witt, Rochelle
; TITLE OF INVENTION: METHOD AND MEANS FOR PRODUCING HIGH
; TITLE OF INVENTION: TITER, SAFE, RECOMBINANT LENTIVIRUS VECTORS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MILO, ZINN, MACPHEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,394
FILING DATE: 12-DEC-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Nakamura, Dean H.
REGISTRATION NUMBER: 33,981
REFERENCE/DOCKET NUMBER: A7086
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-989-394-10

Query Match 19.6%; Score 51.8; DB 2; Length 74;
Best Local Similarity 96.4%; Pred. No. 5.5e-09;
Matches 53; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 176 AAATTCGCGATTGCGAGATATTGTTTAAAGTGGCTAGCTCGATACATAAAGC 230
|||
Db 1 AATTGCGCGATTGCGAGATATTGTTTAAAGTGGCTAGCTCGATACATAAAGC 55
|||

RESULT 65
US-09-271-365-10
Sequence 10, Application US/09271365
Patent No. 6165782
GENERAL INFORMATION:
APPLICANT: Naldini, Luigi
Dull, Thomas
Parson, Deborah A.
Witt, Rochelle
TITLE OF INVENTION: METHOD AND MEANS FOR PRODUCING HIGH
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/271,365
FILING DATE: 18-Mar-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/989,394
FILING DATE: 12-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Nakamura, Dean H.
REGISTRATION NUMBER: 33,981
REFERENCE/DOCKET NUMBER: A7086
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-271-365-10

Query Match 19.6%; Score 51.8; DB 3; Length 74;
Best Local Similarity 96.4%; Pred. No. 5.5e-09;
Matches 53; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 176 AAATTCGCGATTGCGAGATATTGTTTAAAGTGGCTAGCTCGATACATAAAGC 230
|||
Db 1 AATTGCGCGATTGCGAGATATTGTTTAAAGTGGCTAGCTCGATACATAAAGC 55
|||

RESULT 66
US-09-604-013A-10
Sequence 10, Application US/09604013A
Patent No. 6428953
GENERAL INFORMATION:
APPLICANT: Naldini, Luigi
Dull, Thomas
Parson, Deborah A.
Witt, Rochelle
TITLE OF INVENTION: METHOD AND MEANS FOR PRODUCING HIGH
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/604,013A
FILING DATE: 26-Jun-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/271,365
FILING DATE: 18-Mar-1999
APPLICATION NUMBER: 08/989,394
FILING DATE: 12-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Nakamura, Dean H.
REGISTRATION NUMBER: 33,981
REFERENCE/DOCKET NUMBER: A7086
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-604-013A-10

Query Match 19.6%; Score 51.8; DB 4; Length 74;
Best Local Similarity 96.4%; Pred. No. 5.5e-09;
Matches 53; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 176 AAATTCGCGATTGCGAGATATTGTTTAAAGTGGCTAGCTCGATACATAAAGC 230
|||
Db 1 AATTGCGCGATTGCGAGATATTGTTTAAAGTGGCTAGCTCGATACATAAAGC 55
|||

RESULT 67
US-08-989-394-11/c
; Sequence 11, Application US/08989394
; Patent No. 5994136
; GENERAL INFORMATION:
; APPLICANT: Naldini, Luigi
; APPLICANT: Dull, Thomas
; APPLICANT: Farson, Deborah A.
; APPLICANT: Witt, Rochelle
; TITLE OF INVENTION: METHOD AND MEANS FOR PRODUCING HIGH
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/989,394
; FILING DATE: 12-DEC-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Dean H.
; REGISTRATION NUMBER: 33,981
; REFERENCE/DOCKET NUMBER: A7086
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7860
; TELEFAX: (202)293-7860
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 74 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; APPLICATION NUMBER: US/08/989,394
; FILING DATE: 12-DEC-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Dean H.
; REGISTRATION NUMBER: 33,981
; REFERENCE/DOCKET NUMBER: A7086
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7860
; TELEFAX: (202)293-7860
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 74 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-989-394-11

Query Match 18.9%; Score 50; DB 2; Length 74;
Best Local Similarity 100.0%; Pred. No. 2.4e-08;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 181 CGCATTGCAGAGATATTGTTTAAAGTCCCTAGCTCGATACATAAAG 230
DB 73 CGCATTGCAGAGATATTGTTTAAAGTCCCTAGCTCGATACATAAAG 24

RESULT 68
US-09-271-365-11/c
; Sequence 11, Application US/09271365
; Patent No. 6165782
; GENERAL INFORMATION:
; APPLICANT: Naldini, Luigi
; APPLICANT: Dull, Thomas
; APPLICANT: Farson, Deborah A.
; APPLICANT: Witt, Rochelle
; TITLE OF INVENTION: METHOD AND MEANS FOR PRODUCING HIGH
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20037

Query Match 18.9%; Score 50; DB 2; Length 74;
Best Local Similarity 100.0%; Pred. No. 2.4e-08;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 181 CGCATTGCAGAGATATTGTTTAAAGTCCCTAGCTCGATACATAAAG 230
DB 73 CGCATTGCAGAGATATTGTTTAAAGTCCCTAGCTCGATACATAAAG 24

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/271,365
FILING DATE: 18-Mar-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/989,394
FILING DATE: 12-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Nakamura, Dean H.
REGISTRATION NUMBER: 33,981
REFERENCE/DOCKET NUMBER: A7086
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-271-365-11

Query Match 18.9%; Score 50; DB 3; Length 74;
Best Local Similarity 100.0%; Pred. No. 2.4e-08;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 181 CGCATTGCAGAGATATTGTTTAAAGTCCCTAGCTCGATACATAAAG 230
DB 73 CGCATTGCAGAGATATTGTTTAAAGTCCCTAGCTCGATACATAAAG 24

RESULT 69
US-09-604-013A-11/c
; Sequence 11, Application US/09604013A
; Patent No. 6428953
; GENERAL INFORMATION:
; APPLICANT: Naldini, Luigi
; APPLICANT: Dull, Thomas
; APPLICANT: Farson, Deborah A.
; APPLICANT: Witt, Rochelle
; TITLE OF INVENTION: METHOD AND MEANS FOR PRODUCING HIGH
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/604,013A
; FILING DATE: 26-Jun-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/271,365
; FILING DATE: 18-Mar-1999
; APPLICATION NUMBER: 08/989,394
; FILING DATE: 12-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Dean H.

```

;
;   REGISTRATION NUMBER: 33,981
;   REFERENCE/DOCKET NUMBER: A7086
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (202)293-7060
;   TELEFAX: (202)293-7860
;   INFORMATION FOR SEQ ID NO: 11:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 74 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA
;   SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-604-013A-11

Query Match      18.9%; Score 50; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 2.4e-08;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 181 CCGCATTGCAGAGATATTTGATTTAAGTGCCTAGCTCGATACATAAAGC 230
DB 73 CCGCATTGCAGAGATATTTGATTTAAGTGCCTAGCTCGATACATAAAGC 24

RESULT 70
US-08-272-513-1
; Sequence 1, Application US/08272513
; Patent No. 5558867
; GENERAL INFORMATION:
; APPLICANT: Sakaguchi, Masashi
; APPLICANT: Yamamoto, Michitaka
; TITLE OF INVENTION: RECOMBINANT MAREK'S DISEASE VIRUS,
; TITLE OF INVENTION: PROCESS FOR PREPARING THE SAME AND VACCINE CONTAINING THE
; TITLE OF INVENTION: SAME
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wegner, Cantor, Mueller & Player
; STREET: 1233 20th Street, N.W.
; CITY: Washington
; STATE: D.C.
; ZIP: 20036-8218
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/272,513
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/910,554
; FILING DATE: 08-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: P-500-23477
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-0400
; TELEFAX: 202-835-0605
; TELEX: 440706
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3001 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Marek's disease gammaherpesvirus
; STRAIN: 61-554 and BC-1
US-08-272-513-1
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Query Match      17.0%; Score 44.8; DB 1; Length 3001;
Best Local Similarity 81.2%; Pred. No. 8.3e-06;
Matches 52; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 200 TATTTAAGTGCCTAGCTCGATACATAAAGCCATTTCACCATTCACCATTCGTCGC 259
DB 2108 TATATAAGCTGTTGCCACCATCAATAAAGCCATTTCACCATTCACCATTCGTCGC 2167

QY 260 ACCT 263
DB 2168 ACCT 2171

RESULT 71
US-08-379-452-9/c
; Sequence 9, Application US/08379452
; Patent No. 6040174
; GENERAL INFORMATION:
; APPLICANT: IMLER, Jean-Luc
; APPLICANT: MEHTALI, Majid
; APPLICANT: PAVIRANI, Andrea
; TITLE OF INVENTION: DEFECTIVE ADENOVIRUSES AND CORRESPONDING
; TITLE OF INVENTION: COMPLEMENTATION LINES
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: 1737 King Street, Suite 500
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22314-2756
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/379,452
; FILING DATE: 26-JAN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR94/00624
; FILING DATE: 27-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93 06482
; FILING DATE: 28-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Radio, Susan M.
; REGISTRATION NUMBER: 40,373
; REFERENCE/DOCKET NUMBER: 029395-002
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 47 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; ORIGINAL SOURCE:
; ORGANISM: Synthetic oligonucleotide (ONG5893)
US-08-379-452-9

Query Match      12.5%; Score 33; DB 3; Length 47;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 231 CCATTGACCATTCACCATTCGTCGCACCT 263
DB 47 CCATTGACCATTCACCATTCGTCGCACCT 15

RESULT 72
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US-08-682-794-5/c
; Sequence 5, Application US/08682794
; Patent No. 6110735
; GENERAL INFORMATION:
; APPLICANT: CILE CHARTIER et al.
; TITLE OF INVENTION: METHOD OF PREPARING A VIRAL VECTOR BY INTERMOLECULAR
; FILE REFERENCE: 032751-002
; CURRENT APPLICATION NUMBER: US/08/682,794
; CURRENT FILING DATE: 1996-08-01
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 5
; LENGTH: 47
; TYPE: DNA
; ORGANISM: rous sarcoma virus
US-08-682-794-5

Query Match      12.5%; Score 33; DB 3; Length 47;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      231 CCATTGACCATTCACCATTCGTTGGTGCACCT 263
Db      47 CCATTGACCATTCACCATTCGTTGGTGCACCT 15

RESULT 73
US-09-409-670-9/c
; Sequence 9, Application US/09409670
; Patent No. 6133028
; GENERAL INFORMATION:
; APPLICANT: IMLER, Jean-Irac
; APPLICANT: MEHTALI, Majid
; APPLICANT: PAVIRANI, Andrea
; TITLE OF INVENTION: DEFECTIVE ADENOVIRUSES AND CORRESPONDING
; FILE REFERENCE: 032751-002
; CURRENT APPLICATION NUMBER: US/09/467,952
; EARLIER FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: 08/682,794
; EARLIER FILING DATE: 1996-08-01
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 5
; LENGTH: 47
; TYPE: DNA
; ORGANISM: rous sarcoma virus
US-09-467-952-5/c
; Sequence 5, Application US/09467952
; Patent No. 6281000
; GENERAL INFORMATION:
; APPLICANT: CILE CHARTIER et al.
; TITLE OF INVENTION: METHOD OF PREPARING A VIRAL VECTOR BY INTERMOLECULAR
; FILE REFERENCE: 032751-002
; CURRENT APPLICATION NUMBER: US/09/467,952
; EARLIER FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: 08/682,794
; EARLIER FILING DATE: 1996-08-01
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 5
; LENGTH: 47
; TYPE: DNA
; ORGANISM: rous sarcoma virus
US-09-467-952-5

Query Match      12.5%; Score 33; DB 3; Length 47;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      231 CCATTGACCATTCACCATTCGTTGGTGCACCT 263
Db      47 CCATTGACCATTCACCATTCGTTGGTGCACCT 15

RESULT 74
US-09-467-952-5/c
; Sequence 5, Application US/09467952
; Patent No. 6281000
; GENERAL INFORMATION:
; APPLICANT: CILE CHARTIER et al.
; TITLE OF INVENTION: METHOD OF PREPARING A VIRAL VECTOR BY INTERMOLECULAR
; FILE REFERENCE: 032751-002
; CURRENT APPLICATION NUMBER: US/09/467,952
; EARLIER FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: 08/682,794
; EARLIER FILING DATE: 1996-08-01
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 5
; LENGTH: 47
; TYPE: DNA
; ORGANISM: rous sarcoma virus
US-09-467-952-5

Query Match      12.5%; Score 33; DB 3; Length 47;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      231 CCATTGACCATTCACCATTCGTTGGTGCACCT 263
Db      47 CCATTGACCATTCACCATTCGTTGGTGCACCT 15

RESULT 75
US-09-167-322-10
; Sequence 10, Application US/09167322
; Patent No. 6365151
; GENERAL INFORMATION:
; APPLICANT: Allegheny University of the Health
; Sciences, Halpern, Michael S.
; England, James M.
; TITLE OF INVENTION: CANCER VACCINE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seidel, Gorda, Lavorina & Monaco, P.C.
; STREET: Suite 1800, Two Penn Center Plaza
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; APPLICATION NUMBER: WO PCT/FR94/00624
; FILING DATE: 27-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93 06482
; FILING DATE: 28-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Padio, Susan M.
; REGISTRATION NUMBER: 40,373
; REFERENCE/DOCKET NUMBER: 029395-002
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 47 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

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; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; ORIGINAL SOURCE:
; ORGANISM: Synthetic oligonucleotide (OTG5893)
US-09-409-670-9

Query Match      12.5%; Score 33; DB 3; Length 47;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      231 CCATTGACCATTCACCATTCGTTGGTGCACCT 263
Db      47 CCATTGACCATTCACCATTCGTTGGTGCACCT 15

RESULT 76
US-09-167-322-10
; Sequence 10, Application US/09167322
; Patent No. 6365151
; GENERAL INFORMATION:
; APPLICANT: Allegheny University of the Health
; Sciences, Halpern, Michael S.
; England, James M.
; TITLE OF INVENTION: CANCER VACCINE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seidel, Gorda, Lavorina & Monaco, P.C.
; STREET: Suite 1800, Two Penn Center Plaza
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; APPLICATION NUMBER: WO PCT/FR94/00624
; FILING DATE: 27-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93 06482
; FILING DATE: 28-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Padio, Susan M.
; REGISTRATION NUMBER: 40,373
; REFERENCE/DOCKET NUMBER: 029395-002
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 47 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

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; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 7933-33 PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1897 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-167-322-10

Query Match          11.9%; Score 31.4; DB 4; Length 1897;
Best Local Similarity 75.4%; Pred. No. 0.37;
Matches 52; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

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Db 1748 AATGTACTTAAGCTTGTGTTGCTAACAATAAAGTCCATTCCTCTCACCACATTTGG 1807

QY 255 TGTGCACCT 263
Db 1808 TGTGCACCT 1816

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Search completed: March 11, 2004, 11:10:00
Job time : 56.7624 secs

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OM nucleic - nucleic search, using sw model

Run on: March 11, 2004, 08:24:22 ; Search time 191.633 Seconds
(without alignments)
5071.893 Million cell updates/sec

Title: US-09-733-368a-1_COPY_349_612

Perfect score: 264

Sequence: 1 aatgtatttattgcaatac.....accacattgtgtgcaatc 264

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Searched: 2432557 seqs, 1840798884 residues

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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- 3: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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- 18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	262.4	99.4	8238	10	US-09-482-682-50
2	262.4	99.4	33622	15	US-10-403-337-44
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4	262.4	99.4	35211	15	US-10-403-337-43
5	262.4	99.4	35211	15	US-10-351-890-43
6	257.2	97.4	262	9	US-09-965-703-69
7	257.2	97.4	262	12	US-10-239-134-61
8	248.2	94.0	6836	14	US-10-331-329-18
9	248.2	94.0	8902	9	US-09-729-416A-1
10	248.2	94.0	9737	14	US-10-331-329-22
11	248.2	94.0	9737	14	US-10-331-329-23
12	248.2	94.0	9737	14	US-10-331-329-28
13	248.2	94.0	9871	14	US-10-331-329-24
14	248.2	94.0	10060	14	US-10-331-329-25
15	248.2	94.0	11265	14	US-10-185-799-1

16	248.2	94.0	11265	14	US-10-185-799-1
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18	232	87.9	5130	10	US-09-897-511A-9
19	217.4	82.3	10469	14	US-10-155-736A-1
20	205.2	77.7	11282	9	US-09-733-042-1
21	205.2	77.7	11282	10	US-09-275-883-1
22	187.6	71.1	5283	11	US-09-921-143-36
23	174.2	66.0	6250	12	US-10-182-327-16
24	174.2	66.0	6250	15	US-10-182-329-109
25	173.4	65.7	11600	9	US-09-847-101B-35
26	173.4	65.7	11600	10	US-09-482-682-49
27	173.4	65.7	11600	15	US-10-403-337-42
28	173.4	65.7	11600	15	US-10-351-890-42
29	171.8	65.1	6279	15	US-10-182-329-1
30	171.8	65.1	8513	15	US-10-182-329-9
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32	77	29.2	7492	14	US-10-267-117-5
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37	33	12.5	47	9	US-09-938-491-5
38	33	12.5	47	10	US-09-739-007-9
39	33	12.5	542	15	US-10-027-632-81543
40	33	12.5	542	15	US-10-027-632-301875
41	33	12.5	573	15	US-10-027-632-50648
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43	31.4	11.9	669	12	US-10-424-599-52313
44	31	11.7	595	12	US-10-424-599-132712
45	30.8	11.7	1330	12	US-10-424-599-14875
46	30.8	11.7	2664	15	US-10-027-632-112120
47	30.6	11.6	5214	15	US-10-027-632-175173
48	30.4	11.5	3300	12	US-10-425-114-31887
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53	30.2	11.4	1452	9	US-09-739-254-34
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61	29.6	11.2	302250	9	US-09-962-832-154
62	29.2	11.1	183	15	US-10-027-632-63861
63	29.2	11.1	637	15	US-10-027-632-64765
64	29.2	11.1	752	15	US-10-027-632-63862
65	29.2	11.1	752	15	US-10-027-632-64766
66	29.2	11.1	752	15	US-10-027-632-310455
67	29.2	11.1	752	15	US-10-027-632-310456
68	29.2	11.1	766	15	US-10-027-632-35424
69	29.2	11.1	5297	14	US-10-311-455-820
70	29.2	11.1	5297	16	US-10-257-166-84
71	29	11.0	518	12	US-10-424-599-17797
72	29	11.0	1438	9	US-09-764-847-1659
73	29	11.0	1438	14	US-10-092-154-1659
74	29	11.0	3308	15	US-10-220-891-5
75	29	11.0	6302	14	US-10-097-534-5
76	29	11.0	6396	14	US-10-037-270-226
77	29	11.0	6396	15	US-10-117-722-226
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79	28.8	10.9	577	14	US-09-796-692-6990
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87	28.6	10.8	676	15	US-10-027-632-134758
88	28.6	10.8	676	15	US-10-027-632-134759

Sequence 1, Appli

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c 89 28.6 10.8 676 15 US-10-027-632-134760 Sequence 134760,
c 90 28.6 10.8 835 12 US-10-424-599-11801 Sequence 11801, A
c 91 28.6 10.8 2932 15 US-10-027-632-112341 Sequence 112341,
c 92 28.4 10.8 39 10 US-09-996-073-27 Sequence 27, Appl
c 93 28.4 10.8 668 12 US-10-424-599-130378 Sequence 130378,
c 94 28.4 10.8 1008 12 US-10-282-122A-28910 Sequence 28910, A
c 95 28.4 10.8 1011 12 US-10-282-122A-29797 Sequence 29797, A
c 96 28.4 10.8 2368 12 US-10-424-599-120123 Sequence 120123,
c 97 28.2 10.7 271 12 US-10-424-599-42230 Sequence 42230, A
c 98 28.2 10.7 750 14 US-10-161-051-39 Sequence 39, Appl
c 99 28.2 10.7 30352 9 US-09-764-869-1768 Sequence 1768, Ap
c 100 28.2 10.7 30352 14 US-10-091-504-1768 Sequence 1768, Ap

ALIGNMENTS

RESULT 1
US-09-482-682-50
; Sequence 50, Application US/09482682
; Publication No. US2003015768A1
; GENERAL INFORMATION:
; APPLICANT: VON SEGGERN, DANIEL
; APPLICANT: NEMEROW, GLEN R.
; APPLICANT: HALLENBECK, PAUL
; APPLICANT: STEVENSON, SUSAN
; APPLICANT: SKRIPCENKO, YELENA
; TITLE OF INVENTION: ADENOVIRUS VECTORS, PACKAGING CELL LINES, COMPOSITIONS,
; FILE REFERENCE: 1294.0010001
; CURRENT APPLICATION NUMBER: US/09/482,682
; CURRENT FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 8238
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-09-482-682-50

Query Match 99.4%; Score 262.4; DB 10; Length 8238;
Best Local Similarity 99.6%; Pred. No. 1.4e-79;
Matches 263; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 AATGAGCTTATGCAATACCTCTTGTAGCTTGCACATGCTTAACGATGAGTTAGCAACA 60
DB 541 AATGAGCTTATGCAATACCTCTTGTAGCTTGCACATGCTTAACGATGAGTTAGCAACA 600
QY 61 TGCCTTACAAGGAGAGAAAAGCACCGTGCATGCGATGCTGAAGTAAAGTGGTAGCA 120
DB 601 TGCCTTACAAGGAGAGAAAAGCACCGTGCATGCGATGCTGAAGTAAAGTGGTAGCA 660
QY 121 TCGTCCCTTATTAGGAGCAACAGACGGGTCTGCATGCTGAAGTAAAGTGGTAGCAATT 180
DB 661 TCGTCCCTTATTAGGAGCAACAGACGGGTCTGCATGCTGAAGTAAAGTGGTAGCAATT 720
QY 181 CGCATTTGCAGAGATATTGTTATTAAAGTGCCTAGCTCGATACATAAAGCCATTGGACC 240
DB 721 CGCATTTGCAGAGATATTGTTATTAAAGTGCCTAGCTCGATACATAAAGCCATTGGACC 780
QY 241 ATTCACCAATTTGGTGTGCACCTC 264
DB 781 ATTCACCAATTTGGTGTGCACCTC 804

RESULT 2
US-10-403-337-44
; Sequence 44, Application US/10403337
; Publication No. US20030215948A1
; GENERAL INFORMATION:
; APPLICANT: Kaleko, Michael

; APPLICANT: Nemerow, Glen R.
; APPLICANT: Smith, Theodore
; APPLICANT: Stevenson, Susan C.
; TITLE OF INVENTION: Fiber Shaft Modifications for Efficient Targeting
; FILE REFERENCE: 22908-1236B
; CURRENT APPLICATION NUMBER: US/10/403,337
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: 10/351,890
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 60/350,388
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/391,967
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 44
; LENGTH: 33622
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid Av3nBg
US-10-403-337-44

Query Match 99.4%; Score 262.4; DB 15; Length 33622;
Best Local Similarity 99.6%; Pred. No. 2.7e-79;
Matches 263; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 AATGAGCTTATGCAATACCTCTTGTAGCTTGCACATGCTTAACGATGAGTTAGCAACA 60
DB 533 AATGAGCTTATGCAATACCTCTTGTAGCTTGCACATGCTTAACGATGAGTTAGCAACA 592
QY 61 TGCCTTACAAGGAGAGAAAAGCACCGTGCATGCGATGCTGAAGTAAAGTGGTAGCA 120
DB 593 TGCCTTACAAGGAGAGAAAAGCACCGTGCATGCGATGCTGAAGTAAAGTGGTAGCA 652
QY 121 TCGTCCCTTATTAGGAGCAACAGACGGGTCTGCATGCTGAAGTAAAGTGGTAGCAATT 180
DB 653 TCGTCCCTTATTAGGAGCAACAGACGGGTCTGCATGCTGAAGTAAAGTGGTAGCAATT 712
QY 181 CGCATTTGCAGAGATATTGTTATTAAAGTGCCTAGCTCGATACATAAAGCCATTGGACC 240
DB 713 CGCATTTGCAGAGATATTGTTATTAAAGTGCCTAGCTCGATACATAAAGCCATTGGACC 772
QY 241 ATTCACCAATTTGGTGTGCACCTC 264
DB 773 ATTCACCAATTTGGTGTGCACCTC 796

RESULT 3
US-10-351-890-44
; Sequence 44, Application US/10351890
; Publication No. US20040002060A1
; GENERAL INFORMATION:
; APPLICANT: Stevenson, Susan C.
; APPLICANT: Kaleko, Michael
; APPLICANT: Smith, Theodore
; APPLICANT: Nemerow, Glen R.
; TITLE OF INVENTION: Fiber Shaft Modifications for Efficient Targeting
; FILE REFERENCE: 22908-1236
; CURRENT APPLICATION NUMBER: US/10/351,890
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: 60/350,388
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/391,967
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 44
; LENGTH: 33622
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid Av3nBg

QY	1	AAATGTA	GTCTTATG	CAATACTCT	TAGTCTT	GTCAACAT	GGTAA	CGATGAT	GTAGT	TAGCAACA	60
Db	647	AAATGTA	GTCTTATG	CAATACTCT	TAGTCTT	GTCAACAT	GGTAA	CGATGAT	GTAGT	TAGCAACA	706
QY	61	TGCCTT	ACAGGAG	GAAGAAAG	CACCGT	CGATCGCGAT	TGGT	TGGAAGT	TAAGT	TGTGTGCA	120
Db	707	TGCCTT	ACAGGAG	GAAGAAAG	CACCGT	CGATCGCGAT	TGGT	TGGAAGT	TAAGT	TGTGTGCA	766
QY	121	TGTGT	CCCTTAT	TAGGAAG	GGCAACAG	ACGGGTCTG	CATCGAT	TGGAG	CGAACCACT	TAATTT	180
Db	767	TGTGT	CCCTTAT	TAGGAAG	GGCAACAG	ACGGGTCTG	CATCGAT	TGGAG	CGAACCACT	TAATTT	826
QY	181	CCGCAT	TGCAG	ATATTTGT	ATTTAA	GTGGCTT	CGATCGAT	ACAATAA	ACGCCAT	TTTGACC	240

; CURRENT FILING DATE: 2001-09-26

QY	2	ATGTAGTCTTATGCAATACTCTTGTAGTCTTGCACACATGCTAACAGTACGATGAGTTACACACAT	61
Db	1	ATGTAGTCTTATGCAATACTCTTGTAGTCTTGCACACATGCTAACAGTACGATGAGTTACACACAT	61
QY	62	GCCTTACAAGGAGAGAAAAAGCACCGTGCATCGCGATTGGTTCGAACTAAGGTGGTACGAT	121
Db	61	GCCTTACAAGGAGAGAAAAAGCACCGTGCATCGCGATTGGTTCGAACTAAGGTGGTACGAT	120
QY	122	CGTGCCTTATTAGGAAGGCAACAGACGGGTCTGACATGGATTGGAGCAACACACTAAATTC	181
Db	121	CGTGCCTTATTAGGAAGGCAACAGACGGGTCTGACATGGATTGGAGCAACACACTGAATTC	180
QY	182	CGCATTTGCAGAGATATTGTTATTAAAGTGCTAGCTCGATACATATAAGCGCCATTTGACCA	241
Db	181	CGCATTTGCAGAGATATTGTTATTAAAGTGCTAGCTCGATACATATAAGCGCCATTTGACCA	240
QY	242	TTTCAACCAATTGGTGTGCACCT	263
Db	241	TTTCAACCAATTGGTGTGCACCT	262
RESULT 8			
US-10-331-329-18			
; Sequence 18, Application US/10331329			
; Publication No. US20030180267A1			
; GENERAL INFORMATION:			
; APPLICANT: HARRINGTON, JOHN J.			
; APPLICANT: SHERP, BRUCE			
; APPLICANT: RUNDETT, STEPHEN			
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF			
; TITLE OF INVENTION: ENDOGENOUS GENES			
; FILE REFERENCE: 0221-0003CON			
; CURRENT APPLICATION NUMBER: US/10/331,329			
; CURRENT FILING DATE: 2002-12-30			
; PRIOR APPLICATION NUMBER: 09/276,820			
; PRIOR FILING DATE: 1999-03-26			
; PRIOR APPLICATION NUMBER: 09/263,814			
; PRIOR FILING DATE: 1999-03-08			
; PRIOR APPLICATION NUMBER: 09/253,022			
; PRIOR FILING DATE: 1999-02-19			
; PRIOR APPLICATION NUMBER: 09/159,643			
; PRIOR FILING DATE: 1998-09-24			
; PRIOR APPLICATION NUMBER: 08/941,223			
; PRIOR FILING DATE: 1997-09-26			
; NUMBER OF SEQ ID NOS: 33			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 18			
; LENGTH: 6836			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-331-329-18			
Query Match 94.0%; Score 248.2; DB 14; Length 6836;			
Best Local Similarity 98.5%; Pred. No. 1e-74;			
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1			
QY	1	AATGTAGTCTTATGCAATACTCTTGTAGTCTTGCACACATGCTAACAGTACGATGAGTTACACCA	60
Db	1558	AATGTAGTCTTATGCAATACTCTTGTAGTCTTGCACACATGCTAACAGTACGATGAGTTACACCA	161
QY	61	TGCTTACAAGGAGAGAAAAAGCACCGTGCATCGCGATTGGTTCGAACTAAGGTGGTACGA	120
Db	1618	TGCTTACAAGGAGAGAAAAAGCACCGTGCATCGCGATTGGTTCGAACTAAGGTGGTACGA	167
QY	121	TCGTGCTTATTAGGAAGGCAACAGACGGGTCTGACATGGATTGGAGCAACACACTAAATT	180
Db	1678	TCGTGCTTATTAGGAAGGCAACAGACGGGTCTGACATGGATTGGAGCAACACACTGAATT	173
QY	181	CCGCATTGCAGAGAT-ATTGTATTAAAGTGCCTTAGCTCGATACATTAACCGCAATTGAC	239
Db	1738	CCGCATTGCAGAGATATTGTATTAAAGTGCCTTAGCTCGATACATTAACCGCAATTGAC	179

; PRIOR APPLICATION NUMBER: 08/941,223
 ; PRIOR FILING DATE: 1997-09-26
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 22
 ; LENGTH: 9737
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: modified_base
 ; LOCATION: (8347)
 ; OTHER INFORMATION: a, c, t, g, other or unknown
 ; FEATURE:
 ; NAME/KEY: modified_base
 ; LOCATION: (8499)
 ; OTHER INFORMATION: a, c, t, g, other or unknown
 US-10-331-329-22

Query Match 94.0%; Score 248.2; DB 14; Length 9737;
 Best Local Similarity 98.5%; Pred. No. 1.2e-74; Indels 1; Gaps 1;
 Matches 261; Conservative 0; Mismatches 3;

QY 1 AATGTAGTCTTATGCCAATACCTTTGTAGTCTTTGCCAATCATGTTAAAGCATGAGTTAGCAACA 60
 Db 1411 AATGTAGTCTTATGCCAATACCTTTGTAGTCTTTGCCAATCATGTTAAAGCATGAGTTAGCAACA 1470
 QY 61 TGCCTTACAGGAGAGAAAGACACCGTCATGCGGATTTGGTGGAGTAAGCTGGTTACGA 120
 Db 1471 TGCCTTACAGGAGAGAAAGACACCGTCATGCGGATTTGGTGGAGTAAGCTGGTTACGA 1530
 QY 121 TCGTGCCCTTATTAGGAAGGCAACAGACGGGCTCTGACATGCAATGGACGAACCACTAAATT 180
 Db 1531 TCGTGCCCTTATTAGGAGGCAACAGACGGTCTGACATGCAATGGACGAACCACTGAATT 1590
 QY 181 CGCATTCGACAGAT-ATTGTAATTAAAGTGCCTAGCTCGATACATATAAGCCCAATTGGAC 239
 Db 1591 CGGCATTCGACAGATTAATTGTAATTAAAGTGCCTAGCTCGATACATATAAGCCCAATTGGAC 1650
 QY 240 CATTCCACCATAATGGTGTGCACCTC 264
 Db 1651 CATTCCACCATAATGGTGTGCACCTC 1675

RESULT 11
 US-10-331-329-23
 ; Sequence 23, Application No. 10331329
 ; Publication No. US20030180267A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HARRINGTON, JOHN J.
 ; APPLICANT: SHERF, BRUCE
 ; APPLICANT: RUNDLETT, STEPHEN
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
 ; TITLE OF INVENTION: ENDOGENOUS GENES
 ; FILE REFERENCE: 0221-0003CON
 ; CURRENT APPLICATION NUMBER: US/10/331,329
 ; CURRENT FILING DATE: 2002-12-30
 ; PRIOR APPLICATION NUMBER: 09/276,820
 ; PRIOR FILING DATE: 1999-03-26
 ; PRIOR APPLICATION NUMBER: 09/263,814
 ; PRIOR FILING DATE: 1999-03-08
 ; PRIOR APPLICATION NUMBER: 09/253,022
 ; PRIOR FILING DATE: 1999-02-19
 ; PRIOR APPLICATION NUMBER: 09/159,643
 ; PRIOR FILING DATE: 1998-09-24
 ; PRIOR APPLICATION NUMBER: 08/941,223
 ; PRIOR FILING DATE: 1997-09-26
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 23
 ; LENGTH: 9737
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:

; NAME/KEY: modified_base
 ; LOCATION: (8347)
 ; OTHER INFORMATION: a, c, t, g, other or unknown
 ;
 ; FEATURE:
 ; NAME/KEY: modified_base
 ; LOCATION: (8499)
 ; OTHER INFORMATION: a, c, t, g, other or unknown
 US-10-331-329-23

Query Match 94.0%; Score 248.2; DB 14; Length 9737;
 Best Local Similarity 98.5%; Pred. No. 1.2e-74;
 Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 QY 1 AATGTAGTCTTATGCAATACCTTGTAGTCTTGCACATGTAACGATGAGTTAGCAACA 60
 Db 1411 AATGTAGTCTTATGCAATACCTTGTAGTCTTGCACATGTAACGATGAGTTAGCAACA 1470
 QY 61 TGCCTTACAAGGAGAGAAAAGCACCGTGCATGCGGTCCTGACATGATGGAGCAACCACTTAATT 180
 Db 1471 TGCCTTACAAGGAGAGAAAAGCACCGTGCATGCGGTCCTGACATGATGGAGCAACCACTTAATT 1590
 QY 121 TCGTGCCTTATTAGGAGGCAACAGACAGGTCCTGACATGATGGAGCAACCACTTAATT 180
 Db 1471 TGCCTTACAAGGAGAGAAAAGCACCGTGCATGCGGTCCTGACATGATGGAGCAACCACTTAATT 1590
 QY 181 CGCATTCGAGAGAT-ATTGTATTAAAGTGCCTAGCTGCATACATAAAGCAACCACTTAATT 239
 Db 1591 CGCATTCGAGAGATATTGTATTAAAGTGCCTAGCTGCATACATAAAGCAACCACTTAATT 1650
 QY 240 CATTCAACACATTTGGTGTGCACCTC 264
 Db 1651 CATTCAACACATTTGGTGTGCACCTC 1675

RESULT 12

US-10-331-329-28
 ; Sequence 28, Application US/10331329
 ; Publication No. US20030180267A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HARRINGTON, JOHN J.
 ; APPLICANT: SHERP, BRUCE
 ; APPLICANT: RUNDLETT, STEPHEN
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
 ; FILE REFERENCE: 0221-0003CON
 ; CURRENT APPLICATION NUMBER: US/10/331,329
 ; PRIOR FILING DATE: 2002-12-30
 ; PRIOR FILING DATE: 1999-03-26
 ; PRIOR FILING DATE: 1999-03-08
 ; PRIOR FILING DATE: 1999-02-19
 ; PRIOR FILING DATE: 1998-09-24
 ; PRIOR FILING DATE: 1997-09-26
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 28
 ; LENGTH: 9737
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: modified_base
 ; LOCATION: (8347)
 ; OTHER INFORMATION: a, c, t, g, other or unknown
 ;
 ; FEATURE:
 ; NAME/KEY: modified_base
 ; LOCATION: (8499)
 ; OTHER INFORMATION: a, c, t, g, other or unknown
 US-10-331-329-28

Query Match 94.0%; Score 248.2; DB 14; Length 9737;
 Best Local Similarity 98.5%; Pred. No. 1.2e-74;
 Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 QY 1 AATGTAGTCTTATGCAATACCTTGTAGTCTTGCACATGTAACGATGAGTTAGCAACA 60
 Db 1411 AATGTAGTCTTATGCAATACCTTGTAGTCTTGCACATGTAACGATGAGTTAGCAACA 1470
 QY 61 TGCCTTACAAGGAGAGAAAAGCACCGTGCATGCGGTCCTGACATGATGGAGCAACCACTTAATT 180
 Db 1471 TGCCTTACAAGGAGAGAAAAGCACCGTGCATGCGGTCCTGACATGATGGAGCAACCACTTAATT 1590
 QY 121 TCGTGCCTTATTAGGAGGCAACAGACAGGTCCTGACATGATGGAGCAACCACTTAATT 180
 Db 1531 TCGTGCCTTATTAGGAGGCAACAGACAGGTCCTGACATGATGGAGCAACCACTTAATT 1590
 QY 181 CGCATTCGAGAGAT-ATTGTATTAAAGTGCCTAGCTGCATACATAAAGCAACCACTTAATT 239
 Db 1591 CGCATTCGAGAGATATTGTATTAAAGTGCCTAGCTGCATACATAAAGCAACCACTTAATT 1650
 QY 240 CATTCAACACATTTGGTGTGCACCTC 264
 Db 1651 CATTCAACACATTTGGTGTGCACCTC 1675

RESULT 13

US-10-331-329-24
 ; Sequence 24, Application US/10331329
 ; Publication No. US20030180267A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HARRINGTON, JOHN J.
 ; APPLICANT: SHERP, BRUCE
 ; APPLICANT: RUNDLETT, STEPHEN
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
 ; FILE REFERENCE: 0221-0003CON
 ; CURRENT APPLICATION NUMBER: US/10/331,329
 ; PRIOR FILING DATE: 2002-12-30
 ; PRIOR FILING DATE: 1999-03-26
 ; PRIOR FILING DATE: 1999-03-08
 ; PRIOR FILING DATE: 1999-02-19
 ; PRIOR FILING DATE: 1998-09-24
 ; PRIOR FILING DATE: 1997-09-26
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 24
 ; LENGTH: 9871
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: modified_base
 ; LOCATION: (8481)
 ; OTHER INFORMATION: a, c, t, g, other or unknown
 ;
 ; NAME/KEY: modified_base
 ; LOCATION: (8633)
 ; OTHER INFORMATION: a, c, t, g, other or unknown
 US-10-331-329-24

Query Match 94.0%; Score 248.2; DB 14; Length 9871;
 Best Local Similarity 98.5%; Pred. No. 1.2e-74;
 Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 QY 1 AATGTAGTCTTATGCAATACCTTGTAGTCTTGCACATGTAACGATGAGTTAGCAACA 60
 Db 1545 AATGTAGTCTTATGCAATACCTTGTAGTCTTGCACATGTAACGATGAGTTAGCAACA 1604
 QY 61 TGCCTTACAAGGAGAGAAAAGCACCGTGCATGCGGTCCTGACATGATGGAGCAACCACTTAATT 120

RESULT 15
US-10-1B5-318-1
; Sequence 1, Application US/10185318
; Publication No. US20030035793A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, JEFFREY S.
; APPLICANT: BEADY, JAMIE T.

```

/ / TITLE OF INVENTION: NOVEL IMMUNE RESPONSE TARGETING MOLECULES
/ /
/ / FILE REFERENCE: FBRC:009USC2
/ /
/ / CURRENT APPLICATION NUMBER: US/10/185,318
/ /
/ / CURRENT FILING DATE: 2002-06-28
/ /
/ / PRIOR APPLICATION NUMBER: 09/402,020
/ /
/ / PRIOR FILING DATE: 1999-09-27
/ /
/ / PRIOR APPLICATION NUMBER: PCT/AU98/00208
/ /
/ / PRIOR FILING DATE: 1998-03-26
/ /
/ / PRIOR APPLICATION NUMBER: AU PP5891
/ /
/ / PRIOR FILING DATE: 1997-03-27
/ /
/ / PRIOR APPLICATION NUMBER: AU PP1830
/ /
/ / PRIOR FILING DATE: 1998-02-13
/ /
/ / NUMBER OF SEQ ID NOS: 1
/ /
/ / SOFTWARE: PatentIn Ver. 2.1
/ /
/ / SEQ ID NO 1
/ /
/ / LENGTH: 11265
/ /
/ / TYPE: DNA
/ /
/ / ORGANISM: Murine
/ /
/ / US-10-185-318-1

```

```

QY      240 CATTCAACCATTTGGTGTGCACCTC   264
          |||||
Db      609 CATTCAACCATTTGGTGTGCACCTC   633
          |||||

RESULT 16
US-10-185-799-1
; Sequence 1, Application US/10185799
; Publication No. US2003007242A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, JEFFREY S.
; APPLICANT: BRADY, JAMIE L.
; APPLICANT: LEW, ANDREW M.
; TITLE OF INVENTION: ENHANCEMENT OF IMMUNE RESPONSE USING TARGETING
; TITLE OF INVENTION: MOLECULES
; FILE REFERENCE: PERC:009USC1
; CURRENT APPLICATION NUMBER: US/10/185,799
; CURRENT FILING DATE: 2002-06-28
```

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; PRIOR APPLICATION NUMBER: 09/402,020
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: PCT/AU98/00208
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: AU PP5891
; PRIOR FILING DATE: 1997-03-27
; PRIOR APPLICATION NUMBER: AU P21830
; PRIOR FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 1
; TYPE: DNA
; ORGANISM: Murine
US-10-185-799-1

Query Match          94.0%; Score 248.2; DB 14; Length 11265;
Best Local Similarity 98.5%; Pred. No. 1.3e-74;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGGACACATGTAACGATGAGTTAGCAACA 60
DB 369 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGGACACATGTAACGATGAGTTAGCAACA 428
QY 61 TGCCTTACAAGGAGAGAAAAGCACCGTGCATGCCGATTGGTGGAAAGTAAGTGGTACGA 120
DB 429 TGCCTTACAAGGAGAGAAAAGCACCGTGCATGCCGATTGGTGGAAAGTAAGTGGTACGA 488
QY 121 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGATTTGGAGCAACCACTAAATT 180
DB 489 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGATTTGGAGCAACCACTAAATT 548
QY 181 CGCATTTGCAGAGAT-ATTGTATTAAAGTGCCTCGATACATAATAACGCCATTGAC 239
DB 549 CGCATTTGCAGAGATTAATTGTTTAAAGTGCCTCGATACATAATAACGCCATTGAC 608
QY 240 CATTACCAACATTTGGTGCACCTC 264
DB 609 CATTACCAACATTTGGTGCACCTC 633

RESULT 17
US-09-897-006-9
; Sequence 9, Application US/09897006
; Patent No. US20020106729A1
; GENERAL INFORMATION:
; APPLICANT: Bleck, Gregory
; TITLE OF INVENTION: Expression Vectors
; FILE REFERENCE: GALA-06415
; CURRENT APPLICATION NUMBER: US/09/897,006
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/215,851
; PRIOR FILING DATE: 2000-07-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 9
; LENGTH: 5130
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-897-006-9

Query Match          87.9%; Score 232; DB 9; Length 5130;
Best Local Similarity 97.0%; Pred. No. 3.6e-69;
Matches 258; Conservative 0; Mismatches 5; Indels 3; Gaps 2;

QY 1 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGGACACATGTAACGATGAGTTAGCAACA 60
DB 2325 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGGACACATGTAACGATGAGTTAGCAACA 2384
QY 61 TGCCTTACAAGGAGAGAAAAGCACCGTGCATGCCGATTGGTGGAAAGTAAGTGGTACGA 120
DB 2385 TGCCTTACAAGGAGAGAAAAGCACCGTGCATGCCGATTGGTGGAAAGTAAGTGGTACGA 2444
QY 121 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGATTTGGAGCAACCACTAAATT 180
DB 2445 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGATTTGGAGCAACCACTAAATT 2504
QY 181 CGCATTTGCAGAGAT-ATTGTATTAAAGTGCCTCGATACATAATAACGCCCA--TTTG 237
DB 2505 CGCATTTGCAGAGATTAATTGTTTAAAGTGCCTCGATACATAATAACGCCCA--TTTG 2564
QY 238 ACCATTACACATTTGGTGCACCT 263
DB 2565 ACCATTACACATTTGGTGCACCT 2590

RESULT 18
US-09-897-511A-9
; Sequence 9, Application US/09897511A
; Publication No. US20030092882A1
; GENERAL INFORMATION:
; APPLICANT: Brenel, Robert
; APPLICANT: Miller, Linda
; APPLICANT: Bleck, Gregory
; TITLE OF INVENTION: Host Cells Containing Multiple Integrating Vectors
; FILE REFERENCE: GALA-06416
; CURRENT APPLICATION NUMBER: US/09/897,511A
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/215,925
; PRIOR FILING DATE: 2000-07-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 9
; LENGTH: 5130
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-897-511A-9

Query Match          87.9%; Score 232; DB 10; Length 5130;
Best Local Similarity 97.0%; Pred. No. 3.6e-69;
Matches 258; Conservative 0; Mismatches 5; Indels 3; Gaps 2;

QY 1 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGGACACATGTAACGATGAGTTAGCAACA 60
DB 2325 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGGACACATGTAACGATGAGTTAGCAACA 2384
QY 61 TGCCTTACAAGGAGAGAAAAGCACCGTGCATGCCGATTGGTGGAAAGTAAGTGGTACGA 120
DB 2385 TGCCTTACAAGGAGAGAAAAGCACCGTGCATGCCGATTGGTGGAAAGTAAGTGGTACGA 2444
QY 121 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGATTTGGAGCAACCACTAAATT 180
DB 2445 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGATTTGGAGCAACCACTAAATT 2504
QY 181 CGCATTTGCAGAGAT-ATTGTATTAAAGTGCCTCGATACATAATAACGCCCA--TTTG 237
DB 2505 CGCATTTGCAGAGATTAATTGTTTAAAGTGCCTCGATACATAATAACGCCCA--TTTG 2564
QY 238 ACCATTACACATTTGGTGCACCT 263
DB 2565 ACCATTACACATTTGGTGCACCT 2590

RESULT 19
US-10-155-736A-1
; Sequence 1, Application US/10155736A
; Publication No. US20030095948A1
; GENERAL INFORMATION:
; APPLICANT: Universit. di Torino
; TITLE OF INVENTION: Vector and methods of use for selective expression of genes in si
; FILE OF INVENTION: of angiogenesis in vivo
; FILE REFERENCE: 36019/MMN

```

Query Match	77.7%;	Score 205.2;	DB 9;	Length 11282;
Best Local Similarity	98.6%;	Pred. No. 9.6e-60;		
Matches 207;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;
QY	2	ATGTAGCTTTATGCCAATACTCTTCTAGTCTTGCACATGTTGACGATGAGTTGACACAT	61	
Db	564	ATCCAGTCTTTATGCCAATACTCTTCTAGTCTTGCACATGTTGACGATGAGTTGACACAT	723	
QY	62	GCCTTACAGGAGAGAAAAAGCACCCGTGATCCGATTTGGTGGAGTGAAGTGTGTACGAT	121	
Db	724	GCCTTACAGGAGAGAAAAAGCACCCGTGATCCGATTTGGTGGAGTGAAGTGTGTACGAT	783	
QY	122	CGTGCCTTTATTAGGAGGCAACACAGCGGGTCTGCATCGATTGGACGACCACTAAATTC	181	
Db	784	CGTGCCTTTATTAGGAGGCAACACAGCGGGTCTGCATCGATTGGACGACCACTGAATTC	843	
QY	182	CSCATTGCAGAGATATTGTATTAAAGTGCC	211	
Db	844	CSCATTGCAGAGATATTGTATTAAAGTGCC	873	

Query Match 71.1%; Score 187.6; DB 11; Length 5283;
Best Local Similarity 91.5%; Pred. No. 8,26-54;
Matches 214; Conservative 0; Mismatches 9; Indels 11; Gaps 1;
QY 41 GTAACGATGAGTTACGACATCGCTTACAGGAGAGAAAGCCGTGATCGCATG 100

Db 252 GTACGGTGGATTAGCAACATCGCTTATATAGGAGGAGAAAAGCACCGTGCATGCCGATTG 311
QY 101 GTGGAGTAAG-----GTGGPACATCGTGGCTTATATAGGAGGCAACAGACGG 149
Db 312 GTGGAGTAAGTGGTATCGTGGTATCGTGGCTTATATAGGAGGCAACAGACGG 371
QY 150 GTCTGACATGGATTGGACCAACCACTAAATTCGGATTGCAGAGATATTTGATTAAAGTG 209
Db 372 GTCTAACCAGATTGAGCAACCACTGAATTCGGATTGCAGAGATATTTGATTAAAGTG 431
QY 210 CCTGATCGATCAATAAAGCCATTGACCACTTGCACATTCACACATTTGGTGTCACT 263
Db 432 CCGAGCTGATACAATAAAGCCATTGACCACTTGCACATTCACACATTTGGTGTCACT 485

RESULT 23

US-10-182-327-16
; Sequence 16, Application US/10182327
; Publication No. US20040043468A1
; GENERAL INFORMATION:
; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
; APPLICANT: THE NEUROSCIENCE INSTITUTE
; APPLICANT: MAURO, Vincent P.
; APPLICANT: EDELMAN, Gerald M.
; APPLICANT: CHAPPELL, Stephen A.
; APPLICANT: OWENS, Geoffrey
; APPLICANT: PINKSTAFF, Jason K.
; APPLICANT: KRUSHEL, Leslie
; APPLICANT: ZHOU, Wei
; TITLE OF INVENTION: SYNTHETIC INTERNAL RIBOSOME ENTRY SITES AND METHODS OF IDENTIFYING
; FILE REFERENCE: SCRIPT360-1
; CURRENT APPLICATION NUMBER: US/10/182,327
; CURRENT FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: PCT/US 01/02586
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/261,312
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/230,956
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/230,852
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/207,804
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: US 60/186,496
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/178,816
; PRIOR FILING DATE: 2000-01-28
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 6250
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: VECTOR
US-10-182-327-16

Query Match 66.0%; Score 174.2; DB 12; Length 6250;
Best Local Similarity 98.3%; Pred. No. 3.8e-49;
Matches 176; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 AATGATGCTTATGCAATACCTTGTAGTCTTGCAACATGTTACCAATGTTAGTACCA 60
Db 3165 AATGATGCTTATGCAATACCTTGTAGTCTTGCAACATGTTACCAATGTTAGTACCA 3224
QY 61 TGCCTTACAGGAGAGAAAAGCACCGTGCATGCCGATTGGTAAGTAAAGTGTACGA 120
Db 3225 TGCCTTACAGGAGAGAAAAGCACCGTGCATGCCGATTGGTAAGTAAAGTGTACGA 3284
QY 121 TCGTGCCCTTATTAGGAAGCAACAGACGCGTCTTGACATGGATTGGACGACCACTAAAT 179
Db 3285 TCGTGCCCTTATTAGGAAGCAACAGACGCGTCTTGACATGGATTGGACGACCACTAGAT 3343

RESULT 24

US-10-182-329-109
; Sequence 109, Application US/10182329
; Publication No. US2004005564A1
; GENERAL INFORMATION:
; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
; APPLICANT: MAURO, Vincent P.
; APPLICANT: EDELMAN, Gerald M.
; APPLICANT: CHAPPELL, Stephen A.
; APPLICANT: JONES, Frederick S.
; APPLICANT: OWENS, Geoffrey
; APPLICANT: MEECH, Robin
; TITLE OF INVENTION: METHODS OF IDENTIFYING SYNTHETIC TRANSCRIPTIONAL AND TRANSLATIONA
; FILE REFERENCE: SCRIPT380-1
; CURRENT APPLICATION NUMBER: US/10/182,329
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: PCT/US 01/02733
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/261,312
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/230,956
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/230,852
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/207,804
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: US 60/186,496
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/178,816
; PRIOR FILING DATE: 2000-01-28
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 109
; LENGTH: 6250
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: vector
US-10-182-329-109

Query Match 66.0%; Score 174.2; DB 15; Length 6250;
Best Local Similarity 98.3%; Pred. No. 3.8e-49;
Matches 176; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATGATGCTTATGCAATACCTTGTAGTCTTGCAACATGTTACCAATGTTAGTACCA 60
Db 3165 AATGATGCTTATGCAATACCTTGTAGTCTTGCAACATGTTACCAATGTTAGTACCA 3224
QY 61 TGCCTTACAGGAGAGAAAAGCACCGTGCATGCCGATTGGTAAGTAAAGTGTACGA 120
Db 3225 TGCCTTACAGGAGAGAAAAGCACCGTGCATGCCGATTGGTAAGTAAAGTGTACGA 3284
QY 121 TCGTGCCCTTATTAGGAAGCAACAGACGCGTCTTGACATGGATTGGACGACCACTAAAT 179
Db 3285 TCGTGCCCTTATTAGGAAGCAACAGACGCGTCTTGACATGGATTGGACGACCACTAGAT 3343

RESULT 25

US-09-847-101B-35
; Sequence 35, Application US/09847101B
; Publication No. US2002019327A1
; GENERAL INFORMATION:
; APPLICANT: VON SEGGERN, DANIEL
; APPLICANT: NEMEROW, GLEN R.
; APPLICANT: FRIEDLANDER, MARTIN
; TITLE OF INVENTION: VECTORS FOR OCULAR TRANSDUCTION AND USE THEREFOR FOR GENETIC THER
; FILE REFERENCE: 22908-1226B
; CURRENT APPLICATION NUMBER: US/09/847,101B
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/562,934
; PRIOR FILING DATE: 2000-05-01

; NUMBER OF SEQ ID NOS: 50
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 35
 ; LENGTH: 11600
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: plasmid MMTV-E2a-SV40-Neo
 US-09-847-101B-35

Query Match 65.7%; Score 173.4; DB 9; Length 11600;
 Best Local Similarity 99.4%; Pred. No. 9.7e-49;
 Matches 174; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 AATGAGTCTTATGCAATACCTCTTGTAGTCTTGCACATGTAACGATGAGTTAGCAACA 60
 DB 11426 AATGAGTCTTATGCAATACCTCTTGTAGTCTTGCACATGTAACGATGAGTTAGCAACA 11485
 QY 61 TGCCTTCAAGGAGAGAAAAGCCCGTGCATGCCGATGGTGAAGTAAGGTGGTACGA 120
 DB 11486 TGCCTTCAAGGAGAGAAAAGCCCGTGCATGCCGATGGTGAAGTAAGGTGGTACGA 11545
 QY 121 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGCATGATGATGGAGCAACCACT 175
 DB 11546 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGCATGATGATGGAGCAACCACT 11600

RESULT 26
 US-09-482-682-49
 ; Sequence 49, Application US/09482682
 ; Publication No. US20030157688A1
 ; GENERAL INFORMATION:
 ; APPLICANT: VON SEGGERN, DANIEL
 ; APPLICANT: NEMEROW, GLEN R.
 ; APPLICANT: HALLENBECK, PAUL
 ; APPLICANT: STEVENSON, SUSAN
 ; APPLICANT: SKRIPCHENKO, YELENA
 ; TITLE OF INVENTION: ADENOVIRUS VECTORS, PACKAGING CELL LINES, COMPOSITIONS,
 ; TITLE OF INVENTION: AND METHODS FOR PREPARATION AND USE
 ; FILE REFERENCE: 1294.0010001
 ; CURRENT APPLICATION NUMBER: US/09/482,682
 ; CURRENT FILING DATE: 2000-01-14
 ; NUMBER OF SEQ ID NOS: 76
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 49
 ; LENGTH: 11600
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: plasmid
 US-09-482-682-49

Query Match 65.7%; Score 173.4; DB 10; Length 11600;
 Best Local Similarity 99.4%; Pred. No. 9.7e-49;
 Matches 174; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 AATGAGTCTTATGCAATACCTCTTGTAGTCTTGCACATGTAACGATGAGTTAGCAACA 60
 DB 11426 AATGAGTCTTATGCAATACCTCTTGTAGTCTTGCACATGTAACGATGAGTTAGCAACA 11485
 QY 61 TGCCTTCAAGGAGAGAAAAGCCCGTGCATGCCGATGGTGAAGTAAGGTGGTACGA 120
 DB 11486 TGCCTTCAAGGAGAGAAAAGCCCGTGCATGCCGATGGTGAAGTAAGGTGGTACGA 11545
 QY 121 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGCATGATGATGGAGCAACCACT 175
 DB 11546 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGCATGATGATGGAGCAACCACT 11600

RESULT 27
 US-10-403-337-42
 ; Sequence 42, Application US/10403337
 ; Publication No. US20030215948A1

; GENERAL INFORMATION:
 ; APPLICANT: Kaleko, Michael
 ; APPLICANT: Nemerow, Glen R.
 ; APPLICANT: Smith, Theodore
 ; APPLICANT: Stevenson, Susan C.
 ; TITLE OF INVENTION: Fiber Shaft Modifications for Efficient Targeting
 ; FILE REFERENCE: 22908-1236B
 ; CURRENT APPLICATION NUMBER: US/10/403,337
 ; CURRENT FILING DATE: 2003-03-27
 ; PRIOR APPLICATION NUMBER: 10/351,890
 ; PRIOR FILING DATE: 2003-01-24
 ; PRIOR APPLICATION NUMBER: 60/350,388
 ; PRIOR FILING DATE: 2002-01-24
 ; PRIOR APPLICATION NUMBER: 60/391,967
 ; PRIOR FILING DATE: 2002-06-26
 ; NUMBER OF SEQ ID NOS: 72
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 42
 ; LENGTH: 11600
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Plasmid MMTV-E2a-SV40-Neo
 US-10-403-337-42

Query Match 65.7%; Score 173.4; DB 15; Length 11600;
 Best Local Similarity 99.4%; Pred. No. 9.7e-49;
 Matches 174; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 AATGAGTCTTATGCAATACCTCTTGTAGTCTTGCACATGTAACGATGAGTTAGCAACA 60
 DB 11426 AATGAGTCTTATGCAATACCTCTTGTAGTCTTGCACATGTAACGATGAGTTAGCAACA 11485
 QY 61 TGCCTTCAAGGAGAGAAAAGCCCGTGCATGCCGATGGTGAAGTAAGGTGGTACGA 120
 DB 11486 TGCCTTCAAGGAGAGAAAAGCCCGTGCATGCCGATGGTGAAGTAAGGTGGTACGA 11545
 QY 121 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGCATGATGATGGAGCAACCACT 175
 DB 11546 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGCATGATGATGGAGCAACCACT 11600

RESULT 28
 US-10-351-890-42
 ; Sequence 42, Application US/10351890
 ; Publication No. US20040002060A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Stevenson, Susan C.
 ; APPLICANT: Kaleko, Michael
 ; APPLICANT: Smith, Theodore
 ; APPLICANT: Nemerow, Glen R.
 ; TITLE OF INVENTION: Fiber Shaft Modifications for Efficient Targeting
 ; FILE REFERENCE: 22908-1236
 ; CURRENT APPLICATION NUMBER: US/10/351,890
 ; CURRENT FILING DATE: 2003-01-28
 ; PRIOR APPLICATION NUMBER: 60/350,388
 ; PRIOR FILING DATE: 2002-01-24
 ; PRIOR APPLICATION NUMBER: 60/391,967
 ; PRIOR FILING DATE: 2002-06-26
 ; NUMBER OF SEQ ID NOS: 72
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 42
 ; LENGTH: 11600
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Plasmid MMTV-E2a-SV40-Neo
 US-10-351-890-42

Query Match 65.7%; Score 173.4; DB 15; Length 11600;
 Best Local Similarity 99.4%; Pred. No. 9.7e-49;
 Matches 174; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGCACATGGTACGATGAGTTAGCAACA 60
Db 11426 AATGTAGTCTTATGCAATACCTTGTAGTCTTGCACATGGTACGATGAGTTAGCAACA 11485
QY 61 TGCCTTACAAGGAGAGAAAAGCACCCTGTCATGCCGATTCGTAAGTGAAGTGGTACGA 120
Db 11486 TGCCTTACAAGGAGAGAAAAGCACCCTGTCATGCCGATTCGTAAGTGAAGTGGTACGA 11545
QY 121 TCGTCCCTTATTAGGAAGGCAACAGACGCGGTCTGCATGGATTGGACGAACCACT 175
Db 11546 TCGTCCCTTATTAGGAAGGCAACAGACGCGGTCTGCATGGATTGGACGAACCACT 11600

RESULT 29

US-10-182-329-1
; Sequence 1, Application US/10182329
; Publication No. US20040005564A1
; GENERAL INFORMATION:
; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
; APPLICANT: MAURO, Vincent P.
; APPLICANT: EDELMAN, Gerald M.
; APPLICANT: CHAPPELL, Stephen A.
; APPLICANT: JONES, Frederick S.
; APPLICANT: OWENS, Geoffrey
; APPLICANT: MEECH, Robin
; TITLE OF INVENTION: METHODS OF IDENTIFYING SYNTHETIC TRANSCRIPTIONAL AND TRANSLATION
; FILE REFERENCE: SCRIPI380-1
; CURRENT APPLICATION NUMBER: US/10/182,329
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: PCT/US 01/02733
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/261,312
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/230,956
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/207,804
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: US 60/186,496
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/178,816
; PRIOR FILING DATE: 2000-01-28
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 6279
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: vector
US-10-182-329-1

Query Match 65.1%; Score 171.8; DB 15; Length 6279;
Best Local Similarity 98.9%; Pred. No. 2.6e-48;
Matches 173; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGCACATGGTAAAGTGGTACGA 60
Db 203 AATGTAGTCTTATGCAATACCTTGTAGTCTTGCACATGGTAAAGTGGTACGA 262
QY 61 TGCCTTACAAGGAGAGAAAAGCACCCTGTCATGCCGATTCGTAAGTGAAGTGGTACGA 120
Db 263 TGCCTTACAAGGAGAGAAAAGCACCCTGTCATGCCGATTCGTAAGTGAAGTGGTACGA 322
QY 121 TCGTCCCTTATTAGGAAGGCAACAGACGCGGTCTGCATGGATTGGACGAACCACT 175
Db 323 TCGTCCCTTATTAGGAAGGCAACAGACGCGGTCTGCATGGATTGGACGAACCACT 377

RESULT 30

US-10-182-329-9

; Sequence 9, Application US/10182329
; Publication No. US20040005564A1
; GENERAL INFORMATION:
; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
; APPLICANT: MAURO, Vincent P.
; APPLICANT: EDELMAN, Gerald M.
; APPLICANT: CHAPPELL, Stephen A.
; APPLICANT: JONES, Frederick S.
; APPLICANT: OWENS, Geoffrey
; APPLICANT: MEECH, Robin
; TITLE OF INVENTION: METHODS OF IDENTIFYING SYNTHETIC TRANSCRIPTIONAL AND TRANSLATION
; FILE REFERENCE: SCRIPI380-1
; CURRENT APPLICATION NUMBER: US/10/182,329
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: PCT/US 01/02733
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/261,312
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/230,956
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/230,852
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/207,804
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: US 60/186,496
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/178,816
; PRIOR FILING DATE: 2000-01-28
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 8513
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: vector
US-10-182-329-9

Query Match 65.1%; Score 171.8; DB 15; Length 8513;
Best Local Similarity 98.9%; Pred. No. 3e-48;
Matches 173; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGCACATGGTAAAGTGGTACGA 60
Db 203 AATGTAGTCTTATGCAATACCTTGTAGTCTTGCACATGGTAAAGTGGTACGA 262
QY 61 TGCCTTACAAGGAGAGAAAAGCACCCTGTCATGCCGATTCGTAAGTGAAGTGGTACGA 120
Db 263 TGCCTTACAAGGAGAGAAAAGCACCCTGTCATGCCGATTCGTAAGTGAAGTGGTACGA 322
QY 121 TCGTCCCTTATTAGGAAGGCAACAGACGCGGTCTGCATGGATTGGACGAACCACT 175
Db 323 TCGTCCCTTATTAGGAAGGCAACAGACGCGGTCTGCATGGATTGGACGAACCACT 377

RESULT 31

US-10-264-237-633
; Sequence 633, Application US/10264237
; Publication No. US20040009491A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; PRIOR FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 633

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/
/ LENGTH: 766
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURES:
/ NAME/KEY: misc_feature
/ LOCATION: (56)..(56)
/ OTHER INFORMATION: n equals a,t,g, or c
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (91)..(91)
/ OTHER INFORMATION: n equals a,t,g, or c
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (141)..(141)
/ OTHER INFORMATION: n equals a,t,g, or c
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (652)..(652)
/ OTHER INFORMATION: n equals a,t,g, or c
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (753)..(753)
/ OTHER INFORMATION: n equals a,t,g, or c
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (763)..(763)
/ OTHER INFORMATION: n equals a,t,g, or c
US-10-264-237-633

Query Match 61.1%; Score 161.2; DB 15; Length 766;
Best Local Similarity 89.8%; Pred. No. 4.4e-45;
Matches 199; Conservative 0; Mismatches 10; Indels 13; Gaps 2;

QY 55 GCAACATGCTTACAAAGGAGAGAAAAAGCACCGTCATGCGATTGGTGAAGTAA-GGT 113
Db 9 GCAACATGCTTATAGGAGAGAAAGACCGTCATGCGATTGGGAGTAGGGT 68

QY 114 GTACGATCGTG-----CCTTAGGAAGCAACAGACGGTCTGCATGGA 161
Db 69 GGTATGATCGTGATGATGCTGTCCTTTAGGAAGCAACAGACGGTCTTAACAGGA 128

QY 162 TTGACCAACCACTAATTCGCGATTCAGAGATTTATTATTAGTGCCTAGCTCGATA 221
Db 129 TTGACCAACCACTAATTCGCGATTCAGAGATTTATTATTAGTGCCTAGCTCGATA 188

QY 222 CAATAAAGCGCATTTGACCATTCACCACTTGGTGTGCACT 263
Db 189 CAATAAAGCGCATTTGACCATTCACCACTTGGTGTGCACT 230

RESULT 32
US-10-267-117-5
/ Sequence 5, Application US/10267117
/ Publication No. US20030082162A1
/ GENERAL INFORMATION:
/ APPLICANT: FLOTTE, TERENCE R.
/ APPLICANT: SONG, SIHONG
/ APPLICANT: BYRNE, BARRY J.
/ APPLICANT: MORGAN, MICHAEL
/ TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
/ CURRENT APPLICATION NUMBER: US/10/267,117
/ PRIOR FILING DATE: 2002-10-08
/ PRIOR FILING DATE: 1999-04-23
/ PRIOR FILING DATE: 1999-04-23
/ PRIOR FILING DATE: 1999-04-23
/ NUMBER OF SEQ ID NOS: 13
/ SOFTWARE: Patent in Ver. 2.0
/ SEQ ID NO 5
/ LENGTH: 7492
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:p43C-AT-IN
US-10-267-117-5
```

```
/
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:p43C-AT-IN
US-10-267-117-5

Query Match 29.2%; Score 77; DB 14; Length 7492;
Best Local Similarity 98.9%; Pred. No. 1.7e-15;
Matches 88; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 177 AATTCGCATTGCAGAGAT-ATTGTATTAAAGTGCCTAGCTCGATACAAATAAAGCCATT 235
Db 1 AATTCGCATTGCAGAGATATTGTATTAAAGTGCCTAGCTCGATACAAATAAAGCCATT 60

QY 236 TGACCATTCACACATTTGGTGTGCACCTC 264
Db 61 TGACCATTCACACATTTGGTGTGCACCTC 89

RESULT 33
US-10-340-112-5
/ Sequence 5, Application US/10340112
/ Publication No. US20030095949A1
/ GENERAL INFORMATION:
/ APPLICANT: FLOTTE, TERENCE R.
/ APPLICANT: SONG, SIHONG
/ APPLICANT: BYRNE, BARRY J.
/ APPLICANT: MORGAN, MICHAEL
/ TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
/ FILE REFERENCE: 4300.011800
/ CURRENT APPLICATION NUMBER: US/10/340,112
/ PRIOR FILING DATE: 2003-01-10
/ PRIOR FILING DATE: 1999-04-23
/ PRIOR FILING DATE: 1999-04-23
/ PRIOR FILING DATE: 1999-04-23
/ NUMBER OF SEQ ID NOS: 13
/ SOFTWARE: Patent in Ver. 2.0
/ SEQ ID NO 5
/ LENGTH: 7492
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:p43C-AT-IN
US-10-340-112-5

Query Match 29.2%; Score 77; DB 14; Length 7492;
Best Local Similarity 98.9%; Pred. No. 1.7e-15;
Matches 88; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 177 AATTCGCATTGCAGAGAT-ATTGTATTAAAGTGCCTAGCTCGATACAAATAAAGCCATT 235
Db 1 AATTCGCATTGCAGAGATATTGTATTAAAGTGCCTAGCTCGATACAAATAAAGCCATT 60

QY 236 TGACCATTCACACATTTGGTGTGCACCTC 264
Db 61 TGACCATTCACACATTTGGTGTGCACCTC 89

RESULT 34
US-10-192-085-10
/ Sequence 10, Application US/10192085
/ Publication No. US20020173030A1
/ GENERAL INFORMATION:
/ APPLICANT: Naldini, Luigi
/ APPLICANT: Dull, Thomas
/ APPLICANT: Parson, Deborah A.
/ APPLICANT: Witt, Rochelle
/ TITLE OF INVENTION: METHOD AND MEANS FOR PRODUCING HIGH
/ TITER, SAFE, RECOMBINANT LENTIVIRUS VECTORS
/ NUMBER OF SEQUENCES: 22
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: SUGHRUE, MION, ZINN, MACPHEAK & SEAS
/ STREET: 2100 Pennsylvania Avenue, N.W.
/ CITY: Washington
```

```

; STATE: D.C.
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/10/192,085
; APPLICATION NUMBER: US/10/192,085
; FILING DATE: 10-Jul-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/271,365
; FILING DATE: 18-Mar-1999
; APPLICATION NUMBER: 08/389,394
; FILING DATE: 12-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Dean H.
; REFERENCE/DOCKET NUMBER: A7086
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 74 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-192-085-10

Query Match 19.6%; Score 51.8; DB 13; Length 74;
Best Local Similarity 96.4%; Pred. No. 9.7e-08;
Matches 53; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 176 AATTCGCGATTCCAGAGATATTGTTTAAAGTCGCTAGCTCGATACAATAACG 230
Db 1 AATTCGCGATTCCAGAGATATTGTTTAAAGTCGCTAGCTCGATACAATAACG 55

RESULT 35
US-10-192-085-11/c
; Sequence 11, Application US/10192085
; Publication No. US20020173030A1
; GENERAL INFORMATION:
; APPLICANT: Naldini, Luigi
; Dull, Thomas
; Parson, Deborah A.
; Witt, Rochelle
; TITLE OF INVENTION: METHOD AND MEANS FOR PRODUCING HIGH
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/192,085
; FILING DATE: 10-Jul-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/271,365

```

```

; FILING DATE: 18-Mar-1999
; APPLICATION NUMBER: 08/389,394
; FILING DATE: 12-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Dean H.
; REGISTRATION NUMBER: 33,981
; REFERENCE/DOCKET NUMBER: A7086
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 74 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-192-085-11

Query Match 18.9%; Score 50; DB 13; Length 74;
Best Local Similarity 100.0%; Pred. No. 4.1e-07;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 181 CGCATTCCAGAGATATTGTTTAAAGTCGCTAGCTCGATACAATAACG 230
Db 73 CGCATTCCAGAGATATTGTTTAAAGTCGCTAGCTCGATACAATAACG 24

RESULT 36
US-09-725-720-9/c
; Sequence 9, Application US/09725720
; Patent No. US20010049136A1
; GENERAL INFORMATION:
; APPLICANT: IMLER, Jean-Luc
; APPLICANT: MEHTALI, Majid
; APPLICANT: PAVITANI, Andrea
; TITLE OF INVENTION: DEFECTIVE ADENOVIRUSES AND CORRESPONDING
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: 1737 King Street, Suite 500
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22314-2756
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/725,720
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/379,452
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93 06482
; FILING DATE: 28-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Dadio, Susan M.
; REGISTRATION NUMBER: 40,373
; REFERENCE/DOCKET NUMBER: 029395-002
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 47 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

```

```
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; ORIGINAL SOURCE:
; ORGANISM: Synthetic oligonucleotide (OTG5893)
US-09-725-720-9

Query Match      12.5%; Score 33; DB 9; Length 47;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 231 CCATTGACCATTCACCATTTGGTGGACCT 263
Db 47 CCATTGACCATTCACCATTTGGTGGACCT 15

RESULT 37
US-09-938-491-5/c
; Sequence 5, Application US/09938491
; Patent No. US20020090715A1
; GENERAL INFORMATION:
; APPLICANT: Cgile CHARTIER et al.
; TITLE OF INVENTION: METHOD OF PREPARING A VIRAL VECTOR BY INTERMOLECULAR
; TITLE OF INVENTION: HOMOLOGOUS RECOMBINATION
; FILE REFERENCE: 032751-002
; CURRENT APPLICATION NUMBER: US/09/938,491
; PRIOR FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: 08/682,794
; PRIOR FILING DATE: 1996-08-01
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 47
; TYPE: DNA
; ORGANISM: rous sarcoma virus
US-09-938-491-5

Query Match      12.5%; Score 33; DB 9; Length 47;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 231 CCATTGACCATTCACCATTTGGTGGACCT 263
Db 47 CCATTGACCATTCACCATTTGGTGGACCT 15

RESULT 38
US-09-739-007-9/c
; Sequence 9, Application US/09739007
; Publication No. US20030170885A1
; GENERAL INFORMATION:
; APPLICANT: IMMLER, Jean-Luc
; MEHTALI, Majid
; PAVIRANI, Andrea
; TITLE OF INVENTION: DEFECTIVE ADENOVIRUSES AND CORRESPONDING
; COMPLEMENTATION LINES
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: 1737 King Street, Suite 500
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22314-2756
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/739,007
; FILING DATE: 19-Dec-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
```

```
; APPLICATION NUMBER: 08/379,452
; FILING DATE: <Unknown>
; APPLICATION NUMBER: FR 93 06482
; FILING DATE: 28-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Dadio, Susan M.
; REGISTRATION NUMBER: 40,373
; REFERENCE/DOCKET NUMBER: 029395-002
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 47 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Synthetic oligonucleotide (OTG5893)
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-739-007-9

Query Match      12.5%; Score 33; DB 10; Length 47;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 231 CCATTGACCATTCACCATTTGGTGGACCT 263
Db 47 CCATTGACCATTCACCATTTGGTGGACCT 15

RESULT 39
US-10-027-632-81543
; Sequence 81543, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81543
; LENGTH: 542
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-81543

Query Match      12.5%; Score 33; DB 15; Length 542;
Best Local Similarity 54.5%; Pred. No. 0.8;
Matches 66; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 46 GATGAGTTAGCAACATGCTTCAAGGAGAGAGAAAAGCACCGTGCATGCCGATTTGGTGA 105
Db 46 GAGAGAGTCACTGATCTGACTCACACACTGAGATAGGTAGGAGGACCGGTGGAGACGA 105
QY 106 AGTAGGTGTGATGATGCTGCTTATTAGGAGGCAACAGACGGTCTGACATGATTGG 165
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Db 106 GCCCAGTTAGGAGGTATTGATTATGTTGGTAGGCAAGACACTACTGCTTGGATTGG 165
QY 166 A 166
Db 166 A 166

RESULT 40

US-10-027-632-301875
; Sequence 301875, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 301875
; LENGTH: 542
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-301875

Query Match 12.5%; Score 33; DB 15; Length 542;
Best Local Similarity 54.5%; Pred. No. 0.8;
Matches 66; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
QY 46 GATGAGTTAGCAACATGCTTACAGGAGAGAAAGCACCGTCAATGCGATTGGTGA 105
Db 46 GAGAAGTGAATGCTGACTCCTGACTCAGACCTGAGATAGGTAGGAGACCGGTGGGAGCAGGA 105
QY 106 AGTAAGTGGTACGATCGTGCCTTATTAGGAAGCAACAGACGGGTGACATGGATTGG 165
Db 106 GCCCAGTTAGGAGGTATTGATTATGTTGGTAGGCAAGACACTACTGCTTGGATTGG 165
QY 166 A 166
Db 166 A 166

RESULT 41

US-10-027-632-50648
; Sequence 50648, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20

; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 50648
; LENGTH: 573
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-50648

Query Match 12.5%; Score 33; DB 15; Length 573;
Best Local Similarity 54.5%; Pred. No. 0.82;
Matches 66; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
QY 46 GATGAGTTAGCAACATGCTTACAGGAGAGAAAGCACCGTCAATGCGATTGGTGA 105
Db 54 GAGAAGTGAATGCTGACTCCTGACTCAGACCTGAGATAGGTAGGAGACCGGTGGGAGCAGGA 113
QY 106 AGTAAGTGGTACGATCGTGCCTTATTAGGAAGCAACAGACGGGTGACATGGATTGG 165
Db 114 GCCCAGTTAGGAGGTATTGATTATGTTGGTAGGCAAGACACTACTGCTTGGATTGG 173
QY 166 A 166
Db 174 A 174

RESULT 42

US-10-369-493-25133/c
; Sequence 25133, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-1052052/B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 25133
; LENGTH: 2877
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-10-369-493-25133

Query Match 12.2%; Score 32.2; DB 15; Length 2877;
Best Local Similarity 51.0%; Pred. No. 3.4;
Matches 76; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
QY 88 TGCATGCCGATGGTGGAAAGTGGTGGTACGATCGTGCCTTATTAGGAAGGCAACAGAC 147
Db 2193 TGGATTCGATGAAAGATGTGAGTAGTCCCTTTGTTTACAGGTATGGAACCCGTC 2134
QY 148 GGGTCTGATGGATTGGACGAACCCACTAAATTCGCAATTCGAGATATGTATTAAAG 207
Db 2133 GAGTCTGCAATGTGACATCCAGCCATATTCATCAAAUUTTCATATATATCCATGTTTG 2074
QY 208 TGCCTAGCTCGATACAAATAAACGCCATTT 236

; SOFTWARE: FastSEO for Windows Version 4.0

SEQ ID NO 112120
 LENGTH: 2664
 TYPE: DNA
 ORGANISM: Human
 US-10-027-632-112120

Query Match 11.7% Score 30.8; DB 15; Length 2664;
 Best Local Similarity 61.0%; Pred. No. 9.9;
 Matches 50; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
 QY 10 TTATGCAATATCTTGTAGTCTTGCACATGGTAAGCATGAGTTAGCAACATGCCCTTACA 69
 Db 600 TTATGTAATACACTTATAGATATGTCACACTGTAACTCAATATATTACATCACCTTAAA 541

QY 70 AGGAGAGAAAAAGCAGCCGTGCA 91
 Db 540 GGAATATAAAGCAGCATGCA 519

RESULT 47

US-10-027-632-175173
 ; Sequence 175173, Application US/10027632
 ; Publication No. US20030204075A9
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
 ; FILE REFERENCE: 108827.129
 ; CURRENT APPLICATION NUMBER: US/10/027,632
 ; CURRENT FILING DATE: 2002-04-30
 ; PRIOR APPLICATION NUMBER: US 60/218,006
 ; PRIOR FILING DATE: 2000-07-12
 ; PRIOR APPLICATION NUMBER: US 60/198,676
 ; PRIOR FILING DATE: 2000-04-20
 ; PRIOR APPLICATION NUMBER: US 60/193,483
 ; PRIOR FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: US 60/185,218
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: US 60/167,363
 ; PRIOR FILING DATE: 1999-11-23
 ; PRIOR APPLICATION NUMBER: US 60/156,358
 ; PRIOR FILING DATE: 1999-09-28
 ; PRIOR APPLICATION NUMBER: US 60/146,002
 ; PRIOR FILING DATE: 1999-08-09
 ; NUMBER OF SEQ ID NOS: 325720
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 175173
 ; LENGTH: 5214
 ; TYPE: DNA
 ; ORGANISM: Human
 US-10-027-632-175173

Query Match 11.6% Score 30.6; DB 15; Length 5214;
 Best Local Similarity 50.3%; Pred. No. 16;
 Matches 75; Conservative 0; Mismatches 74; Indels 0; Gaps 0;
 QY 8 TCTTATGCAATATCTTGTAGTCTTGCACATGGTAAGCATGAGTTAGCAACATGCCCTTA 67
 Db 3021 TATAAGGTATTCTTTTAAAGAAAGAAATGGCAATCTGACTTAGAAAAATCGGCTC 3080
 QY 68 CAAAGAGAGAAAAAGCAGCCGTGCGATTGGTGAAGTAAGGTGAGCATCGTCC 127
 Db 3081 AAAGAGATCTAGAGACACCGCATCCATAGGTGCATGCTGTAGATGGTATTGTGCT 3140
 QY 128 TTATTAGGAAGCAACAGACGGGTCTGAC 156
 Db 3141 AAGTTAGCAATCTATCATCATGGGGCTCTCAC 3169

RESULT 48

US-10-425-114-31887
 ; Sequence 31887, Application US/10425114
 ; Publication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong
 APPLICANT: Zhou, Yihua
 APPLICANT: Kovalic, David K.
 APPLICANT: Screen, Steven E
 APPLICANT: Tabaska, Jack E
 APPLICANT: Cao, Yongwei
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 FILE REFERENCE: 38-21(53313)B
 CURRENT APPLICATION NUMBER: US/10/425,114
 CURRENT FILING DATE: 2003-04-28
 NUMBER OF SEQ ID NOS: 73128
 SEQ ID NO 31887
 LENGTH: 3300
 TYPE: DNA
 ORGANISM: Zea mays
 FEATURE:
 OTHER INFORMATION: Clone ID: UC-ZMFLB73227A02_FLI
 US-10-425-114-31887

Query Match 11.5% Score 30.4; DB 12; Length 3300;
 Best Local Similarity 50.7%; Pred. No. 15;
 Matches 73; Conservative 0; Mismatches 71; Indels 0; Gaps 0;
 QY 110 AGGTGTACGATCGTCCCTTATTAGGAAGGCAACAGACGGGTCTGCATGATTGGACGA 169
 Db 2354 AGTCCGACCAACTTGNACATGGAGAGCCCAATCAAAAGGAGCTTGAAGATGGATAT 2413
 QY 170 ACCATAAATTCGCATTCGACAGATATGTTTAAAGTGCTAGCTCGATACAAATAAC 229
 Db 2414 ACCAATGAAGTTGTGTTTGAATAGAGTGTGTTGAAAGAAAGCTACCCACGTCGCCGACC 2473
 QY 230 GCCATTGACCATTCACCACATTG 253
 Db 2474 GTGATTAGGCATTTTTCCTTATAG 2497

RESULT 49

US-09-739-254-63
 ; Sequence 63, Application US/09739254
 ; Patent No. US20010021700A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: 49 Human Secreted Proteins
 ; FILE REFERENCE: PZ032P1
 ; CURRENT APPLICATION NUMBER: US/09/739,254
 ; CURRENT FILING DATE: 2000-12-19
 ; EARLIER APPLICATION NUMBER: 09/511,554
 ; EARLIER FILING DATE: 2000-02-23
 ; EARLIER APPLICATION NUMBER: PCT/US99/19330
 ; EARLIER FILING DATE: 1999-08-24
 ; EARLIER APPLICATION NUMBER: 60/097,917
 ; EARLIER FILING DATE: 1998-08-25
 ; EARLIER APPLICATION NUMBER: 60/098,634
 ; EARLIER FILING DATE: 1998-08-31
 ; NUMBER OF SEQ ID NOS: 170
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 63
 ; LENGTH: 1202
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (282)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (596)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (607)

US-10-054-988-63
: Sequence 63, Application US/10054988


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; FEATURE:
; NAME/KEY: SITE
; LOCATION: (282)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (596)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (607)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1200)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-055-098-63

Query Match      11.4%; Score 30.2; DB 14; Length 1202;
Best Local Similarity 53.4%; Pred. No. 11;
Matches 62; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 17 ATACTCTTTGAGTCTTGCACATGTAACGATGAGTTAGCAACATGCTTTACAAGGAGAG 76
Db 485 ACACCCAGGTGGTGAAGTCTTAAGGATAAGGTGAATTTGCCCATAGCTGCTCGACAG 544
QY 77 AAAAGCACCGTGCATGCCGATTGGTGAAGTAAGTGGTACGATCGTCCCTATT 132
Db 545 AAACGTCCAGAGAGATGAATGAGGACATAGGGCTCTGTGGTCCCAACNTTTT 600

RESULT 53
US-09-739-254-34
; Sequence 34, Application US/09739254
; Patent No. US20010021700A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 49 Human Secreted Proteins
; FILE REFERENCE: PZ032P1
; CURRENT APPLICATION NUMBER: US/09/739,254
; PRIOR FILING DATE: 2000-12-19
; EARLIER APPLICATION NUMBER: US/09/511,554
; EARLIER FILING DATE: 2000-02-23
; EARLIER APPLICATION NUMBER: PCT/US99/19330
; EARLIER FILING DATE: 1999-08-24
; EARLIER APPLICATION NUMBER: 60/097,917
; EARLIER FILING DATE: 1998-08-25
; EARLIER APPLICATION NUMBER: 60/098,634
; EARLIER FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 34
; LENGTH: 1452
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (283)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (596)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (607)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1275)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1284)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-739-254-34
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```

Query Match      11.4%; Score 30.2; DB 9; Length 1452;
Best Local Similarity 53.4%; Pred. No. 12;
Matches 62; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 17 ATACTCTTTGAGTCTTGCACATGTAACGATGAGTTAGCAACATGCTTTACAAGGAGAG 76
Db 485 ACACCCAGGTGGTGAAGTCTTAAGGATAAGGTGAATTTGCCCATAGCTGCTCGACAG 544
QY 77 AAAAGCACCGTGCATGCCGATTGGTGAAGTAAGTGGTACGATCGTCCCTATT 132
Db 545 AAACGTCCAGAGAGATGAATGAGGACATAGGGCTCTGTGGTCCCAACNTTTT 600

RESULT 54
US-09-904-615-34
; Sequence 34, Application US/09904615
; Patent No. US20020026040A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 49 Human Secreted Proteins
; FILE REFERENCE: PZ032P1
; CURRENT APPLICATION NUMBER: US/09/904,615
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/511,554
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/097,917
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: 60/098,634
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 34
; LENGTH: 1452
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (283)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (596)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (607)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1275)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1284)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-904-615-34
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; FEATURE:
; NAME/KEY: SITE
; LOCATION: (282)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (596)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (607)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1200)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-055-098-63

Query Match      11.4%; Score 30.2; DB 14; Length 1202;
Best Local Similarity 53.4%; Pred. No. 11;
Matches 62; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 17 ATACTCTTTGAGTCTTGCACATGTAACGATGAGTTAGCAACATGCTTTACAAGGAGAG 76
Db 485 ACACCCAGGTGGTGAAGTCTTAAGGATAAGGTGAATTTGCCCATAGCTGCTCGACAG 544
QY 77 AAAAGCACCGTGCATGCCGATTGGTGAAGTAAGTGGTACGATCGTCCCTATT 132
Db 545 AAACGTCCAGAGAGATGAATGAGGACATAGGGCTCTGTGGTCCCAACNTTTT 600

RESULT 53
US-09-739-254-34
; Sequence 34, Application US/09739254
; Patent No. US20010021700A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 49 Human Secreted Proteins
; FILE REFERENCE: PZ032P1
; CURRENT APPLICATION NUMBER: US/09/739,254
; PRIOR FILING DATE: 2000-12-19
; EARLIER APPLICATION NUMBER: US/09/511,554
; EARLIER FILING DATE: 2000-02-23
; EARLIER APPLICATION NUMBER: PCT/US99/19330
; EARLIER FILING DATE: 1999-08-24
; EARLIER APPLICATION NUMBER: 60/097,917
; EARLIER FILING DATE: 1998-08-25
; EARLIER APPLICATION NUMBER: 60/098,634
; EARLIER FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 34
; LENGTH: 1452
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (283)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (596)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (607)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1275)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1284)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-739-254-34
```

```

Query Match      11.4%; Score 30.2; DB 9; Length 1452;
Best Local Similarity 53.4%; Pred. No. 12;
Matches 62; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 17 ATACTCTTTGAGTCTTGCACATGTAACGATGAGTTAGCAACATGCTTTACAAGGAGAG 76
Db 485 ACACCCAGGTGGTGAAGTCTTAAGGATAAGGTGAATTTGCCCATAGCTGCTCGACAG 544
QY 77 AAAAGCACCGTGCATGCCGATTGGTGAAGTAAGTGGTACGATCGTCCCTATT 132
Db 545 AAACGTCCAGAGAGATGAATGAGGACATAGGGCTCTGTGGTCCCAACNTTTT 600

RESULT 55
US-10-054-988-34
; Sequence 34, Application US/10054988
; Publication No. US20030087341A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 49 Human Secreted Proteins
; FILE REFERENCE: PZ032P1
; CURRENT APPLICATION NUMBER: US/10/054,988
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/511,554
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/097,917
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: 60/098,634
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 34
; LENGTH: 1452
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (283)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (596)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (607)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1275)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1284)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-054-988-34
```

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; TITLE OF INVENTION: 49 Human Secreted Proteins
; FILE REFERENCE: P2032P1
; CURRENT APPLICATION NUMBER: US/10/054,988
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: 09/904,615
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/511,554
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/097,917
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: 60/098,634
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 1452
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (283)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (596)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (607)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1275)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1284)
; OTHER INFORMATION: n equals a,t,g, or c
; US-10-054-988-34
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Query Match 11.4%; Score 30.2; DB 14; Length 1452;
Best Local Similarity 53.4%; Pred. No. 12;
Matches 62; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 17 ATACTCTTGTAGTCTTGCACATGTAAGCATGTAAGTGTAGCAATGCTTACAGGAGAG 76
Db 485 ACACCCAGTGTGAGTCTTAAAGATAGGTGGAATTTGCCCATAGTGTCTCTGGACAG 544

QY 77 AAAAAGCAGCGTCGATCGCGATTGCTGGAGTAAGTGTGATGATGCTGCTTATT 132
Db 545 AAATGCCAGAGAGATGATGAGGACATAGGCTCTGTGTGCCACCNTTTT 600
```

```
RESULT 56
US-10-055-098-34
; Sequence 34, Application US/10055098
; Publication No. US20030139954A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 49 Human Secreted Proteins
; FILE REFERENCE: P2032P1
; CURRENT APPLICATION NUMBER: US/10/055,098
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 2000-02-23
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 2000-02-23
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-08-24
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 60/097,917
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 60/098,634
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 1452
; TYPE: DNA
; ORGANISM: Homo sapiens
```

```
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (283)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (596)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (607)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1275)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1284)
; OTHER INFORMATION: n equals a,t,g, or c
; US-10-055-098-34
```

```
Query Match 11.4%; Score 30.2; DB 14; Length 1452;
Best Local Similarity 53.4%; Pred. No. 12;
Matches 62; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 17 ATACTCTTGTAGTCTTGCACATGTAAGCATGTAAGTGTAGCAATGCTTACAGGAGAG 76
Db 485 ACACCCAGTGTGAGTCTTAAAGATAGGTGGAATTTGCCCATAGTGTCTCTGGACAG 544

QY 77 AAAAAGCAGCGTCGATCGCGATTGCTGGAGTAAGTGTGATGATGCTGCTTATT 132
Db 545 AAATGCCAGAGAGATGATGAGGACATAGGCTCTGTGTGCCACCNTTTT 600
```

```
RESULT 57
US-10-027-632-165752/c
; Sequence 165752, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 165752
; LENGTH: 834
; TYPE: DNA
; ORGANISM: Human
; US-10-027-632-165752
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```
Query Match 11.4%; Score 30; DB 15; Length 834;
Best Local Similarity 55.9%; Pred. No. 11;
Matches 57; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 153 TGACATGATTTGGACAGCAACCACTTAATTCGCAATTCGAGATATTTATTAAAGTGCCT 212
Db 325 TGAACATATCTTTTGTATCCACCTGTAATCTTTTGGCAATTTATATATAGCTT 266

QY 213 AGCTCGATACATAAAGCAATTTGACCAATTCACCAATGG 254
```

Db 265 AGCTCTAAGGATTAAAGTATTCAGTTTTCACCACTCTG 224
||||| | | | | | | | | | | | | | | | | | | | |

RESULT 58
US-10-027-632-165753/c
; Sequence 165753, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 165753
; LENGTH: 834
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-165753

Query Match 11.4%; Score 30; DB 15; Length 834;
Best Local Similarity 55.9%; Pred. No. 11;
Matches 57; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 153 TGACATGATTTGACGACCACTAAATTCGCTTTCAGAGATATTTTAAAGTGCCT 212
Db 325 TGAATATCTTTTGGCTATCCACTGGTATCTTTTGGCAATTTTATTATTAAGCCT 266
QY 213 AGCTGATACATAAAGCCATTGACCAATTCACACATTCG 254
Db 265 AGCTCTAAGGATTAAAGTATTCAGTTTTCACCACTCTG 224

RESULT 59
US-10-398-221-1044
; Sequence 1044, Application US/10398221
; Publication No. US20040018514A1
; GENERAL INFORMATION:
; APPLICANT: KUNST, Frederik
; APPLICANT: GLASER, Philippe
; TITLE OF INVENTION: Listeria innocua, genome and applications
; FILE REFERENCE: 344 702 - US
; CURRENT APPLICATION NUMBER: US/10/398,221
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: FR 00/12 697
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 4025
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1044
; LENGTH: 2271
; TYPE: DNA
; ORGANISM: Listeria monocytogenes-EGD
US-10-398-221-1044

Query Match 11.2%; Score 29.6; DB 15; Length 2271;
Best Local Similarity 68.3%; Pred. No. 24;
Matches 41; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 25 GTAGTCTTGCAACATGTAACGATGAGTTAGCAACATGCTTTACAGGAGAGAAAAAGCA 84
Db 2020 GAAGTCGTGCACTTTATATTCATGATGGAAGCAAGCATTACTTAGAAGAAAAAGAA 2079
RESULT 60
US-10-398-221-2861
; Sequence 2861, Application US/10398221.
; Publication No. US20040018514A1
; GENERAL INFORMATION:
; APPLICANT: KUNST, Frederik
; APPLICANT: GLASER, Philippe
; TITLE OF INVENTION: Listeria innocua, genome and applications
; FILE REFERENCE: 344 702 - US
; CURRENT APPLICATION NUMBER: US/10/398,221
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: FR 00/12 697
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 4025
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2861
; LENGTH: 2271
; TYPE: DNA
; ORGANISM: Listeria monocytogenes EGD
US-10-398-221-2861

Query Match 11.3%; Score 29.6; DB 15; Length 2271;
Best Local Similarity 68.3%; Pred. No. 24;
Matches 41; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 25 GTAGTCTTGCAACATGTAACGATGAGTTAGCAACATGCTTTACAGGAGAGAAAAAGCA 84
Db 2020 GAAGTCGTGCACTTTATATTCATGATGGAAGCAAGCATTACTTAGAAGAAAAAGAA 2079

RESULT 61
US-09-962-832-154
; Sequence 154, Application US/09962832
; Patent No. US20020110821A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; FILE REFERENCE: 689290-74
; CURRENT APPLICATION NUMBER: US/09/962,832
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/60/235,077
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,280
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 154
; LENGTH: 302250
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-962-832-154

Query Match 11.2%; Score 29.6; DB 9; Length 302250;
Best Local Similarity 56.0%; Pred. No. 2.4e+02;
Matches 56; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 158 TGGATTGGACGAACCACTAAATTCGCAATTCGAGAGATATTGTATTAAAGTGCCTAGCTC 217
Db 95902 TGTATAGAGGTACTAGCCAGTGCAGTAAATGCTAAGCAGATGAATCAAGGGCTAGAGA 95961

QY 218 GATACATAACGCCATTGACCAATTCACCAATTTGGTGT 257

Db 95962 TAAAAATAAACAAATTTGGCTAATTACAGATGGTTT 96001

RESULT 62

US-10-027-632-63861/c

; Sequence 63861, Application US/10027632

; Publication No. US20030204075A9

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

; POLYMERIZATION: Polymorphisms in the Human Genome

; FILE REFERENCE: 108827.129

; CURRENT APPLICATION NUMBER: US/10/027,632

; CURRENT FILING DATE: 2002-04-30

; PRIOR FILING DATE: 2000-07-12

; PRIOR FILING DATE: 2000-07-12

; PRIOR FILING DATE: 2000-07-12

; PRIOR FILING DATE: 2000-07-12

; PRIOR FILING DATE: 2000-07-12

; PRIOR FILING DATE: 2000-07-12

; PRIOR FILING DATE: 2000-07-12

; PRIOR FILING DATE: 2000-07-12

; PRIOR FILING DATE: 2000-07-12

; PRIOR FILING DATE: 2000-07-12

; PRIOR FILING DATE: 2000-07-12

; PRIOR FILING DATE: 2000-07-12

; PRIOR FILING DATE: 2000-07-12

; PRIOR FILING DATE: 2000-07-12

; PRIOR FILING DATE: 2000-07-12

; PRIOR FILING DATE: 2000-07-12

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; PRIOR FILING DATE: 2000-07-12

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; PRIOR FILING DATE: 2000-07-12

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; PRIOR FILING DATE: 2000-07-12

; PRIOR FILING DATE: 2000-07-12

; PRIOR FILING DATE: 2000-07-12

; PRIOR FILING DATE: 2000-07-12

; PRIOR FILING DATE: 2000-07-12

; PRIOR FILING DATE: 2000-07-12

; PRIOR FILING DATE: 2000-07-12

Query Match 11.1%; Score 29.2; DB 15; Length 183;
Best Local Similarity 50.7%; Pred. No. 9.8;
Matches 70; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 113 TGGTACGATCGCTGCTTATTAGGAGGCAACAGACGGGCTCGACATGGATTGGACGAACC 172

Db 145 TGGAGGTACATGAGTGCTCTGAGGCGAGGGAATAAGTATTTCATGGGCGGAGT 86

QY 173 ACTAAATTCGGCATTCGACAGATATGTTTAAAGTGGCTAGCTCGATACATAAAGCC 232

Db 85 ACTGGTTCTTAAATTTTCAATTTGTTAAGTGGCTCTCTTAAATCCAGTCTGTAC 26

QY 233 ATTGACCATTCACACA 250

Db 25 ATTCTAGAACTGAGRCA 8

RESULT 63

US-10-027-632-64765/c

; Sequence 64765, Application US/10027632

; Publication No. US20030204075A9

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

; POLYMERIZATION: Polymorphisms in the Human Genome

; FILE REFERENCE: 108827.129

; CURRENT APPLICATION NUMBER: US/10/027,632

; CURRENT FILING DATE: 2002-04-30

; PRIOR FILING DATE: 2000-07-12

; PRIOR FILING DATE: 2000-07-12

; PRIOR FILING DATE: 2000-07-12

; PRIOR FILING DATE: 2000-07-12

; PRIOR FILING DATE: 2000-07-12

; PRIOR FILING DATE: 2000-07-12

; PRIOR FILING DATE: 2000-07-12

; PRIOR FILING DATE: 2000-07-12

; PRIOR FILING DATE: 2000-07-12

; PRIOR FILING DATE: 2000-07-12

; PRIOR FILING DATE: 2000-07-12

; PRIOR FILING DATE: 2000-07-12

; PRIOR FILING DATE: 2000-07-12

; PRIOR FILING DATE: 2000-07-12

; PRIOR FILING DATE: 2000-07-12

; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64765
; LENGTH: 637
; TYPE: DNA
; ORGANISM: Human
; US-10-027-632-64765

Query Match 11.1%; Score 29.2; DB 15; Length 637;
Best Local Similarity 50.7%; Pred. No. 18;
Matches 70; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 113 TGGTACGATCGCTGCTTATTAGGAGGCAACAGACGGGCTCGACATGGATTGGACGAACC 172

Db 599 TGGAGGTACATGAGTGCTCTGAGGCGAGGGAATAAGTATTTCATGGGCGGAGT 540

QY 173 ACTAAATTCGGCATTCGACAGATATGTTTAAAGTGGCTAGCTCGATACATAAAGCC 232

Db 539 ACTGGTTCTTAAATTTTCAATTTGTTAAGTGGCTCTCTTAAATCCAGTCTGTAC 480

QY 233 ATTGACCATTCACACA 250

Db 479 ATTCTAGAACTGAGRCA 462

RESULT 64

US-10-027-632-63862/c

; Sequence 63862, Application US/10027632

; Publication No. US20030204075A9

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

; POLYMERIZATION: Polymorphisms in the Human Genome

; FILE REFERENCE: 108827.129

; CURRENT APPLICATION NUMBER: US/10/027,632

; CURRENT FILING DATE: 2002-04-30

; PRIOR FILING DATE: 2000-07-12

; PRIOR FILING DATE: 2000-07-12

; PRIOR FILING DATE: 2000-07-12

; PRIOR FILING DATE: 2000-07-12

; PRIOR FILING DATE: 2000-07-12

; PRIOR FILING DATE: 2000-07-12

; PRIOR FILING DATE: 2000-07-12

; PRIOR FILING DATE: 2000-07-12

; PRIOR FILING DATE: 2000-07-12

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; PRIOR FILING DATE: 2000-07-12

; PRIOR FILING DATE: 2000-07-12

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; PRIOR FILING DATE: 2000-07-12

; PRIOR FILING DATE: 2000-07-12

; PRIOR FILING DATE: 2000-07-12

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Db 654 ACTGTTCTAAATTTTACATTTGTTATGTTTAAAGTGAATCTCTTAATCCAGTGTGTAC 595
QY 233 ATTTCACCAATTCACCA 250
Db 594 ATTCTAGAAGTGAAGCA 577

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RESULT 65
US-10-027-632-64766/c
; Sequence 64766, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64766
; LENGTH: 752
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-64766

```

```

Query Match 11.1%; Score 29.2; DB 15; Length 752;
Best Local Similarity 50.7%; Pred. No. 19;
Matches 70; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 113 TGGTAGCATCTGCTTATTAGGAAGGCAACAGCGGTCTGCATCGATTCGACGAACC 172
Db 714 TGAAGGTACATGAGTCTCTCGAGCGAGTGAAGGGAATAGTATTTCATGGACGGAGT 655
QY 173 ACTAAATTCGCAATTCGAGATATTGTTAAAGTCTAGCTCGATCAATAAAGCC 232
Db 654 ACTGTTTCTAAATTTTACATTTGTTATGTTTAAAGTGAATCTCTTAATCCAGTGTGTAC 595
QY 233 ATTTCACCAATTCACCA 250
Db 594 ATTCTAGAAGTGAAGCA 577

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RESULT 66
US-10-027-632-310455/c
; Sequence 310455, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20

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; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 310455
; LENGTH: 752
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-310455

Query Match 11.1%; Score 29.2; DB 15; Length 752;
Best Local Similarity 50.7%; Pred. No. 19;
Matches 70; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 113 TGGTAGCATCTGCTTATTAGGAAGGCAACAGCGGTCTGCATCGATTCGACGAACC 172
Db 714 TGAAGGTACATGAGTCTCTCGAGCGAGTGAAGGGAATAGTATTTCATGGACGGAGT 655
QY 173 ACTAAATTCGCAATTCGAGATATTGTTAAAGTCTAGCTCGATCAATAAAGCC 232
Db 654 ACTGTTTCTAAATTTTACATTTGTTATGTTTAAAGTGAATCTCTTAATCCAGTGTGTAC 595
QY 233 ATTTCACCAATTCACCA 250
Db 594 ATTCTAGAAGTGAAGCA 577

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RESULT 67
US-10-027-632-310456/c
; Sequence 310456, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 310456
; LENGTH: 752
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-310456

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Query Match 11.1%; Score 29.2; DB 15; Length 752;
Best Local Similarity 50.7%; Pred. No. 19;
Matches 70; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 113 TGGTAGCATCTGCTTATTAGGAAGGCAACAGCGGTCTGCATCGATTCGACGAACC 172

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Db 714 TGAAGGTACATGAGTGTCTCTGAGCGAGTACAGAGGAATAAGTATTCATGCGGACGGAGT 655
QY 173 ACTAAATTCGGCATTCGACAGATATTGTATTAAAGTGGCTAGCTCGATACATTAACGCC 232
Db 654 ACTGGTTCCTAAATTTACAAATGTTATGTTTAAGTGAAGTCTCTTAATCCAGTGTGTAC 595
QY 233 ATTGACCATTCACCA 250
Db 594 ATTCTAGAACTGAGGCA 577

RESULT 68
US-10-027-632-35424/c
; Sequence 35424, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35424
; LENGTH: 766
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-35424

Query Match 11.1%; Score 29.2; DB 15; Length 766;
Best Local Similarity 50.7%; Pred. No. 19;
Matches 70; Conservative 0; Mismatches 68; Indels 0; Gaps 0;
QY 113 TGGTACGATCGGCGCTTATTAGAGGCAACAGACGGGTCTGCATGATGGACGACACC 172
Db 714 TGGAGGTACATGAGTGTCTCTGAGCGAGTACAGAGGAATAAGTATTCATGCGGACGGAGT 655
QY 173 ACTAAATTCGGCATTCGACAGATATTGTATTAAAGTGGCTAGCTCGATACATTAACGCC 232
Db 654 ACTGGTTCCTAAATTTACAAATGTTATGTTTAAGTGAAGTCTCTTAATCCAGTGTGTAC 595
QY 233 ATTGACCATTCACCA 250
Db 594 ATTCTAGAACTGAGGCA 577

RESULT 69
US-10-311-455-820
; Sequence 820, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining
; TITLE OF INVENTION: cytosine methylation
; FILE REFERENCE: 5013.1014

; CURRENT APPLICATION NUMBER: US/10/311.455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 820
; LENGTH: 5297
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-820

Query Match 11.1%; Score 29.2; DB 14; Length 5297;
Best Local Similarity 50.7%; Pred. No. 49;
Matches 70; Conservative 0; Mismatches 68; Indels 0; Gaps 0;
QY 70 AGGAGAGAAAAGCACCGTGCATGCCGATTTGGTGAAGTAAGTGGTACATCGTCCTT 129
Db 2592 AAGAAAGGAGAGAGTATAAATTTATGATAGTGAATTTATAATGTTGTTTTTTT 2651
QY 130 ATTAGGAAGCAACAGACGGGTCTGCATGATGGAGCAACCACTAAATCCGCATTGC 189
Db 2652 TTTAGAAGTAAGTAAGTGTAGTTATAATTTATTGAGGTATAGATTAAATTTATTGA 2711
QY 190 AGAGATATTGTTTAAAG 207
Db 2712 GTATTATTATTATGTTAG 2729

RESULT 70
US-10-257-166-84
; Sequence 84, Application US/10257166
; Publication No. US2004002320A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Method and Nucleic Acids for Analysing the Methylation of
; TITLE OF INVENTION: Genes Implicated in Pharmacogenomics
; FILE REFERENCE: 5013.1011
; CURRENT APPLICATION NUMBER: US/10/257.166
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: PCT/EP01/07470
; DE 10032529.7
; DE 10043826.1
; PRIOR FILING DATE: 2001-06-29
; PRIOR FILING DATE: 2000-06-30
; 2000-09-01
; NUMBER OF SEQ ID NOS: 178
; SEQ ID NO 84
; LENGTH: 5297
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-257-166-84

Query Match 11.1%; Score 29.2; DB 16; Length 5297;
Best Local Similarity 50.7%; Pred. No. 49;
Matches 70; Conservative 0; Mismatches 68; Indels 0; Gaps 0;
QY 70 AGGAGAGAAAAGCACCGTGCATGCCGATTTGGTGAAGTAAGTGGTACATCGTCCTT 129
Db 2592 AAGAAAGGAGAGTATAAATTTATGATAGTGAATTTATAATGTTGTTTTTTT 2651
QY 130 ATTAGGAAGCAACAGACGGGTCTGCATGATGGAGCAACCACTAAATCCGCATTGC 189
Db 2652 TTTAGAAGTAAGTAAGTGTAGTTATAATTTATTGAGGTATAGATTAAATTTATTGA 2711


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; Sequence 5, Application US/10097534
; Publication No. US20030049607A1
; GENERAL INFORMATION:
; APPLICANT: GREENER, TSVIKA
; APPLICANT: MOSKOWITZ, HAIM
; APPLICANT: REISS, YUVAL
; APPLICANT: ALROY, IRIS
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE MODULATION OF VIRAL
; TITLE OF INVENTION: MATURATION
; FILE REFERENCE: PLV-001.01
; CURRENT APPLICATION NUMBER: US/10/097,534
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/275,224
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/308,958
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/340,170
; PRIOR FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 6102
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-097-534-5
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Query Match      11.0%; Score 29; DB 14; Length 6102;
Best Local Similarity 55.4%; Pred. No. 61;
Matches 56; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY      16 AATACCTCTGTAGTCTGCAACATGGTAAAGATGAGTTAGCACATGCGCTTACAGGAGA 75
Db      3248 AACATTTTGAATCTGCAAGAGCGTTCAGCCAGCTTAGCAAGAAACCCACACACTCAGG 3307

QY      76 GAAAAAGCACCGTCATGCCGATTTGGTGGAGTAAAGTGGT 116
Db      3308 GAGAAATCCATTACATTGCGACTGAGGGTATCACGGGCT 3348
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Search completed: March 11, 2004, 11:20:22
Job time : 194.633 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 11, 2004, 05:54:28 ; Search time 352.355 Seconds
(without alignments)
7749.556 Million cell updates/sec

Title: US-09-733-368a-1_COPY_550_612

Perfect score: 63

Sequence: 1 tttaagtgcctagtcgata.....accacattgtgtgcacctc 63

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_hrg.*

3: gb_in.*

4: gb_em.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vi.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htg_mus.*

34: em_htg_pln.*

35: em_htg_rod.*

36: em_htg_mam.*

37: em_htg_vrt.*

38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	63	100.0	648	6	AX175190	AX175190 Sequence
3	63	100.0	648	6	AX175195	AX175195 Sequence
4	63	100.0	2309	12	EVU67090	U67090 Expression
5	63	100.0	2794	12	EVU51722	U51722 Expression
6	63	100.0	2856	12	AY229985	AY229985 Expressio
7	63	100.0	2895	12	AY229986	AY229986 Expressio
8	63	100.0	2981	12	EVU51721	U51721 Expression
9	63	100.0	3059	12	EVU67091	U67091 Expression
10	63	100.0	3189	6	A30504	A30504 plasmid p79
11	63	100.0	3277	6	A30505	A30505 plasmid p23
12	63	100.0	3277	6	A30507	A30507 plasmid p23
13	63	100.0	3384	6	A30503	A30503 plasmid p79
14	63	100.0	3427	6	A30513	A30513 plasmid p26
15	63	100.0	3427	6	A30515	A30515 plasmid p26
16	63	100.0	3557	12	SYNRSV3MV	M83240 Cloning vec
17	63	100.0	3979	6	A30511	A30511 plasmid p26
18	63	100.0	3980	6	A30509	A30509 plasmid p26
19	63	100.0	4059	6	AR071324	AR071324 Sequence
20	63	100.0	4341	6	A38214	A38214 Sequence 58
21	63	100.0	4341	6	AX286570	AX286570 Sequence
22	63	100.0	4457	6	AX743954	AX743954 Sequence
23	63	100.0	4839	12	SYNRSV5GPT	M83236 Cloning vec
24	63	100.0	5108	12	SYNRSV5NEO	M83237 cDNA expres
25	63	100.0	5564	12	SYNTCRC	L36555 Cloning vec
26	63	100.0	5653	6	I56772	I56772 Sequence 3
27	63	100.0	5653	6	I95540	I95540 Sequence 1
28	63	100.0	5736	12	SYNRSVNEO	M7786 prsVneo clo
29	63	100.0	6836	6	AR215114	AR215114 Sequence
30	63	100.0	6836	6	AR302356	AR302356 Sequence
31	63	100.0	6836	6	AR373228	AR373228 Sequence
32	63	100.0	6836	6	AR401614	AR401614 Sequence
33	63	100.0	6836	12	AP346624	AP346624 PAGE vect
34	63	100.0	6864	12	XXU19931	U19931 Cloning vec
35	63	100.0	6926	6	A48775	A48775 Sequence 2
36	63	100.0	6926	6	AR018703	AR018703 Sequence
37	63	100.0	7086	6	AX743955	AX743955 Sequence
38	63	100.0	7334	6	AX743956	AX743956 Sequence
39	63	100.0	7492	6	AR235458	AR235458 Sequence
40	63	100.0	8238	6	BD268239	BD268239 Adenoviru
41	63	100.0	8413	12	XXU02432	U02432 Cloning vec
42	63	100.0	8475	12	XXU02430	U02430 Cloning vec
43	63	100.0	8591	6	I58322	I58322 Sequence 6
44	63	100.0	8591	6	I58323	I58323 Sequence 8
45	63	100.0	8591	6	I60508	I60508 Sequence 6
46	63	100.0	8591	6	I60509	I60509 Sequence 6
47	63	100.0	8591	6	I77052	I77052 Sequence 8
48	63	100.0	8591	6	I77053	I77053 Sequence 8
49	63	100.0	8591	6	I87173	I87173 Sequence 6
50	63	100.0	8591	6	I87174	I87174 Sequence 8
51	63	100.0	9184	12	XXU02431	U02431 Cloning vec
52	63	100.0	9737	6	AR215118	AR215118 Sequence
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54	63	100.0	9737	6	AR215124	AR215124 Sequence
55	63	100.0	9737	6	AR302360	AR302360 Sequence
56	63	100.0	9737	6	AR302361	AR302361 Sequence
57	63	100.0	9737	6	AR302366	AR302366 Sequence
58	63	100.0	9737	6	AR373232	AR373232 Sequence
59	63	100.0	9737	6	AR373233	AR373233 Sequence
60	63	100.0	9737	6	AR373238	AR373238 Sequence
61	63	100.0	9737	6	AR401618	AR401618 Sequence
62	63	100.0	9737	6	AR401619	AR401619 Sequence
63	63	100.0	9737	6	AR401624	AR401624 Sequence
64	63	100.0	9871	6	AR215120	AR215120 Sequence
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Pred. No. is the number of results predicted by chance to have a

ALIGNMENTS

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1. .101
Location/Qualifiers
/organism="Rous sarcoma virus"
/mol_type="genomic DNA"
/db_xref="taxon:11896"

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Best Local Similarity 100.0%; Pred. No. 1.5e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TTTAAGTGCTAGCTGCGATACATAAAGCCATTGACCATTCACCAATTGGTGTGCAC 60
Db      32  TTTAAGTGCTAGCTGCGATACATAAAGCCATTGACCATTCACCAATTGGTGTGCAC 91

QY      61  CTC 63
Db      92  CTC 94

RESULT 2
AXI175190
LOCUS      AXI175190
DEFINITION Sequence 1 from Patent WO0142444.
ACCESSION  AXI175190
VERSION     AXI175190.1 GI:14598581
KEYWORDS    .
SOURCE      Synthetic construct
            Synthetic construct
            artificial sequences.
ORGANISM    1
            Rivera,V., Zoltick,P. and Wilson,J.M.
REFERENCE   1
            Methods for expression of genes in primates
            Patent: WO 0142444-A 1 14-JUN-2001;
            ARIAD GENE THERAPEUTICS, INC. (US) ; THE UNIVERSITY OF PENNSYLVANIA
            (US)
FEATURES
    source      Location/Qualifiers
                1. .648
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="vector/BSV promoter/vector"

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ORIGIN					
 Query Match 100.0%; Score 63; DB 6; Length 648;					
Best Local Similarity 100.0%; Pred. No. 1.5e-13;					
Matches	63;	Conservative	0;	Mismatches	0; Indels 0; Gaps 0;
QY	1	TTTAAAGTCCTAGCTCGATACATAAAGCCATTGACCATTCACCACCATGGTGTCAC	60		
Dd	550	TTTAAAGTCCTAGCTCGATACATAAAGCCATTGACCATTCACCACCATGGTGTCAC	609		
QY	61	CTC	63		
Dd	610	CTC	612		
RESULT 3					
AXI75195					
LOCUS	AXI75195	648 bp	DNA	linear	PAT 03-JUL-2001
DEFINITION	Sequence 6 from Patent WO0142444.				
ACCESSION	AXI75195				
VERSION	AXI75195.1	GI:14598586			
KEYWORDS	synthetic construct				
SOURCE	synthetic construct				
ORGANISM	artificial sequences.				
REFERENCE	1				
AUTHORS	Rivera,V., Zoltick,P. and Wilson,J.M.				
TITLE	Methods for expression of genes in primates				
JOURNAL	Patent: WO 014244-A 6 14-JUN-2001;				
	ARIAD GENE THERAPEUTICS, INC. [US]; THE UNIVERSITY OF PENNSYLVANIA				
FEATURES	(US)	Location/Qualifiers			
source	1..648				
	/organism="synthetic construct"				
	/mol_type="unassigned DNA"				
	/db_xref="taxon:32630"				

/note="MluI/RSV promoter/BglI"

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Best Local Similarity 100.0%; Pred. No. 1.5e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTGATACAAATAAGCGCATTTGACCATTCACCATTTGGTGTGCAC 60
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Db 550 TTTAAGTCCTAGCTGATACAAATAAGCGCATTTGACCATTCACCATTTGGTGTGCAC 609

QY 61 CTC 63
    |||
Db 610 CTC 612

RESULT 4
LOCUS EVU67090 2309 bp mRNA linear SYN 29-OCT-2001
DEFINITION Expression vector pNEX2 beta-lactamase mRNA, complete cds.
ACCESSION U67090
VERSION U67090.1 GI:1561767
KEYWORDS Expression vector pNEX2
SOURCE artificial sequences; vectors.
ORGANISM Kaang,B.K.
REFERENCE 1 (bases 1 to 2309)
AUTHORS Kaang,B.K.
TITLE Parameters influencing ectopic gene expression in Aplysia neurons
JOURNAL Neurosci. Lett. 221 (1), 29-32 (1996)
MEDLINE 97166442
PUBMED 9014173
REFERENCE 2 (bases 1 to 2309)
AUTHORS Kaang,B.-K.
TITLE Direct Submission
JOURNAL Submitted (16-AUG-1996) Inst. for Mol. Biol. & Genet., Seoul
National University, San 56-1, Silim-dong, Kwanak-gu, Seoul
151-742, Korea
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        1. .2309
            /organism="Expression vector pNEX2"
            /mol_type="mRNA"
            /db_xref="taxon:51257"
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        9. .15
            /bound_moiety="AP-1"
        17. .103
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        107. .169
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        190. .331
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        454. .1314
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            /note="selection marker"
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            /protein_id="AAB08871.1"
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            YSPVTEKHLDGMVRELCSAAITWSDNTAANLLLTIGGPKELTAFIHNMGDVTFL
            DRWPELNAIEDERDTTPVAMATTLKLTGELLTLASRQQLIDWMEADKVGFL
            LRSLAPAGWFIADKSGAGERSGIIAALGPDGKPSRIIVITVTSQATMDERNRQIA
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            /note="ColEI origin of replication from pUC19"
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Query Match          100.0%; Score 63; DB 12; Length 2309;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTGATACAAATAAGCGCATTTGACCATTCACCATTTGGTGTGCAC 60
    |||
Db 550 TTTAAGTCCTAGCTGATACAAATAAGCGCATTTGACCATTCACCATTTGGTGTGCAC 609

QY 61 CTC 63
    |||
Db 610 CTC 612

RESULT 5
LOCUS EVU51722 2794 bp DNA circular SYN 14-SEP-1996
DEFINITION Expression vector pNEX delta, complete sequence.
ACCESSION U51722
VERSION U51722.1 GI:1277160
KEYWORDS Expression vector pNEX delta
SOURCE Expression vector pNEX delta
ORGANISM Expression vector pNEX delta
REFERENCE 1 (sites)
AUTHORS Kaang,B.K., Kandel,E.R. and Grant,S.G.
TITLE Activation of cAMP-responsive genes by stimuli that produce
long-term facilitation in Aplysia sensory neurons
JOURNAL Neuron 10 (3), 427-435 (1993)
MEDLINE 93213500
PUBMED 8384857
REFERENCE 2 (bases 1 to 2794)
AUTHORS Kaang,B.-K.
TITLE Direct Submission
JOURNAL Submitted (19-MAR-1996) Bong-Kiun Kaang, Seoul National University,
Inst. for Mol. Biol. & Genet., San 56-1, Silim-dong, Kwanak-gu,
Seoul, Korea, 151-742
FEATURES
    source
        1. .2794
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            /db_xref="taxon:51098"
        14. .53
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            /evidence=experimental
        89. .176
            /note="minimal promoter from RSV LTR for transcription"
            /evidence=experimental
        180. .242
            /note="polylinker region from pUC19, pNEXdelta derived
            from pNEX to generate two more cloning sites, HindIII and
            PvuII"
            /function="multiple cloning sites"
            /evidence=experimental
        551. .682
            /note="polyadenylation signal sequences from simian virus
            40"
            /evidence=experimental
        939. .1799
            /function="ampicillin resistance"
            /note="selection marker"
            /codon_start=1
            /evidence=experimental
            /transl_table=11
            /product="beta-lactamase"
            /protein_id="AAB08055.1"
            /db_xref="GI:1277161"
            /translation="MSIQHFRVALIPFFAFCPLVFAHPETLVKVKDAEDQLGARVGY
            IEIDLSNGKILSPFEPERFPMSTFKVLICGAVLSRIDAGQQLGRIRHYSDNLYVE
            YSPVTEKHLDGMVRELCSAAITWSDNTAANLLLTIGGPKELTAFIHNMGDVTFL
            DRWPELNAIEDERDTTPVAMATTLKLTGELLTLASRQQLIDWMEADKVGFL
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            /note="ColEI origin of replication from pUC19"
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    ORIGIN

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Query Match          100.0%; Score 63; DB 12; Length 2794;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCCTAGCTCGATACAAATAAAGCCATTGACCATTCACCACATTGGTGTGCAC 60
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Db 116 TTTAAGTGCCTAGCTCGATACAAATAAAGCCATTGACCATTCACCACATTGGTGTGCAC 175

QY 61 CTC 63
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Db 176 CTC 178

RESULT 6
AY229985      2856 bp      DNA      circular SYN 29-AUG-2003
LOCUS      Expression vector pNEX delta F, complete sequence.
DEFINITION      AY229985
ACCESSION      AY229985
VERSION      AY229985.1 GI:29469036
KEYWORDS
SOURCE      Expression vector pNEX delta F
ORGANISM      Expression vector pNEX delta F
artificial sequences; vectors.
REFERENCE      1 (bases 1 to 2856)
AUTHORS      Lee, Y., Han, J.-H., Lim, C.-S., Chang, D.-J., Lee, Y.-S., Soh, H., Park, C.-S.
and Kaang, B.-K.
TITLE      Impairment of a parabolic bursting rhythm by the ectopic expression
of a small conductance Ca(2+)-activated K(+) channel in Aplysia
neuron R15
JOURNAL      Neurosci. Lett. 349 (1), 53-57 (2003)
MEDLINE      22827995
PubMed      12946585
REFERENCE      2 (bases 1 to 2856)
AUTHORS      Lee, Y., Han, J.-H., Lim, C.-S., Chang, D.-J., Lee, Y.-S., Park, C.-S.
and Kaang, B.-K.
TITLE      Direct Submission
JOURNAL      Submitted (04-FEB-2003) School of Biological Science, Seoul
National University, San56-1 Silim-dong Kwanak-gu, Seoul 151-742,
Korea
FEATURES
     source              Location/Qualifiers
     1..2856
     /organism="Expression vector pNEX delta F"
     /mol_type="other DNA"
     /db_xref="taxon:221894"
     /note="derived from pNEX delta, altered to generate
additional cloning sites in the polylinker"
protein_bind          14..53
     /bound_moiety="AP-1"
promoter              89..176
     /notes="minimal RSV LTR promoter"
misc_feature          198..285
     /notes="polylinker region from pNEX delta and Litmus28"
CDS                  1001..1861
     /note="ampicillin resistance; selection marker"
     /codon_start=1
     /product="beta-lactamase"
     /protein_id="AA049810.1"
     /db_xref="GI:29469037"
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YSFVTEKHLTDGMTVRELCSAAITWSDNTAANLLITIGPKELTAFIHNMGDHTRL
DRWPELNEALPNDERDTTPVAMATTIRKLITGLLTLASQQLIDWMEADKVAQPL
LRSLAPAGNFIADKSGAGRGSRGIIAALGPDGKPSRIIVYITGSOATMDERNRQIA
EIGASLIKHW"
ORIGIN
EVU51721
LOCUS      EVU51721      2981 bp      DNA      circular SYN 17-SEP-1996
DEFINITION      Expression vector pNEX, complete sequence.
ACCESSION      U51721
VERSION      U51721.1 GI:1277158
KEYWORDS
SOURCE      Expression vector pNEX
ORGANISM      Expression vector pNEX
artificial sequences, vectors.
REFERENCE      1 (bases 1 to 2981)

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QY 61 CTC 63
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Db 176 CTC 178

RESULT 7
AY229986      2895 bp      DNA      circular SYN 01-APR-2003
LOCUS      Expression vector pNEX delta R, complete sequence.
DEFINITION      AY229986
ACCESSION      AY229986
VERSION      AY229986.1 GI:29423755
KEYWORDS
SOURCE      Expression vector pNEX delta R
ORGANISM      Expression vector pNEX delta R
artificial sequences; vectors.
REFERENCE      1 (bases 1 to 2895)
AUTHORS      Lee, Y.-S. and Kaang, B.-K.
TITLE      Direct Submission
JOURNAL      Submitted (04-FEB-2003) School of Biological Science, Seoul
National University, San 56-1 Silim-dong Kwanak-gu, Seoul 151-742,
Korea
FEATURES
     source              Location/Qualifiers
     1..2895
     /organism="Expression vector pNEX delta R"
     /mol_type="genomic DNA"
     /db_xref="taxon:225583"
     /note="polylinker region derived from pNEX delta and
Litmus28 to include more cloning sites"
protein_bind          14..53
     /bound_moiety="AP-1 protein"
promoter              89..176
     /notes="minimal promoter from RSV LTR for transcription"
misc_feature          197..306
     /note="polylinker region derived from pNEX delta and
Litmus28 to include more cloning sites"
CDS                  1040..1900
     /function="ampicillin resistance"
     /codon_start=1
     /product="beta-lactamase"
     /protein_id="AA073815.1"
     /db_xref="GI:29423756"
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YSFVTEKHLTDGMTVRELCSAAITWSDNTAANLLITIGPKELTAFIHNMGDHTRL
DRWPELNEALPNDERDTTPVAMATTIRKLITGLLTLASQQLIDWMEADKVAQPL
LRSLAPAGNFIADKSGAGRGSRGIIAALGPDGKPSRIIVYITGSOATMDERNRQIA
EIGASLIKHW"
ORIGIN
Query Match          100.0%; Score 63; DB 12; Length 2895;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCCTAGCTCGATACAAATAAAGCCATTGACCATTCACCACATTGGTGTGCAC 60
   |||||
Db 116 TTTAAGTGCCTAGCTCGATACAAATAAAGCCATTGACCATTCACCACATTGGTGTGCAC 175

QY 61 CTC 63
   |||
Db 176 CTC 178

RESULT 8
EVU51721
LOCUS      EVU51721      2981 bp      DNA      circular SYN 17-SEP-1996
DEFINITION      Expression vector pNEX, complete sequence.
ACCESSION      U51721
VERSION      U51721.1 GI:1277158
KEYWORDS
SOURCE      Expression vector pNEX
ORGANISM      Expression vector pNEX
artificial sequences, vectors.
REFERENCE      1 (bases 1 to 2981)

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AUTHORS Kaang,B.-K., Pfaffinger,P.J., Grant,S.G., Kandel,E.R. and Furukawa,Y.
TITLE Overexpression of an Aplysia shaker K⁺ channel gene modifies the electrical properties and synaptic efficacy of identified Aplysia neurons
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 89 (3), 1133-1137 (1992)
MEDLINE 92141216
PUBMED 1310540
REFERENCE 2 (bases 1 to 2981)
AUTHORS Kaang,B.-K.
TITLE Neuronal expression of reporter genes in the intact nervous system of Aplysia
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 2981)
AUTHORS Kaang,B.-K.
TITLE Direct Submission
JOURNAL Submitted (19-MAR-1996) Bong-Kiun Kaang, Seoul National University, Inst. for Mol. Biol. & Genet., San 56-1, Sillim-dong, Kwanak-gu, Seoul, Korea, 151-742
FEATURES Location/Qualifiers
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 /mol_type="genomic DNA"
 /db_xref="taxon:51097"
 protein_bind
 23..82
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 /evidence=experimental
 98..185
 /note="minimal promoter from RSV LTR for transcription"
 /evidence=experimental
 189..245
 /note="polylinker region from pUC19"
 /function="multiple cloning site"
 /evidence=experimental
 560..691
 /note="polyadenylation signal sequence from simian virus 40"
 /evidence=experimental
 948..1808
 /function="ampicillin resistance"
 /note="selection marker"
 /codon_start=1
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 /db_xref="GI:1277159"
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 DRWPELNEAIPIVNDERDTMPVAVATTAKLTGELLTLASRQQLIDWVADKVGAPL
 LRSALPAGWFIADKSGAGERSGRIIAALGPDGKPSRIVVIYITGSGATMDERNRQIA
 EIGASLIKHW"
 2567
 /note="ColE1 origin of replication from pUC19"
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 Best Local Similarity 100.0%; Pred. No. 1.6e-13;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTAAGTCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTCGTTGGTGCAC 60
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 Db 125 TTTAAGTCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTCGTTGGTGCAC 184
 |||||
 QY 61 CTC 63
 |||||
 Db 185 CTC 187

RESULT 9
 EVU67091
 LOCUS
 DEFINITION Expression vector pNEX3 beta-lactamase mRNA, complete cds.
 3059 bp mRNA linear SYN 29-OCT-2001

ACCESSION U67091
VERSION GI:1561769
KEYWORDS Expression vector pNEX3
SOURCE Expression vector pNEX3
ORGANISM artificial sequences; vectors.
REFERENCE 1 (bases 1 to 3059)
AUTHORS Kaang,B.-K.
TITLE Parameters influencing ectopic gene expression in Aplysia neurons
JOURNAL Neurosci. Lett. 221 (1), 29-32 (1996)
MEDLINE 97166442
PUBMED 9014173
REFERENCE 2 (bases 1 to 3059)
AUTHORS Kaang,B.-K.
TITLE Direct Submission
JOURNAL Submitted (16-AUG-1996) Inst. for Mol. Biol. & Genet., Seoul National University, San 56-1, Sillim-dong, Kwanak-gu, Seoul 151-742, Korea
FEATURES Location/Qualifiers
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 1..3059
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 /mol_type="mRNA"
 /db_xref="taxon:51681"
 /note="neuronal expression vector"
 16..160
 /note="eight copies of AP-1 binding site; four copies of AP-1 site inserted into pNEX, GenBank Accession Number U51721"
 /bound_moiety="AP-1"
 180..263
 /note="minimal promoter from RSV LTR for transcription"
 267..323
 /note="polylinker region from pUC19"
 637..770
 /note="polyadenylation signal sequence from simian virus 40"
 1026..1886
 /function="ampicillin resistance"
 /note="selection marker"
 /codon_start=1
 /product="beta-lactamase"
 /protein_id="AAB08872.1"
 /db_xref="GI:1561770"
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 DRWPELNEAIPIVNDERDTMPVAVATTAKLTGELLTLASRQQLIDWVADKVGAPL
 LRSALPAGWFIADKSGAGERSGRIIAALGPDGKPSRIVVIYITGSGATMDERNRQIA
 EIGASLIKHW"
 2645..3059
 /note="ColE1 origin of replication from pUC19"
rep_origin
ORIGIN
 Query Match 100.0%; Score 63; DB 12; Length 3059;
 Best Local Similarity 100.0%; Pred. No. 1.6e-13;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db 203 TTTAAGTCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTCGTTGGTGCAC 262
 |||||
 QY 61 CTC 63
 |||||
 Db 263 CTC 265

RESULT 10
 A30504
 LOCUS
 DEFINITION Plasmid p79DBAM.
 A30504
 ACCESSION A30504
 VERSION A30504.1
 KEYWORDS

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SOURCE      synthetic construct
ORGANISM     synthetic construct
            artificial sequences.
REFERENCE    1 (bases 1 to 3189)
AUTHORS      Fountoulakis,M., Garotta,G. and Stueber,D.
TITLE        Soluble interferon-gamma receptors and methods for their production
JOURNAL      Patent: EP 0393502-A 71 24-OCT-1990;
            F. HOFFMANN-LA ROCHE AG
FEATURES     Location/Qualifiers
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            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
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Query Match      100.0%; Score 63; DB 6; Length 3189;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 TTTAAGTGCCTAGCTCGATACATAAAGCGCCATTGGACCATTCACCAATTGGTGTGCAC 60
        |||||
        251 TTTAAGTGCCTAGCTCGATACATAAAGCGCCATTGGACCATTCACCAATTGGTGTGCAC 310
DB
QY      61 CTC 63
        |||
        311 CTC 313
DB
RESULT 11
A30505
LOCUS      A30505      3277 bp      DNA      linear      PAT 05-JUL-2002
DEFINITION Plasmid p238BGL.
ACCESSION  A30505
VERSION     A30505.1 GI:23957134
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
            artificial sequences.
REFERENCE  1 (bases 1 to 3277)
AUTHORS      Fountoulakis,M., Garotta,G. and Stueber,D.
TITLE        Soluble interferon-gamma receptors and methods for their production
JOURNAL      Patent: EP 0393502-A 72 24-OCT-1990;
            F. HOFFMANN-LA ROCHE AG
FEATURES     Location/Qualifiers
            source
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            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
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Query Match      100.0%; Score 63; DB 6; Length 3277;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 TTTAAGTGCCTAGCTCGATACATAAAGCGCCATTGGACCATTCACCAATTGGTGTGCAC 60
        |||||
        251 TTTAAGTGCCTAGCTCGATACATAAAGCGCCATTGGACCATTCACCAATTGGTGTGCAC 310
DB
QY      61 CTC 63
        |||
        311 CTC 313
DB
RESULT 12
A30507
LOCUS      A30507      3277 bp      DNA      linear      PAT 05-JUL-2002
DEFINITION Plasmid p238BAM.
ACCESSION  A30507
VERSION     A30507.1 GI:23957135
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
            artificial sequences.

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REFERENCE    1 (bases 1 to 3277)
AUTHORS      Fountoulakis,M., Garotta,G. and Stueber,D.
TITLE        Soluble interferon-gamma receptors and methods for their production
JOURNAL      Patent: EP 0393502-A 74 24-OCT-1990;
            F. HOFFMANN-LA ROCHE AG
FEATURES     Location/Qualifiers
            source
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            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
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Query Match      100.0%; Score 63; DB 6; Length 3277;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 TTTAAGTGCCTAGCTCGATACATAAAGCGCCATTGGACCATTCACCAATTGGTGTGCAC 60
        |||||
        251 TTTAAGTGCCTAGCTCGATACATAAAGCGCCATTGGACCATTCACCAATTGGTGTGCAC 310
DB
QY      61 CTC 63
        |||
        311 CTC 313
DB
RESULT 13
A30503
LOCUS      A30503      3384 bp      DNA      linear      PAT 05-JUL-2002
DEFINITION Plasmid p79BGL.
ACCESSION  A30503
VERSION     A30503.1 GI:23957132
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
            artificial sequences.
REFERENCE  1 (bases 1 to 3384)
AUTHORS      Fountoulakis,M., Garotta,G. and Stueber,D.
TITLE        Soluble interferon-gamma receptors and methods for their production
JOURNAL      Patent: EP 0393502-A 69 24-OCT-1990;
            F. HOFFMANN-LA ROCHE AG
FEATURES     Location/Qualifiers
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            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
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Query Match      100.0%; Score 63; DB 6; Length 3384;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 TTTAAGTGCCTAGCTCGATACATAAAGCGCCATTGGACCATTCACCAATTGGTGTGCAC 60
        |||||
        251 TTTAAGTGCCTAGCTCGATACATAAAGCGCCATTGGACCATTCACCAATTGGTGTGCAC 310
DB
QY      61 CTC 63
        |||
        311 CTC 313
DB
RESULT 14
A30513
LOCUS      A30513      3427 bp      DNA      linear      PAT 05-JUL-2002
DEFINITION Plasmid p267BGL.
ACCESSION  A30513
VERSION     A30513.1 GI:23957138
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
            artificial sequences.
REFERENCE  1 (bases 1 to 3427)
AUTHORS      Fountoulakis,M., Garotta,G. and Stueber,D.
TITLE        Soluble interferon-gamma receptors and methods for their production

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JOURNAL Patent: EP 0393502-A 80 24-OCT-1990;
FEATURES F. HOFFMANN-LA ROCHE AG
SOURCE location/Qualifiers
1..3427
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCCTAGCTCGATACATAAAGCGCCATTGACCATTCACCATTTGGTGTGCAC 60
DB 250 TTTAAGTGCCTAGCTCGATACATAAAGCGCCATTGACCATTCACCATTTGGTGTGCAC 309

QY 61 CTC 63
DB 310 CTC 312

RESULT 15
A30515
LOCUS Plasmid p267BAM. 3427 bp DNA linear PAT 05-JUL-2002
DEFINITION A30515
ACCESSION A30515
VERSION A30515.1 GI:23957139
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 3427)
AUTHORS Fountoulakis,M., Garotta,G. and Stueber,D.
TITLE Soluble interferon-gamma receptors and methods for their production
JOURNAL Patent: EP 0393502-A 82 24-OCT-1990;
F. HOFFMANN-LA ROCHE AG
FEATURES location/Qualifiers
SOURCE 1..3427
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 100.0%; Score 63; DB 6; Length 3427;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCCTAGCTCGATACATAAAGCGCCATTGACCATTCACCATTTGGTGTGCAC 60
DB 250 TTTAAGTGCCTAGCTCGATACATAAAGCGCCATTGACCATTCACCATTTGGTGTGCAC 309

QY 61 CTC 63
DB 310 CTC 312

RESULT 16
SYNRSV3MV
LOCUS Cloning vector RSV3. 3557 bp DNA circular SYN 27-APR-1993
DEFINITION M83240
ACCESSION M83240
VERSION M83240.1 GI:209303
KEYWORDS cDNA expression vector.
SOURCE unidentified cloning vector
ORGANISM unidentified cloning vector.
REFERENCE 1 (sites)
AUTHORS Messing,J.
TITLE New M13 vectors for cloning
JOURNAL Meth. Enzymol. 101, 20-78 (1983)
MEDLINE 83296918
PUBMED 6310323

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REFERENCE 2 (sites)
AUTHORS Gorman,C., Padmanabhan,R. and Howard,B.H.
TITLE High efficiency DNA-mediated transformation of primate cells
JOURNAL Science 221 (4610), 551-553 (1983)
MEDLINE 83249156
PUBMED 6306768
REFERENCE 3 (bases 1 to 3557)
AUTHORS Jacobson,S., Sekaly,R.P., Jacobson,C.L., McFarland,H.F. and Long,E.O.
TITLE HLA class II-restricted presentation of cytoplasmic measles virus antigens to cytotoxic T cells
JOURNAL J. Virol. 63 (4), 1756-1762 (1989)
MEDLINE 89178863
PUBMED 2784508
COMMENT Original source text: Cloning vector DNA.
FEATURES location/Qualifiers
SOURCE 1..3557
/organism="unidentified cloning vector"
/mol_type="genomic DNA"
/db_xref="taxon:45196"
misc_feature 1..29
/function="polylinker"
/evidence=experimental
misc_feature 912..3029
/function="ampicillin-resistance, replication origin"
/evidence=experimental
enhancer 3030..3657
/standard_name="5'LTR of Rous Sarcoma Virus"
/citations[2]
/evidence=experimental

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Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCCTAGCTCGATACATAAAGCGCCATTGACCATTCACCATTTGGTGTGCAC 60
DB 3491 TTTAAGTGCCTAGCTCGATACATAAAGCGCCATTGACCATTCACCATTTGGTGTGCAC 3550

QY 61 CTC 63
DB 3551 CTC 3553

RESULT 17
A30511
LOCUS Plasmid p264BAM. 3979 bp DNA linear PAT 05-JUL-2002
DEFINITION A30511
ACCESSION A30511
VERSION A30511.1 GI:23957137
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 3979)
AUTHORS Fountoulakis,M., Garotta,G. and Stueber,D.
TITLE Soluble interferon-gamma receptors and methods for their production
JOURNAL Patent: EP 0393502-A 78 24-OCT-1990;
F. HOFFMANN-LA ROCHE AG
FEATURES location/Qualifiers
SOURCE 1..3979
/organism="synthetic construct"
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ORIGIN
Query Match 100.0%; Score 63; DB 6; Length 3979;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCCTAGCTCGATACATAAAGCGCCATTGACCATTCACCATTTGGTGTGCAC 60

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Db 250 TTTAAGTGCCTAGCTCGATACATAAAAGCCATTGGACCATTCACCACTTGGTGTGCAC 309

QY 61 CTC 63
 Db 310 CTC 312

RESULT 18
 A30509
 LOCUS Plasmid p264BGL
 DEFINITION A30509
 ACCESSION A30509
 VERSION A30509.1 GI:23957136
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1 (bases 1 to 3980)
 AUTHORS Pountoulakis, M., Garotta, G. and Stueber, D.
 TITLE Soluble interferon-gamma receptors and methods for their production
 JOURNAL Patent: EP 0391502-A 76 24-OCT-1990;
 F. HOFFMANN-LA ROCHE AG
 FEATURES Location/Qualifiers
 source
 1..3980
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"

ORIGIN
 Query Match 100.0%; Score 63; DB 6; Length 3980;
 Best Local Similarity 100.0%; Pred. No. 1.6e-13;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCCTAGCTCGATACATAAAAGCCATTGGACCATTCACCACTTGGTGTGCAC 60
 Db 251 TTTAAGTGCCTAGCTCGATACATAAAAGCCATTGGACCATTCACCACTTGGTGTGCAC 310

QY 61 CTC 63
 Db 311 CTC 313

RESULT 19
 AR071324/c
 LOCUS
 DEFINITION Sequence 2 from patent US 5910488.
 ACCESSION AR071324
 VERSION AR071324.1 GI:722212
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 4059)
 AUTHORS Nabel, G.J., Nabel, E.G., Lew, D. and Marquet, M.
 TITLE Plasmids suitable for gene therapy
 JOURNAL Patent: US 5910488-A 2 08-JUN-1999;
 FEATURES Location/Qualifiers
 source
 1..4059
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN
 Query Match 100.0%; Score 63; DB 6; Length 4059;
 Best Local Similarity 100.0%; Pred. No. 1.6e-13;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCCTAGCTCGATACATAAAAGCCATTGGACCATTCACCACTTGGTGTGCAC 60
 Db 2954 TTTAAGTGCCTAGCTCGATACATAAAAGCCATTGGACCATTCACCACTTGGTGTGCAC 2895

QY 61 CTC 63
 Db 2894 CTC 2892

RESULT 20
 A38214
 LOCUS
 DEFINITION Sequence 58 from Patent WO9408008.
 ACCESSION A38214
 VERSION A38214.1 GI:2294819
 KEYWORDS
 SOURCE unidentified
 ORGANISM unidentified
 REFERENCE 1 (bases 1 to 4341)
 AUTHORS Hawkins, R.E., Russell, S.J., Stevenson, F.K. and Winter, G.P.
 TITLE IMPROVEMENTS IN OR RELATING TO IMMUNE RESPONSE MODIFICATION
 JOURNAL Patent: WO 9408008-A 58 14-APR-1994;
 MEDICAL RES COUNCIL (GB)
 COMMENT Other publication CA 2145064 940414
 Other publication AU 4832493 940426
 Other publication JP 8501699T 960227.
 FEATURES Location/Qualifiers
 source
 1..4341
 /organism="unidentified"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32644"

ORIGIN
 Query Match 100.0%; Score 63; DB 6; Length 4341;
 Best Local Similarity 100.0%; Pred. No. 1.6e-13;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCCTAGCTCGATACATAAAAGCCATTGGACCATTCACCACTTGGTGTGCAC 60
 Db 542 TTTAAGTGCCTAGCTCGATACATAAAAGCCATTGGACCATTCACCACTTGGTGTGCAC 601

QY 61 CTC 63
 Db 602 CTC 604

RESULT 21
 AX286570
 LOCUS
 DEFINITION Sequence 1 from Patent WO0179510.
 ACCESSION AX286570
 VERSION AX286570.1 GI:17048664
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 REFERENCE 1
 AUTHORS Rice, J.H. and Stevenson, F.M.
 TITLE Materials and methods relating to immune responses to fusion
 JOURNAL Proteins
 Patent: WO 0179510-A 1 25-OCT-2001;
 Cancer Research Ventures Limited (GB)
 FEATURES Location/Qualifiers
 source
 1..4341
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Vector pVAC1"

ORIGIN
 Query Match 100.0%; Score 63; DB 6; Length 4341;
 Best Local Similarity 100.0%; Pred. No. 1.6e-13;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCCTAGCTCGATACATAAAAGCCATTGGACCATTCACCACTTGGTGTGCAC 60
 Db 542 TTTAAGTGCCTAGCTCGATACATAAAAGCCATTGGACCATTCACCACTTGGTGTGCAC 601

QY 61 CTC 63


```

Db          602 CTC 604
||||
RESULT 22
LOCUS      AX743954
DEFINITION Sequence 2 from Patent WO03031630.
ACCESSION  AX743954
VERSION     AX743954.1 GI:30722651
KEYWORDS   .
SOURCE      synthetic construct
ORGANISM    synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Pazio, V., Rinaldi, M., Sonzogni, L., Tonon, G. and Orsini, G.
TITLE       Multi-cistronic vectors for gene transfer protocols
JOURNAL     Patent: WO 03031630-A 2 17-APR-2003;
            Keryos Spa (IT)
FEATURES   Location/Qualifiers
            source
            1..4457
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"

ORIGIN
Query Match      100.0%; Score 63; DB 6; Length 4457;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACATAAAGCGCATTTGACCATTCACCATGCTGTGTCAC 60
Db 918 TTTAAGTCCTAGCTCGATACATAAAGCGCATTTGACCATTCACCATGCTGTGTCAC 977
|||||
QY 61 CTC 63
Db 978 CTC 980

RESULT 23
SYNRSV5GPT
LOCUS      SYNRSV5GPT
DEFINITION Cloning vector RSV.5(gpt).
ACCESSION  M83236
VERSION     M83236.1 GI:209304
KEYWORDS   cDNA expression vector.
SOURCE      Cloning vector pUC19
ORGANISM    Cloning vector pUC19
            artificial sequences; vectors.
REFERENCE   1 (bases 1 to 4839)
AUTHORS     Long, E.O., Rosen-Bronson, S., Karp, D.R., Malnati, M., Sekaly, R.P. and
            Jaraquemada, D.
TITLE       Efficient cDNA expression vectors for stable and transient
            expression of HLA-DR in transfected fibroblast and lymphoid cells
JOURNAL     Hum. Immunol. 31 (4), 229-235 (1991)
MEDLINE     92011006
PUBMED      1655683
FEATURES   Location/Qualifiers
            source
            1..4839
            /organism="Cloning vector pUC19"
            /mol_type="genomic DNA"
            /db_xref="taxon:31851"
            /focus
            1..29
            /organism="Cloning vector pUC12"
            /mol_type="genomic DNA"
            /db_xref="taxon:83674"
            /note="HindIII to BamHI fragment of pUC12"
            30..872
            /organism="Simian virus 40"
            /mol_type="genomic DNA"
            /db_xref="taxon:10633"
            /note="Bi-directional SV40 termination and

poly-adenylation sequences."
873..1929
/organism="Escherichia coli"
/mol_type="genomic DNA"
/db_xref="taxon:562"
1930..2273
/organism="Simian virus 40"
/mol_type="genomic DNA"
/db_xref="taxon:10633"
/note="SV40 early promoter and origin of replication."
2274..4311
/organism="Cloning vector pBR322"
/mol_type="genomic DNA"
/db_xref="taxon:47470"
/note="Ampicillin resistance gene and origin of replication
from the vector pBR322."
4312..4839
/organism="Rous sarcoma virus"
/mol_type="genomic DNA"
/db_xref="taxon:11886"
/note="5' long terminal repeat."
1..29
/function="polylinker"
/evidence=experimental
misc_feature complement (873..1929)
/product="guanine-hypoxanthine phosphoribosyltransferase"
/standard_name="gpt"
/note="gpt gene from E.coli, putative mature peptide -
contains internal stop codons; putative"
2274..4311
/function="ampicillin resistance and origin of
replication"
/evidence=experimental

ORIGIN
Query Match      100.0%; Score 63; DB 12; Length 4839;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACATAAAGCGCATTTGACCATTCACCATGCTGTGTCAC 60
Db 4773 TTTAAGTCCTAGCTCGATACATAAAGCGCATTTGACCATTCACCATGCTGTGTCAC 4832
|||||
QY 61 CTC 63
Db 4833 CTC 4835

RESULT 24
SYNRSV5NEO
LOCUS      SYNRSV5NEO
DEFINITION cDNA expression vector RSV.5(neo).
ACCESSION  M83237
VERSION     M83237.1 GI:209305
KEYWORDS   cDNA expression vector.
SOURCE      Expression vector RSV.5(neo)
ORGANISM    Expression vector RSV.5(neo)
            artificial sequences; vectors.
REFERENCE   1 (bases 1 to 5108)
AUTHORS     Long, E.O., Rosen-Bronson, S., Karp, D.R., Malnati, M., Sekaly, R.P. and
            Jaraquemada, D.
TITLE       Efficient cDNA expression vectors for stable and transient
            expression of HLA-DR in transfected fibroblast and lymphoid cells
JOURNAL     Hum. Immunol. 31 (4), 229-235 (1991)
MEDLINE     92011006
PUBMED      1655683
FEATURES   Location/Qualifiers
            source
            1..5108
            /organism="Expression vector RSV.5(neo)"
            /mol_type="genomic DNA"
            /db_xref="taxon:118308"
            /focus
            1..29
            /organism="Expression vector RSV.5(neo)"
            /mol_type="genomic DNA"
            /db_xref="taxon:118308"
            /focus
            1..29

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/organism="unidentified cloning vector"
/mol_type="genomic DNA"
/db_xref="taxon:45196"
/noife="hindIII to BamHI fragment of pUC12."
30..872
/organism="Simian virus 40"
/mol_type="genomic DNA"
/db_xref="taxon:10633"
/noife="5i-directional SV40 termination and
poly-adenylation sequence."
873..879
/organism="unidentified cloning vector"
/mol_type="genomic DNA"
/db_xref="taxon:45196"
/noife="Remnant of gpt gene from the cDNA expression vector
RSV.5(gpt)."
880..2197
/organism="Cloning vector pSV2neo"
/mol_type="genomic DNA"
/db_xref="taxon:31846"
/noife="TN5 neomycin-resistance gene from cloning vector
pSV2neo."
2198..2542
/organism="Simian virus 40"
/mol_type="genomic DNA"
/db_xref="taxon:10633"
/noife="SV40 early promoter and origin of replication."
2543..4580
/organism="Cloning vector pBR322"
/mol_type="genomic DNA"
/db_xref="taxon:47470"
/noife="Ampicillin resistance gene and origin of
replication from pBR322."
4581..5108
/organism="Rous sarcoma virus"
/mol_type="genomic DNA"
/db_xref="taxon:11886"
/noife="5' long terminal repeat of Rous Sarcoma virus."
5109..5129
/function="polylinker"
/evidence="experimental"
complement(880..2197)
/note="neomycin resistance gene from pSV2neo, putative
mature peptide - contains internal stop codons; putative"
2543..4580
/product="ampicillin resistance"
/function="ampicillin resistance and origin of
replication"
/evidence="experimental"
4581..5108
/standard_name="5' LTR of Rous Sarcoma Virus"
/function="promoter"
/evidence="experimental"

ORIGIN
Query Match 100.0%; Score 63; DB 12; Length 5108;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCCTAGCTCGATACAAATAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
DB 5042 TTTAAGTGCCTAGCTCGATACAAATAAGCCATTGACCATTCACCATTTGGTGTGCAC 60

QY 61 CTC 63
DB 5102 CTC 5104

RESULT 25
SYNTRC
LOCUS 5564 bp DNA linear SYN 27-SEP-1994
DEFINITION Cloning vector murine T-cell receptor C-beta 1 DNA, 3' end of cds.
ACCESSION L36555

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L36555.1 GI:550523
T-cell receptor C-beta 1; T-cell receptor V-beta; cloning vector.
unidentified cloning vector
unidentified cloning vector
artificial sequences; vectors.
1 (bases 1 to 5564)
Palmer,M.S., Bentley,A., Gould,K. and Townsend,A.R.
The T cell receptor from an influenza-A specific murine CTL clone
Nucleic Acids Res. 17 (6), 2353 (1989)
89202046
MEDLINE
PUBMED 2784852
2 (bases 1 to 5564)
Long,E.O., Rosen-Bronson,S., Karp,D.R., Malnati,M., Sekaly,R.P. and
Jaraquemada,D.
Efficient cDNA expression vectors for stable and transient
expression of HLA-DR in transfected fibroblast and lymphoid cells
Hum. Immunol. 31 (4), 229-235 (1991)
92011006
PUBMED 1655683
3 (bases 1 to 5564)
Denis,P., Soudeyria,H., Ringnette,N. and Sekaly,R.-P.
A simple method for the cloning and functional expression of human
T cell receptor Vbeta segments in murine hybridomas
Unpublished (1994)
JOURNAL COMMENT Original source text: Cloning vector DNA.
FEATURES
source
1..5564
/organism="unidentified cloning vector"
/mol_type="genomic DNA"
/db_xref="taxon:45196"
<13..480
/note="murine"
/citation=[3]
/codon_start=1
/evidence="experimental"
/transl_table=11
/product="T-cell receptor C beta 1"
/protein_id="AAA72448.1"
/db_xref="GI:550524"
/translation="VDIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVSTDPOA
YKSNYSYCLSRLEVSATFWNPRHPCOVQPHGLSEEDKWPQSGPKPTQINISAE
AWGRDGGTSASVHQSVLSNTILYEILLKATLIYAVLSGLVLMVWYKKNS"

ORIGIN
Query Match 100.0%; Score 63; DB 12; Length 5564;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCCTAGCTCGATACAAATAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
DB 5498 TTTAAGTGCCTAGCTCGATACAAATAAGCCATTGACCATTCACCATTTGGTGTGCAC 5557

QY 61 CTC 63
DB 5558 CTC 5560

RESULT 26
LOCUS 5564 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 3 from patent US 5650306.
ACCESSION 156772
VERSION 156772.1 GI:2477185
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 5653)
AUTHORS Nabel,G.J., Yang,Z.-Y., Liu,J. and Woffendin,C.
TITLE Recombinant nucleic acids for inhibiting HIV gene expression
JOURNAL Patent: US 5650306-A 3 22-JUL-1997;
FEATURES
Location/Qualifiers
source
1..5653

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ORIGIN
/organism="unknown"
/mol_type="unassigned DNA"

Query Match      100.0%; Score 63; DB 6; Length 5653;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACAAATAAAGCGCCATTGACCAATTCACCAATGTTGTGCAC 60
    |||
Db 542 TTTAAGTCCTAGCTCGATACAAATAAAGCGCCATTGACCAATTCACCAATGTTGTGCAC 601

QY 61 CTC 63
    |||
Db 602 CTC 604

RESULT 27
195540
LOCUS      195540      5653 bp      DNA      linear      PAT 01-DEC-1998
DEFINITION Sequence 1 from patent US 5733543.
ACCESSION 195540
VERSION   195540.1 GI:3940010
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 5653)
AUTHORS   Nabel,G.J.; Woffendin,C.; Yang,N.-S. and Sheehy,M.J.
TITLE     Introduction of HIV-protective genes into cells by
          particle-mediated gene transfer
JOURNAL   Patent: US 5733543-A 1 31-MAR-1998;
FEATURES  Location/Qualifiers
          source          1..5653
                        /organism="unknown"
                        /mol_type="unassigned DNA"

ORIGIN
Query Match      100.0%; Score 63; DB 6; Length 5653;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACAAATAAAGCGCCATTGACCAATTCACCAATGTTGTGCAC 60
    |||
Db 542 TTTAAGTCCTAGCTCGATACAAATAAAGCGCCATTGACCAATTCACCAATGTTGTGCAC 601

QY 61 CTC 63
    |||
Db 602 CTC 604

RESULT 28
SYNPRSVNEO/c
LOCUS      SYNPRSVNEO      5736 bp      DNA      circular SYN 27-APR-1993
DEFINITION PRSVNEO cloning vector for high efficiency gene transfer into
          mammalian cells.
ACCESSION M77786
VERSION   M77786.1 GI:209147
KEYWORDS  synthetic construct
          artificial construct
          artificial sequences.
SOURCE    Gilbert,W.
          Obtained from VecBase 3.0
ORGANISM  Unpublished (1991)
REFERENCE Original source text: Synthetic construct DNA.
          These data and their annotation were supplied to GenBank by Will
          Gilbert under the auspices of the GenBank Curator Program. PRSVNEO
          - Cloning Vector for High Efficiency Gene Transfer into Mammalian
          Cells
ENTRY     PRSVNEO      #TYPE DNA CIRCULAR TITLE PRSVNEO -
          Cloning Vector for High Efficiency Gene Transfer

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into Mammalian Cells
DATE      06-JUN-1986
#sequence 16-DEC-1986
ACCESSION VB0064
SOURCE    artificial
COLLECTION ATCC 37198
REFERENCE
#number 1
#authors  Gorman C.
#book     'DNA cloning Volume II, a practical approach', pp.
143-190,
        edited by D. M. Glover, IRL Press, (1986),
        eds. D. Rickwood and B. D. Hames
COMMENT   Entered by William Gilbert, Whitaker College, MIT, 02-APR-1986
          Revised 16-DEC-1986 by F. Pfeiffer:
          1012/3 'AT' to 'TA' to match revised sequence of PBR322 KEYWORDS
CROSSREFERENCE
#parent   VecBase(3):PBR322, GenBank(50):SV4CG,
          GenBank(50):ALRPROLUTB,
          GenBank(50):Trn5Neo, GenBank(50):Trn5IR1
PARENT    Features of PRSVNEO (5736 bp)
          residue source
          6-529 550- 27 (c) Rous Sarcoma Virus (GenBank(50):
ALRPROLUTB)
          6- 529 3189-2667 (c) GenBank(50):ALRPROLUTB (6 mutations)
          529-2644 2248-4363 PBR322
          2641-3634 1781-2774 SV40
          3631-4244 4100-4713 SV40
          4248-5533 1286- 1 (c) Trn5 (GenBank(50):Trn5NEO)
          5251-5736 1720-1235 (c) Trn5 (GenBank(50):Trn5IR1)
          Conflict (cfl) and Mutations (mut): none
FEATURE    1579-2367 789-1 (c) Ap-R; b-lactamase
          4589-5383 791-1 (c) Neo-R
POLYLINKER
SELECTION #resistance Ap
SUMMARY   PRSVNEO #length 5736 #checksum 3569.
          Location/Qualifiers
          1..5736
          /organism="synthetic construct"
          /mol_type="genomic DNA"
          /db_xref="taxon:32630"

ORIGIN
Query Match      100.0%; Score 63; DB 12; Length 5736;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACAAATAAAGCGCCATTGACCAATTCACCAATGTTGTGCAC 60
    |||
Db 67 TTTAAGTCCTAGCTCGATACAAATAAAGCGCCATTGACCAATTCACCAATGTTGTGCAC 8

QY 61 CTC 63
    |||
Db 7 CTC 5

RESULT 29
AR215114
LOCUS      AR215114      6836 bp      DNA      linear      PAT 25-SEP-2002
DEFINITION Sequence 18 from patent US 6410266.
ACCESSION AR215114
VERSION   AR215114.1 GI:23319242
KEYWORDS
SOURCE    Unknown.
          ORGANISM  Unknown.
          Unclassified.
REFERENCE 1 (bases 1 to 6836)
AUTHORS   Harrington,J.J. and Rundlett,S.
TITLE     Compositions and methods for non-targeted activation of endogenous

```

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genes
JOURNAL Patent: US 6410266-A 18 25-JUN-2002;
FEATURES Location/Qualifiers
source 1..6836
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 63; DB 6; Length 6836;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTAAGTGCTAGCTCGATACATAAAGCGCCATTGGACCATTCACACATTGGTGTGCAC 60
|||||
Db 1760 TTTAAGTGCTAGCTCGATACATAAAGCGCCATTGGACCATTCACACATTGGTGTGCAC 1819

Qy 61 CTC 63
|||
Db 1820 CTC 1822

RESULT 30
AR302356 AR302356 6836 bp DNA linear PAT 12-JUN-2003
LOCUS Sequence 18 from patent US 6541221.
DEFINITION AR302356
ACCESSION AR302356
VERSION AR302356.1 GI:31690610
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 6836)
AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.
TITLE Compositions and methods for non-targeted activation of endogenous genes
JOURNAL Patent: US 6541221-A 18 01-APR-2003;
FEATURES Location/Qualifiers
source 1..6836
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 63; DB 6; Length 6836;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTAAGTGCTAGCTCGATACATAAAGCGCCATTGGACCATTCACACATTGGTGTGCAC 60
|||||
Db 1760 TTTAAGTGCTAGCTCGATACATAAAGCGCCATTGGACCATTCACACATTGGTGTGCAC 1819

Qy 61 CTC 63
|||
Db 1820 CTC 1822

RESULT 31
AR373228 AR373228 6836 bp DNA linear PAT 18-DEC-2003
LOCUS Sequence 18 from patent US 6602686.
DEFINITION AR373228
ACCESSION AR373228
VERSION AR373228.1 GI:40075236
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 6836)
AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.
TITLE Compositions and method for non-targeted activation of endogenous genes
JOURNAL Patent: US 6602686-A 18 05-AUG-2003;
FEATURES Location/Qualifiers
source 1..6836
/mol_type="genomic DNA"

genes
JOURNAL Patent: US 6410266-A 18 25-JUN-2002;
FEATURES Location/Qualifiers
source 1..6836
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 63; DB 6; Length 6836;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTAAGTGCTAGCTCGATACATAAAGCGCCATTGGACCATTCACACATTGGTGTGCAC 60
|||||
Db 1760 TTTAAGTGCTAGCTCGATACATAAAGCGCCATTGGACCATTCACACATTGGTGTGCAC 1819

Qy 61 CTC 63
|||
Db 1820 CTC 1822

RESULT 32
AR401614 AR401614 6836 bp DNA linear PAT 18-DEC-2003
LOCUS Sequence 18 from patent US 6623958.
DEFINITION AR401614
ACCESSION AR401614
VERSION AR401614.1 GI:40149062
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 6836)
AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.
TITLE Compositions and methods for non-targeted activation of endogenous genes
JOURNAL Patent: US 6623958-A 18 23-SEP-2003;
FEATURES Location/Qualifiers
source 1..6836
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 63; DB 6; Length 6836;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTAAGTGCTAGCTCGATACATAAAGCGCCATTGGACCATTCACACATTGGTGTGCAC 60
|||||
Db 1760 TTTAAGTGCTAGCTCGATACATAAAGCGCCATTGGACCATTCACACATTGGTGTGCAC 1819

Qy 61 CTC 63
|||
Db 1820 CTC 1822

RESULT 33
AF346624 AF346624 6836 bp DNA circular SYN 30-AUG-2001
LOCUS RAGE vector pRIG1, complete sequence.
DEFINITION AF346624
ACCESSION AF346624
VERSION AF346624.1 GI:15383987
KEYWORDS
SOURCE RAGE vector pRIG1
ORGANISM RAGE vector pRIG1
artificial sequences; vectors.
REFERENCE 1 (bases 1 to 6836)
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramachandran,R.,
Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Bozer,S.,
Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K.,
Offenbacher,J., Danzig,J. and Ducar,M.
TITLE Creation of genome-wide protein expression libraries using random activation of gene expression
JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)
FEATURES MEDLINE
PUBMED 21227151
REFERENCE 2 (bases 1 to 6836)
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
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/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 63; DB 6; Length 6836;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTAAGTGCTAGCTCGATACATAAAGCGCCATTGGACCATTCACACATTGGTGTGCAC 60
|||||
Db 1760 TTTAAGTGCTAGCTCGATACATAAAGCGCCATTGGACCATTCACACATTGGTGTGCAC 1819

Qy 61 CTC 63
|||
Db 1820 CTC 1822

RESULT 32
AR401614 AR401614 6836 bp DNA linear PAT 18-DEC-2003
LOCUS Sequence 18 from patent US 6623958.
DEFINITION AR401614
ACCESSION AR401614
VERSION AR401614.1 GI:40149062
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 6836)
AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.
TITLE Compositions and methods for non-targeted activation of endogenous genes
JOURNAL Patent: US 6623958-A 18 23-SEP-2003;
FEATURES Location/Qualifiers
source 1..6836
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 63; DB 6; Length 6836;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTAAGTGCTAGCTCGATACATAAAGCGCCATTGGACCATTCACACATTGGTGTGCAC 60
|||||
Db 1760 TTTAAGTGCTAGCTCGATACATAAAGCGCCATTGGACCATTCACACATTGGTGTGCAC 1819

Qy 61 CTC 63
|||
Db 1820 CTC 1822

RESULT 33
AF346624 AF346624 6836 bp DNA circular SYN 30-AUG-2001
LOCUS RAGE vector pRIG1, complete sequence.
DEFINITION AF346624
ACCESSION AF346624
VERSION AF346624.1 GI:15383987
KEYWORDS
SOURCE RAGE vector pRIG1
ORGANISM RAGE vector pRIG1
artificial sequences; vectors.
REFERENCE 1 (bases 1 to 6836)
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramachandran,R.,
Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Bozer,S.,
Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K.,
Offenbacher,J., Danzig,J. and Ducar,M.
TITLE Creation of genome-wide protein expression libraries using random activation of gene expression
JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)
FEATURES MEDLINE
PUBMED 21227151
REFERENCE 2 (bases 1 to 6836)
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
```

Cain, S., Dahl, T., Thornton, M., Ramachandran, R., Whittington, J.,
 Ierner, L., Krashoc, D., McElligott, K., Clark, S., Mays, R., Smith, E.,
 Veloso, N., Hess, J., Cottrill, K., Lo, K., Offenbacher, G., Danzig, U.,
 and Ducar, M.
 Direct Submission
 Submitted (06-FEB-2001) Athersys, Inc., 3201 Carnegie Ave.,
 Cleveland, OH 44115, USA
 JOURNAL

FEATURES
 source
 1..6836
 /organism="BAGE vector pRIG1"
 /mol_type="genomic DNA"
 /db_xref="taxon:161236"

ORIGIN
 Query Match 100.0%; Score 63; DB 12; Length 6836;
 Best Local Similarity 100.0%; Pred. No. 1.6e-13;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTAAGTCCCTAGCTCGATACATAAAGCGCATTTGACCATTCACCATGTTGTGCAC 60
 Db 1760 TTTAAGTCCCTAGCTCGATACATAAAGCGCATTTGACCATTCACCATGTTGTGCAC 1819
 QY 61 CTC 63
 Db 1820 CTC 1822

RESULT 34
 XXU19931
 LOCUS 6864 bp DNA linear SYN 30-MAR-1995
 DEFINITION Cloning vector pGlaRSV, complete sequence.
 ACCESSION U19931
 VERSION U19931.1 GI:644834
 KEYWORDS
 SOURCE
 ORGANISM
 Cloning vector pGlaRSV
 Cloning vector pGlaRSV
 artificial sequences; vectors.
 1 (bases 1 to 6864)
 Gottgens, B.B.
 TITLE A versatile lacZ reporter vector
 JOURNAL Unpublished
 2 (bases 641 to 4011)
 Ravid, K., Beiler, D.L., Rabin, M.S., Ruley, H.E. and Rosenberg, R.D.
 Selective targeting of gene products with the megakaryocyte
 platelet factor 4 promoter
 Proc. Natl. Acad. Sci. U.S.A. 88 (4), 1521-1525 (1991)
 JOURNAL 91142205
 MEDLINE 1899930
 PUBMED 1899930
 3 (bases 1 to 6864)
 Gottgens, B.B.
 AUTHORS Direct Submission
 TITLE Submitted (18-JAN-1995) Berthold B. Gottgens, Hematology, Cambridge
 University, MRC Centre, Hills Road, Cambridge, UK, CB2 2QH
 JOURNAL Location/Qualifiers
 FEATURES
 source
 1..6864
 /organism="Cloning vector pGlaRSV"
 /mol_type="genomic DNA"
 /db_xref="taxon:39038"

misc_feature
 1..37
 /notes="obtained from pGlaC, Genbank Accession Number
 U19930"

misc_feature
 38..631
 /notes="RSV LTR from pRC/RSV cloned as a BglII/HindIII
 fragment"

misc_feature
 632..6864
 /notes="obtained from pGlaC, Genbank Accession Number
 U19930"

misc_feature
 641..4011
 /notes="obtained from pSDXlacZpA containing the E. coli
 lacZ gene followed by an SV40 polyA site"
 /citation=[2]
 662..3727
 /gene="lacZ"

gene

CDS
 662..3727
 /gene="lacZ"
 /codon_start=1
 /transl_table=11
 /product="b-galactosidase"
 /protein_id="AAA64569.1"
 /db_xref="GI:644835"

misc_feature
 4005..6864
 /note="vector backbone from pGI-2basic, Genbank Accession
 Number X65323"

gene
 complement (5081..5941)
 /gene="bla"

CDS
 complement (5081..5941)
 /gene="bla"

misc_feature
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 /transl_table=11
 /product="beta-lactamase"
 /protein_id="AAA64570.1"
 /db_xref="GI:644836"

ORIGIN
 Query Match 100.0%; Score 63; DB 12; Length 6864;
 Best Local Similarity 100.0%; Pred. No. 1.6e-13;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTAAGTCCCTAGCTCGATACATAAAGCGCATTTGACCATTCACCATGTTGTGCAC 60
 Db 567 TTTAAGTCCCTAGCTCGATACATAAAGCGCATTTGACCATTCACCATGTTGTGCAC 626
 QY 61 CTC 63
 Db 627 CTC 629

RESULT 35
 A48775
 LOCUS 6926 bp DNA circular PAT 07-MAR-1997
 DEFINITION Sequence 2 from Patent WO9604388.
 ACCESSION A48775
 VERSION A48775.1 GI:2302445
 KEYWORDS
 SOURCE unidentified
 ORGANISM unidentified
 unclassified.
 1 (bases 1 to 6926)
 Brown, M.J., Murphy, K.E., Chapman, C.G., Clinkenbeard, H.E.,
 Young, P.R. and Shatzman, A.R.
 TITLE NOVEL COMPOUNDS
 JOURNAL Patent: WO 9604388-A 2 15-FEB-1996;

SMITHKLINE BEECHAM PLC (GB)
Other publication AU 3382595 960304.
FEATURES
source
Location/Qualifiers
1..6926
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

ORIGIN

Query Match 100.0%; Score 63; DB 6; Length 6926;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTAAGTCCCTAGCTCGATACATAAAGCCCAATTGACCAATTGACCAATTGCTGTGCAC 60
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Db 709 TTTAAGTCCCTAGCTCGATACATAAAGCCCAATTGACCAATTGACCAATTGCTGTGCAC 768
QY 61 CTC 63
|||
Db 769 CTC 771

RESULT 36
AX743955/c
LOCUS AX743955 6926 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 2 from patent US 5783181.
ACCESSION AX743955
VERSION AX743955.1 GI:3973817
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 6926)
AUTHORS Browne, M. Joseph., Young, P. Ronald., Shatzman, A. Richard.,
Murphy, K. Elizabeth., Chapman, C. Gerald. and
Clinkenbeard, H. Elizabeth.
TITLE Therapeutic uses of fusion proteins between mutant IL 4/IL13
antagonists and immunoglobulins
JOURNAL Patent: US 5783181-A 2 21-JUL-1998;
FEATURES Location/Qualifiers
source
1..6926
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 63; DB 6; Length 6926;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTAAGTCCCTAGCTCGATACATAAAGCCCAATTGACCAATTGACCAATTGCTGTGCAC 60
|||||
Db 709 TTTAAGTCCCTAGCTCGATACATAAAGCCCAATTGACCAATTGACCAATTGCTGTGCAC 768
QY 61 CTC 63
|||
Db 769 CTC 771

RESULT 37
AX743955/c
LOCUS AX743955 7086 bp DNA linear PAT 14-MAY-2003
DEFINITION Sequence 3 from Patent WO0301630.
ACCESSION AX743955
VERSION AX743955.1 GI:30722652
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Fazio, V., Rinaldi, M., Sonzogni, L., Tonon, G. and Orsini, G.
TITLE Multi-cistronic vectors for gene transfer protocols
JOURNAL Patent: WO 03031630-A 3 17-APR-2003;
Keryos Spa (IT)

FEATURES

Location/Qualifiers
1..7086
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 100.0%; Score 63; DB 6; Length 7086;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTAAGTCCCTAGCTCGATACATAAAGCCCAATTGACCAATTGACCAATTGCTGTGCAC 60
|||||
Db 1595 TTTAAGTCCCTAGCTCGATACATAAAGCCCAATTGACCAATTGACCAATTGCTGTGCAC 1536
QY 61 CTC 63
|||
Db 1535 CTC 1533

RESULT 38
AX743956/c
LOCUS AX743956 7334 bp DNA linear PAT 14-MAY-2003
DEFINITION Sequence 4 from Patent WO03031630.
ACCESSION AX743956
VERSION AX743956.1 GI:30722653
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Fazio, V., Rinaldi, M., Sonzogni, L., Tonon, G. and Orsini, G.
TITLE Multi-cistronic vectors for gene transfer protocols
JOURNAL Patent: WO 03031630-A 4 17-APR-2003;
Keryos Spa (IT)
FEATURES Location/Qualifiers
source
1..7334
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 100.0%; Score 63; DB 6; Length 7334;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTAAGTCCCTAGCTCGATACATAAAGCCCAATTGACCAATTGACCAATTGCTGTGCAC 60
|||||
Db 1839 TTTAAGTCCCTAGCTCGATACATAAAGCCCAATTGACCAATTGACCAATTGCTGTGCAC 1780
QY 61 CTC 63
|||
Db 1779 CTC 1777

RESULT 39
AR235458
LOCUS AR235458 7492 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 5 from patent US 6461606.
ACCESSION AR235458
VERSION AR235458.1 GI:27278640
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 7492)
AUTHORS Flotte, T. R., Song, S., Byrne, B. J. and Morgan, M.
TITLE Materials and methods for gene therapy
JOURNAL Patent: US 6461606-A 5 08-OCT-2002;
FEATURES Location/Qualifiers
source
1..7492
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 63; DB 6; Length 7492;
 Best Local Similarity 100.0%; Pred. No. 1.6e-13;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
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 Db 27 TTTAAGTGCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 86
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QY 61 CTC 63
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 Db 87 CTC 89

RESULT 40
 BD268239
 LOCUS
 DEFINITION Adenovirus vector, packaging cell line, composition and method for production and use.
 ACCESSION BD268239
 VERSION BD268239.1 GI:33078007
 KEYWORDS JP 2002534130-A/43.
 SOURCE synthetic construct
 ORGANISM artificial sequences.

REFERENCE 1 (bases 1 to 8238)
 Nemorow, G.R., Seggern, D.J.V., Hallenbeck, P.L., Stevenson, S.C. and Skripchenko, Y.

TITLE Adenovirus vector, packaging cell line, composition and method for production and use

JOURNAL NOVARTIS AG, THE SCRIPPS RESEARCH INSTITUTE

COMMENT OS Artificial Sequence
 PN JP 2002534130-A/43
 PD 15-OCT-2002

PF 14-JAN-2000 JP 2000593765
 PR 14-JAN-1999 US 60/115920
 PI GLEN ROBERT NEMOROW, DANIEL J VON SEGGERN, PAUL L HALLENBECK, PI SUSAN C STEVENSON, YELENA SKRIPCHENKO
 PC C12N15/09, A61K35/76, A61K48/00, A61P35/00, A61P43/00, A61P43/00, PC C12N5/10,
 PC C12N7/00, C12O1/68, G01N33/53, G01N33/566, C12N15/00, C12N5/00 CC
 Description of Artificial Sequence: plasmid
 FH Key Location/Qualifiers
 FT source 1..8238
 /organism='Artificial Sequence'.

FEATURES
 source Location/Qualifiers

1..8238
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"

ORIGIN

Query Match 100.0%; Score 63; DB 6; Length 8238;
 Best Local Similarity 100.0%; Pred. No. 1.6e-13;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
 |||||
 Db 742 TTTAAGTGCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 801
 |||||

QY 61 CTC 63

Db 802 CTC 804

RESULT 41

XXU02432

LOCUS

DEFINITION Cloning vector pMAMneo, complete sequence.

ACCESSION U02432

VERSION U02432.1 GI:413798

XXU02432 8413 bp DNA circular SYN 29-JAN-1997

KEYWORDS

SOURCE Cloning vector pMAMneo
 ORGANISM Cloning vector pMAMneo
 REFERENCE 1 (bases 1 to 8413)
 AUTHORS Kitts, P.A.
 JOURNAL CLONTECH Vectors On Disc version 1.3
 REFERENCE 2 (bases 1 to 8413)
 AUTHORS Kitts, P.A.
 TITLE Direct Submission
 JOURNAL Submitted (07-OCT-1993) Paul A. Kitts, CLONTECH Laboratories, Inc., 1020 East Meadow Circle, Palo Alto, CA 94303, USA

COMMENT This vector can be obtained from CLONTECH Laboratories, Inc., 1020 East Meadow Circle, Palo Alto, CA 94303, USA. To place an order call (415) 424-8222 or (800) 662-2566, extension 1. International customers, please contact your local distributor. For technical information, call (415) 424-8222 or (800) 662-2566, extension 3. This sequence has been compiled from information in the sequence databases, published literature and other sources, together with partial sequences obtained by CLONTECH; this vector has not been completely sequenced. If you suspect there is an error in this sequence, please contact CLONTECH's Technical Service Department at (415) 424-8222 or (800) 662-2566, extension 3 or E-mail TECH@CLONTECH.COM.

FEATURES

Location/Qualifiers

1..8413
 /organism="Cloning vector pMAMneo"
 /mol_type="genomic DNA"
 /db_xref="taxon:31818"

ORIGIN

Query Match 100.0%; Score 63; DB 12; Length 8413;
 Best Local Similarity 100.0%; Pred. No. 1.6e-13;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
 |||||

Db 27 TTTAAGTGCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 86
 |||||

QY 61 CTC 63

Db 87 CTC 89

RESULT 42

XXU02430

LOCUS

DEFINITION Cloning vector pMAMneoBlue, complete sequence.

ACCESSION U02430

VERSION U02430.1 GI:413796

KEYWORDS

SOURCE Cloning vector pMAMneoBlue

ORGANISM Cloning vector pMAMneoBlue

REFERENCE 1 (bases 1 to 8475)

AUTHORS Kitts, P.A.

JOURNAL CLONTECH Vectors On Disc version 1.3

REFERENCE 2 (bases 1 to 8475)

AUTHORS Kitts, P.A.

JOURNAL Direct Submission

Submitted (07-OCT-1993) Paul A. Kitts, CLONTECH Laboratories, Inc., 1020 East Meadow Circle, Palo Alto, CA 94303, USA

COMMENT This sequence has been compiled from information in the sequence databases, published literature and other sources, together with partial sequences obtained by CLONTECH. This vector is no longer available from CLONTECH and CLONTECH will not update or revise this sequence.

FEATURES

source Location/Qualifiers

1..8475
 /organism="Cloning vector pMAMneoBlue"
 /mol_type="genomic DNA"

/db_xref="taxon:31821"

ORIGIN

Query Match 100.0%; Score 63; DB 12; Length 8475;
 Best Local Similarity 100.0%; Pred. No. 1.6e-13;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCCTAGCTCGATACATAAAGCGCATTTGACCATTCACCACATTGGTGTGCAC 60
 |||||
 Db 27 TTTAAGTGCCTAGCTCGATACATAAAGCGCATTTGACCATTCACCACATTGGTGTGCAC 86

QY 61 CTC 63

|||

Db 87 CTC 89

RESULT 43

158322 LOCUS 158322 8591 bp DNA linear PAT 07-OCT-1997
 DEFINITION Sequence 6 from patent US 5652092.
 ACCESSION I58322
 VERSION I58322.1 GI:2477560
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 8591)
 AUTHORS Vitek,M.Peter. and Jacobsen,J.Steven.
 TITLE Amyloid precursor proteins and method of using same to assess agents which down-regulate formation of .beta.-amyloid peptide
 JOURNAL Patent: US 5652092-A 6 29-JUL-1997;
 FEATURES Location/Qualifiers
 source 1..8591
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 63; DB 6; Length 8591;
 Best Local Similarity 100.0%; Pred. No. 1.6e-13;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCCTAGCTCGATACATAAAGCGCATTTGACCATTCACCACATTGGTGTGCAC 60
 |||||
 Db 5177 TTTAAGTGCCTAGCTCGATACATAAAGCGCATTTGACCATTCACCACATTGGTGTGCAC 5236

QY 61 CTC 63

|||

Db 5237 CTC 5239

RESULT 44

158323 LOCUS 158323 8591 bp DNA linear PAT 07-OCT-1997
 DEFINITION Sequence 8 from patent US 5652092.
 ACCESSION I58323
 VERSION I58323.1 GI:2477561
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 8591)
 AUTHORS Vitek,M.Peter. and Jacobsen,J.Steven.
 TITLE Amyloid precursor proteins and method of using same to assess agents which down-regulate formation of .beta.-amyloid peptide
 JOURNAL Patent: US 5652092-A 8 29-JUL-1997;
 FEATURES Location/Qualifiers
 source 1..8591
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 63; DB 6; Length 8591;
 Best Local Similarity 100.0%; Pred. No. 1.6e-13;

Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCCTAGCTCGATACATAAAGCGCATTTGACCATTCACCACATTGGTGTGCAC 60
 |||||
 Db 5177 TTTAAGTGCCTAGCTCGATACATAAAGCGCATTTGACCATTCACCACATTGGTGTGCAC 5236

QY 61 CTC 63

|||

Db 5237 CTC 5239

RESULT 45

160508 LOCUS 160508 8591 bp DNA linear PAT 07-OCT-1997
 DEFINITION Sequence 6 from patent US 5656477.
 ACCESSION I60508
 VERSION I60508.1 GI:2478953
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 8591)
 AUTHORS Vitek,M.Peter. and Jacobsen,J.Steven.
 TITLE Amyloid precursor proteins and method of using same to assess agents which down-regulate formation of .beta.-amyloid peptide
 JOURNAL Patent: US 5656477-A 6 12-AUG-1997;
 FEATURES Location/Qualifiers
 source 1..8591
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 63; DB 6; Length 8591;
 Best Local Similarity 100.0%; Pred. No. 1.6e-13;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCCTAGCTCGATACATAAAGCGCATTTGACCATTCACCACATTGGTGTGCAC 60
 |||||
 Db 5177 TTTAAGTGCCTAGCTCGATACATAAAGCGCATTTGACCATTCACCACATTGGTGTGCAC 5236

QY 61 CTC 63

|||

Db 5237 CTC 5239

RESULT 46

160509 LOCUS 160509 8591 bp DNA linear PAT 07-OCT-1997
 DEFINITION Sequence 8 from patent US 5656477.
 ACCESSION I60509
 VERSION I60509.1 GI:2478954
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 8591)
 AUTHORS Vitek,M.Peter. and Jacobsen,J.Steven.
 TITLE Amyloid precursor proteins and method of using same to assess agents which down-regulate formation of .beta.-amyloid peptide
 JOURNAL Patent: US 5656477-A 8 12-AUG-1997;
 FEATURES Location/Qualifiers
 source 1..8591
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 63; DB 6; Length 8591;
 Best Local Similarity 100.0%; Pred. No. 1.6e-13;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCCTAGCTCGATACATAAAGCGCATTTGACCATTCACCACATTGGTGTGCAC 60
 |||||
 Db 5177 TTTAAGTGCCTAGCTCGATACATAAAGCGCATTTGACCATTCACCACATTGGTGTGCAC 5236

QY 61 CTC 63
Db 5237 CTC 5239

RESULT 47

LOCUS 177052
DEFINITION Sequence 6 from patent US 5693478.
ACCESSION 177052
VERSION 177052.1 GI:3013206
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 8591)
AUTHORS Vitek, M. Peter, and Jacobsen, J. Steven.
TITLE Method of detecting amyloid precursor proteins
JOURNAL Patent: US 5693478-A 6 02-DEC-1997;
FEATURES Location/Qualifiers
source 1..8591
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 63; DB 6; Length 8591;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCCTAGCTCGATACATAAAGCGCAATTGACCAATTCACCAATTTGGTGTGCAC 60
Db 5177 TTTAAGTGCCTAGCTCGATACATAAAGCGCAATTGACCAATTCACCAATTTGGTGTGCAC 5236

QY 61 CTC 63
Db 5237 CTC 5239

RESULT 48

LOCUS 177053
DEFINITION Sequence 8 from patent US 5693478.
ACCESSION 177053
VERSION 177053.1 GI:3013207
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 8591)
AUTHORS Vitek, M. Peter, and Jacobsen, J. Steven.
TITLE Method of detecting amyloid precursor proteins
JOURNAL Patent: US 5693478-A 8 02-DEC-1997;
FEATURES Location/Qualifiers
source 1..8591
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 63; DB 6; Length 8591;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCCTAGCTCGATACATAAAGCGCAATTGACCAATTCACCAATTTGGTGTGCAC 60
Db 5177 TTTAAGTGCCTAGCTCGATACATAAAGCGCAATTGACCAATTCACCAATTTGGTGTGCAC 5236

QY 61 CTC 63
Db 5237 CTC 5239

RESULT 49

LOCUS 187173
DEFINITION Sequence 6 from patent US 5703209.
ACCESSION 187173
VERSION 187173.1 GI:3206891
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 8591)
AUTHORS Vitek, M. Peter, and Jacobsen, J. Steven.
TITLE Amyloid precursor proteins and method of using same to assess agents which down-regulate formation of .beta.-amyloid peptide
JOURNAL Patent: US 5703209-A 6 30-DEC-1997;
FEATURES Location/Qualifiers
source 1..8591
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 63; DB 6; Length 8591;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCCTAGCTCGATACATAAAGCGCAATTGACCAATTCACCAATTTGGTGTGCAC 60
Db 5177 TTTAAGTGCCTAGCTCGATACATAAAGCGCAATTGACCAATTCACCAATTTGGTGTGCAC 5236

QY 61 CTC 63
Db 5237 CTC 5239

RESULT 50

LOCUS 187174
DEFINITION Sequence 8 from patent US 5703209.
ACCESSION 187174
VERSION 187174.1 GI:3206892
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 8591)
AUTHORS Vitek, M. Peter, and Jacobsen, J. Steven.
TITLE Amyloid precursor proteins and method of using same to assess agents which down-regulate formation of .beta.-amyloid peptide
JOURNAL Patent: US 5703209-A 8 30-DEC-1997;
FEATURES Location/Qualifiers
source 1..8591
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 63; DB 6; Length 8591;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCCTAGCTCGATACATAAAGCGCAATTGACCAATTCACCAATTTGGTGTGCAC 60
Db 5177 TTTAAGTGCCTAGCTCGATACATAAAGCGCAATTGACCAATTCACCAATTTGGTGTGCAC 5236

QY 61 CTC 63
Db 5237 CTC 5239

RESULT 51

LOCUS XXU02431
DEFINITION Cloning vector pMAMneo-CAT, complete sequence.
ACCESSION U02431
VERSION U02431.1 GI:413797

KEYWORDS
 SOURCE Cloning vector pMAMneo-CAT
 ORGANISM Cloning vector pMAMneo-CAT
 REFERENCE artificial sequences; vectors.
 AUTHORS 1 (bases 1 to 9184)
 TITLE ClONTECH Vectors On Disc version 1.3
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 9184)
 AUTHORS Kitts,P.A.
 TITLE Direct Submission
 JOURNAL Submitted (07-OCT-1993) Paul A. Kitts, CLONTECH Laboratories, Inc., 1020 East Meadow Circle, Palo Alto, CA 94303, USA
 COMMENT This vector can be obtained from CLONTECH Laboratories, Inc. To place an order call (415) 424-8222 or (800) 662-2566, extension 1. International customers, please contact your local distributor. For technical information, call (415) 424- 8222 or (800) 662-2566, extension 3. This sequence has been compiled from information in the sequence databases, published literature and other sources, together with partial sequences obtained by CLONTECH; this vector has not been completely sequenced. If you suspect there is an error in this sequence, please contact CLONTECH's Technical Service Department at (415) 424-8222 or (800) 662-2566, extension 3 or E-mail TECH@CLONTECH.COM.
 FEATURES
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 Location/Qualifiers
 /organism="Cloning vector pMAMneo-CAT"
 /mol_type="genomic DNA"
 /db_xref="taxon:31819"
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 Best Local Similarity 100.0%; Pred. No. 1.6e-13;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 QY 61 CTC 63
 Db |||||
 87 CTC 89
 RESULT 52
 AR215118
 LOCUS AR215118 9737 bp DNA linear PAT 25-SEP-2002
 DEFINITION Sequence 22 from patent US 6410266.
 ACCESSION AR215118.1 GI:23313246
 VERSION AR215118.1
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE Unclassified.
 1 (bases 1 to 9737)
 AUTHORS Harrington,J.J. and Rundlett,S.
 TITLE Compositions and methods for non-targeted activation of endogenous genes
 JOURNAL Patent: US 6410266-A 22 25-JUN-2002;
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 Location/Qualifiers
 /organism="unknown"
 /mol_type="genomic DNA"
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 Best Local Similarity 100.0%; Pred. No. 1.6e-13;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db |||||
 1613 TTTAAGTGCCTAGCTCGATACAAATAAAGCGCATTTGACCATTCACCACATTGGTGTGCAC 1672
 QY 61 CTC 63
 Db |||||
 1673 CTC 1675

QY 61 CTC 63
 Db |||||
 1673 CTC 1675
 RESULT 53
 AR215119
 LOCUS AR215119 9737 bp DNA linear PAT 25-SEP-2002
 DEFINITION Sequence 23 from patent US 6410266.
 ACCESSION AR215119
 VERSION AR215119.1 GI:23313247
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE Unclassified.
 1 (bases 1 to 9737)
 AUTHORS Harrington,J.J. and Rundlett,S.
 TITLE Compositions and methods for non-targeted activation of endogenous genes
 JOURNAL Patent: US 6410266-A 23 25-JUN-2002;
 FEATURES
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 Location/Qualifiers
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 Best Local Similarity 100.0%; Pred. No. 1.6e-13;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db |||||
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 QY 61 CTC 63
 Db |||||
 1673 CTC 1675
 RESULT 54
 AR215124
 LOCUS AR215124 9737 bp DNA linear PAT 25-SEP-2002
 DEFINITION Sequence 28 from patent US 6410266.
 ACCESSION AR215124
 VERSION AR215124.1 GI:23313252
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE Unclassified.
 1 (bases 1 to 9737)
 AUTHORS Harrington,J.J. and Rundlett,S.
 TITLE Compositions and methods for non-targeted activation of endogenous genes
 JOURNAL Patent: US 6410266-A 28 25-JUN-2002;
 FEATURES
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 1..9737
 Location/Qualifiers
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 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db |||||
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 QY 61 CTC 63
 Db |||||
 1673 CTC 1675

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RESULT 55
AR302360
LOCUS AR302360 9737 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 22 from patent US 6541221.
ACCESSION AR302360
VERSION AR302360.1 GI:31690614
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 9737)
Harrington,J.J., Sherf,B. and Rundlett,S.
AUTHORS
TITLE Compositions and methods for non-targeted activation of endogenous
genes
JOURNAL Patent: US 6541221-A 22 01-APR-2003;
FEATURES
source
Location/Qualifiers
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/organism="unknown"
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QY 61 CTC 63
Db 1673 CTC 1675
RESULT 56
AR302361
LOCUS AR302361 9737 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 23 from patent US 6541221.
ACCESSION AR302361
VERSION AR302361.1 GI:31690615
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 9737)
Harrington,J.J., Sherf,B. and Rundlett,S.
AUTHORS
TITLE Compositions and methods for non-targeted activation of endogenous
genes
JOURNAL Patent: US 6541221-A 23 01-APR-2003;
FEATURES
source
Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"
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Query Match 100.0%; Score 63; DB 6; Length 9737;
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Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1613 TTTAAGTCCTAGCTCGATACATAAAGCGCCATTGACCATTCACCATTCGTTGTGCAC 1672
QY 61 CTC 63
Db 1673 CTC 1675
RESULT 57
AR302366
LOCUS AR302366 9737 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 28 from patent US 6541221.
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ACCESSION AR302366
VERSION AR302366.1 GI:31690620
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 9737)
Harrington,J.J., Sherf,B. and Rundlett,S.
AUTHORS
TITLE Compositions and methods for non-targeted activation of endogenous
genes
JOURNAL Patent: US 6541221-A 28 01-APR-2003;
FEATURES
source
Location/Qualifiers
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/organism="unknown"
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Query Match 100.0%; Score 63; DB 6; Length 9737;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTAAGTCCTAGCTCGATACATAAAGCGCCATTGACCATTCACCATTCGTTGTGCAC 60
Db 1613 TTTAAGTCCTAGCTCGATACATAAAGCGCCATTGACCATTCACCATTCGTTGTGCAC 1672
QY 61 CTC 63
Db 1673 CTC 1675
RESULT 58
AR373232
LOCUS AR373232 9737 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 22 from patent US 6602686.
ACCESSION AR373232
VERSION AR373232.1 GI:40075240
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 9737)
Harrington,J.J., Sherf,B. and Rundlett,S.
AUTHORS
TITLE Compositions and method for non-targeted activation of endogenous
genes
JOURNAL Patent: US 6602686-A 22 05-AUG-2003;
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QY 1 TTTAAGTCCTAGCTCGATACATAAAGCGCCATTGACCATTCACCATTCGTTGTGCAC 60
Db 1613 TTTAAGTCCTAGCTCGATACATAAAGCGCCATTGACCATTCACCATTCGTTGTGCAC 1672
QY 61 CTC 63
Db 1673 CTC 1675
RESULT 59
AR373233
LOCUS AR373233 9737 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 23 from patent US 6602686.
ACCESSION AR373233
VERSION AR373233.1 GI:40075241
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
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Unclassified.
REFERENCE 1 (bases 1 to 9737)
AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.
TITLE Compositions and method for non-targeted activation of endogenous genes
JOURNAL Patent: US 6602686-A 23 05-AUG-2003;
FEATURES Location/Qualifiers
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QY 1 TTTAAGTGCCTAGCTCGATACATAAAGCGCCATTGGACCATTCACCACATTGGTGTGCAC 60
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QY 61 CTC 63
|||
Db 1673 CTC 1675

RESULT 60
AR373238 AR373238 9737 bp DNA linear PAT 18-DEC-2003
LOCUS Sequence 28 from patent US 6602686.
DEFINITION AR373238
ACCESSION AR373238
VERSION AR373238.1 GI:40075246
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 9737)
AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.
TITLE Compositions and method for non-targeted activation of endogenous genes
JOURNAL Patent: US 6602686-A 28 05-AUG-2003;
FEATURES Location/Qualifiers
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ORIGIN

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QY 1 TTTAAGTGCCTAGCTCGATACATAAAGCGCCATTGGACCATTCACCACATTGGTGTGCAC 60
|||||
Db 1613 TTTAAGTGCCTAGCTCGATACATAAAGCGCCATTGGACCATTCACCACATTGGTGTGCAC 1672

QY 61 CTC 63
|||
Db 1673 CTC 1675

RESULT 61
AR401618 AR401618 9737 bp DNA linear PAT 18-DEC-2003
LOCUS Sequence 22 from patent US 6623958.
DEFINITION AR401618
ACCESSION AR401618
VERSION AR401618.1 GI:40149066
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 9737)
AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.
TITLE Compositions and methods for non-targeted activation of endogenous genes

JOURNAL Patent: US 6623958-A 22 23-SEP-2003;
FEATURES Location/Qualifiers
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ORIGIN

Query Match 100.0%; Score 63; DB 6; Length 9737;
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QY 61 CTC 63
|||
Db 1673 CTC 1675

RESULT 62
AR401619 AR401619 9737 bp DNA linear PAT 18-DEC-2003
LOCUS Sequence 23 from patent US 6623958.
DEFINITION AR401619
ACCESSION AR401619
VERSION AR401619.1 GI:40149067
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 9737)
AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.
TITLE Compositions and methods for non-targeted activation of endogenous genes
JOURNAL Patent: US 6623958-A 23 23-SEP-2003;
FEATURES Location/Qualifiers
source 1..9737
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/mol_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 63; DB 6; Length 9737;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCCTAGCTCGATACATAAAGCGCCATTGGACCATTCACCACATTGGTGTGCAC 60
|||||
Db 1613 TTTAAGTGCCTAGCTCGATACATAAAGCGCCATTGGACCATTCACCACATTGGTGTGCAC 1672

QY 61 CTC 63
|||
Db 1673 CTC 1675

RESULT 63
AR401624 AR401624 9737 bp DNA linear PAT 18-DEC-2003
LOCUS Sequence 28 from patent US 6623958.
DEFINITION AR401624
ACCESSION AR401624
VERSION AR401624.1 GI:40149072
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 9737)
AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.
TITLE Compositions and methods for non-targeted activation of endogenous genes
JOURNAL Patent: US 6623958-A 28 23-SEP-2003;
FEATURES Location/Qualifiers
source 1..9737
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ORIGIN

Query Match 100.0%; Score 63; DB 6; Length 9737;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
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QY 1 TTTAAGTCCTAGCTCGATACATAAAGCCATTGACCAATTCACCACTGGTGTGCAC 60
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Db 1613 TTTAAGTCCTAGCTCGATACATAAAGCCATTGACCAATTCACCACTGGTGTGCAC 1672

QY 61 CTC 63
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Db 1673 CTC 1675

RESULT 64

AR215120 LOCUS AR215120 9871 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 24 from patent US 6410266.
ACCESSION AR215120
VERSION AR215120.1 GI:23313248

KEYWORDS

SOURCE

ORGANISM

Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 9871)

AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.

TITLE Compositions and methods for non-targeted activation of endogenous

genes

JOURNAL Patent: US 6410266-A 24 25-JUN-2002;

FEATURES

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Location/Qualifiers

/organism="unknown"

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ORIGIN

Query Match 100.0%; Score 63; DB 6; Length 9871;
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QY 61 CTC 63
|||

Db 1807 CTC 1809

RESULT 65

AR302362 LOCUS AR302362 9871 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 24 from patent US 6541221.
ACCESSION AR302362
VERSION AR302362.1 GI:31690616

KEYWORDS

SOURCE

Unknown.

ORGANISM

Unclassified.

REFERENCE 1 (bases 1 to 9871)

AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.

TITLE Compositions and methods for non-targeted activation of endogenous

genes

JOURNAL Patent: US 6541221-A 24 01-APR-2003;

FEATURES

source

1..9871

Location/Qualifiers

/organism="unknown"

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ORIGIN

Query Match 100.0%; Score 63; DB 6; Length 9871;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACATAAAGCCATTGACCAATTCACCACTGGTGTGCAC 60
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Db 1747 TTTAAGTCCTAGCTCGATACATAAAGCCATTGACCAATTCACCACTGGTGTGCAC 1806

QY 61 CTC 63
|||

Db 1807 CTC 1809

RESULT 66

AR373234 LOCUS AR373234 9871 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 24 from patent US 6602686.
ACCESSION AR373234
VERSION AR373234.1 GI:40075242

KEYWORDS

SOURCE

Unknown.

ORGANISM

Unclassified.

REFERENCE 1 (bases 1 to 9871)

AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.

TITLE Compositions and method for non-targeted activation of endogenous

genes

JOURNAL Patent: US 6602686-A 24 05-AUG-2003;

FEATURES

source

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Location/Qualifiers

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 63; DB 6; Length 9871;
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Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACATAAAGCCATTGACCAATTCACCACTGGTGTGCAC 60
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Db 1747 TTTAAGTCCTAGCTCGATACATAAAGCCATTGACCAATTCACCACTGGTGTGCAC 1806

QY 61 CTC 63
|||

Db 1807 CTC 1809

RESULT 67

AR401620 LOCUS AR401620 9871 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 24 from patent US 6623958.
ACCESSION AR401620
VERSION AR401620.1 GI:40149068

KEYWORDS

SOURCE

Unknown.

ORGANISM

Unclassified.

REFERENCE 1 (bases 1 to 9871)

AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.

TITLE Compositions and methods for non-targeted activation of endogenous

genes

JOURNAL Patent: US 6623958-A 24 23-SEP-2003;

FEATURES

source

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Location/Qualifiers

/organism="unknown"

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ORIGIN

Query Match 100.0%; Score 63; DB 6; Length 9871;
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Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACATAAAGCCATTGACCAATTCACCACTGGTGTGCAC 60
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Qy 61 CTC 63
Db 1807 CTC 1809

RESULT 68
LOCUS AR215121 10060 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 25 from patent US 6410266.
ACCESSION AR215121
VERSION AR215121.1 GI:2313249
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10060)
AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.
TITLE Compositions and methods for non-targeted activation of endogenous genes
JOURNAL Patent: US 6410266-A 25 25-JUN-2002;
FEATURES Location/Qualifiers
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ORIGIN
Query Match 100.0%; Score 63; DB 6; Length 10060;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTAAGTGCTAGCTCGATACATAAAGCCATTGTGACCATTCACCATTTGGTGTGCAC 60
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Db 1936 TTTAAGTGCTAGCTCGATACATAAAGCCATTGTGACCATTCACCATTTGGTGTGCAC 1995

Qy 61 CTC 63
Db 1996 CTC 1998

RESULT 69
LOCUS AR302363 10060 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 25 from patent US 6541221.
ACCESSION AR302363
VERSION AR302363.1 GI:31690617
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10060)
AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.
TITLE Compositions and methods for non-targeted activation of endogenous genes
JOURNAL Patent: US 6541221-A 25 01-APR-2003;
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTAAGTGCTAGCTCGATACATAAAGCCATTGTGACCATTCACCATTTGGTGTGCAC 60
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Db 1936 TTTAAGTGCTAGCTCGATACATAAAGCCATTGTGACCATTCACCATTTGGTGTGCAC 1995

Qy 61 CTC 63
Db 1996 CTC 1998

RESULT 70
LOCUS AR373235 10060 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 25 from patent US 6602686.
ACCESSION AR373235
VERSION AR373235.1 GI:40075243
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10060)
AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.
TITLE Compositions and method for non-targeted activation of endogenous genes
JOURNAL Patent: US 6602686-A 25 05-AUG-2003;
FEATURES Location/Qualifiers
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTAAGTGCTAGCTCGATACATAAAGCCATTGTGACCATTCACCATTTGGTGTGCAC 60
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Db 1936 TTTAAGTGCTAGCTCGATACATAAAGCCATTGTGACCATTCACCATTTGGTGTGCAC 1995

Qy 61 CTC 63
Db 1996 CTC 1998

RESULT 71
LOCUS AR401621 10060 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 25 from patent US 6623958.
ACCESSION AR401621
VERSION AR401621.1 GI:40149069
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10060)
AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.
TITLE Compositions and methods for non-targeted activation of endogenous genes
JOURNAL Patent: US 6623958-A 25 23-SEP-2003;
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Best Local Similarity 100.0%; Pred. No. 1.6e-13;
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Db 1936 TTTAAGTGCTAGCTCGATACATAAAGCCATTGTGACCATTCACCATTTGGTGTGCAC 1995

Qy 61 CTC 63
Db 1996 CTC 1998

RESULT 72
LOCUS U02448 10339 bp DNA circular SYN 29-MAR-1996
DEFINITION Cloning vector pMAMneo-LUC, complete sequence.
ACCESSION U02448

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VERSION      U02448.1  GI:413814
KEYWORDS     Cloning vector pMAmneo-LUC
SOURCE       Cloning vector pMAmneo-LUC
ORGANISM     artificial sequences; vectors.
REFERENCE    1 (bases 1 to 10339)
AUTHORS      Kitts,P.A.
JOURNAL      CLONTECH Vectors On Disc version 1.3
REFERENCE    Unpublished
AUTHORS      Kitts,P.A.
TITLE        Direct Submission
JOURNAL      Submitted (07-OCT-1993) Paul A. Kitts, CLONTECH Laboratories, Inc.,
              1020 East Meadow Circle, Palo Alto, CA 94303, USA
COMMENT      In reference 2, this vector is referred to as pBSpac delta P. This
              vector can be obtained from CLONTECH Laboratories, Inc., 1020 East
              Meadow Circle, Palo Alto, CA 94303, USA. To place an order call
              (415) 424-8222 or (800) 662-2566, extension 1. International
              customers, please contact your local distributor. For technical
              information, call (415) 424- 8222 or (800) 662-2566, extension 3.
              This sequence was compiled by Susana de la Luna. If you suspect
              there is an error in this sequence, please contact CLONTECH's
              Technical Service Department at (415) 424-8222 or (800) 662-2566,
              extension 3 or E-mail TECH@CLONTECH.COM.
FEATURES     Location/Qualifiers
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                /mol_type="genomic DNA"
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QY 61 CTC 63
Db 87 CTC 89
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LOCUS          XXU02428      10737 bp      DNA      circular SYN 29-JAN-1997
DEFINITION     Cloning vector pDR2, complete sequence.
ACCESSION      U02428
VERSION        U02428.1  GI:413794
KEYWORDS       Cloning vector pDR2
SOURCE         Cloning vector pDR2
ORGANISM       artificial sequences; vectors.
REFERENCE      1 (bases 1 to 10737)
AUTHORS        MurphY,A.J., Kung,A.L., Swirski,R.A. and Schimke,R.T.
TITLE          cDNA expression cloning in human cells using the pIamdbADR2
              episomal vector system
JOURNAL        Methods: A Companion to Methods in Enzymology 4, 111-131 (1992)
REFERENCE      2 (bases 1 to 10737)
AUTHORS        Kitts,P.A.
TITLE          Direct Submission
JOURNAL        Submitted (07-OCT-1993) Paul A. Kitts, CLONTECH Laboratories, Inc.,
              1020 East Meadow Circle, Palo Alto, CA 94303, USA
COMMENT        This vector can be obtained from CLONTECH Laboratories, Inc., 1020
              East Meadow Circle, Palo Alto, CA 94303, USA. To place an order
              call (415) 424-8222 or (800) 662-2566, extension 1. International
              customers, please contact your local distributor. For technical
              information, call (415) 424- 8222 or (800) 662-2566, extension 3.

```

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This sequence has been compiled from information in the sequence
databases, published literature and other sources, together with
partial sequences obtained by CLONTECH; this vector has not been
completely sequenced. If you suspect there is an error in this
sequence, please contact CLONTECH's Technical Service Department at
(415) 424-8222 or (800) 662-2566, extension 3 or E-mail
TECH@CLONTECH.COM.
FEATURES     Location/Qualifiers
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Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 CTC 63
Db 669 CTC 671
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DEFINITION     Cloning vector rpDR2, complete sequence.
ACCESSION      U02455
VERSION        U02455.1  GI:413821
KEYWORDS       Cloning vector rpDR2
SOURCE         Cloning vector rpDR2
ORGANISM       artificial sequences; vectors.
REFERENCE      1 (bases 1 to 10950)
AUTHORS        Kitts,P.A.
TITLE          CLONTECH Vectors On Disc version 1.3
JOURNAL        Unpublished
REFERENCE      2 (bases 1 to 10950)
AUTHORS        MurphY,A.J., Kung,A.L., Swirski,R.A. and Schimke,R.T.
TITLE          cDNA expression cloning in human cells using the pIamdbADR2
              episomal vector system
JOURNAL        Methods: A Companion to Methods in Enzymology 4, 111-131 (1992)
REFERENCE      3 (bases 1 to 10950)
AUTHORS        Kitts,P.A.
TITLE          Direct Submission
JOURNAL        Submitted (07-OCT-1993) Paul A. Kitts, CLONTECH Laboratories, Inc.,
              1020 East Meadow Circle, Palo Alto, CA 94303, USA
COMMENT        Lambda DR2 can be obtained from CLONTECH Laboratories, Inc., 1020
              East Meadow Circle, Palo Alto, CA 94303, USA. To place an order
              call (415) 424-8222 or (800) 662-2566, extension 1. International
              customers, please contact your local distributor. For technical
              information, call (415) 424- 8222 or (800) 662-2566, extension 3.
              This sequence was compiled by Andrew Murphy and revised at
              CLONTECH. If you suspect there is an error in this sequence, please
              contact CLONTECH's Technical Service Department at (415) 424-8222
              or (800) 662-2566, extension 3 or E-mail TECH@CLONTECH.COM.
FEATURES     Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 609 TTTAAGTGCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 668
Qy 61 CTC 63
Db 669 CTC 671

RESULT 75
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LOCUS
DEFINITION Sequence 1 from Patent WO9844129.
ACCESSION AX031159
VERSION AX031159.1 GI:10278512

KEYWORDS
SOURCE unidentified
ORGANISM unclassified.

REFERENCE 1
AUTHORS Lew, A.M., Boyle, J.S. and Brady, J.L.
TITLE Enhancement of immune response using targeting molecules
JOURNAL Patent: WO 9844129-A 1 08-OCT-1998;
INST MEDICAL W & E HALL (AU); QUEENSLAND INST MED RES (AU); CSL
LTD (AU); LEW ANDREW MARK (AU); UNIV MELBOURNE (AU); BOYLE
JEFFREY STEPHEN (AU); BRADY JAMIE LOUISE (AU); COMMW SCIENT IND
RES ORG (AU)

FEATURES
Location/Qualifiers
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Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 CTC 63
Db 631 CTC 633

Search completed: March 11, 2004, 09:42:32
Job time : 355.355 secs

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OM nucleic - nucleic search, using sw model

Run on: March 11, 2004, 03:02:06 ; Search time 54.4024 Seconds
(without alignments)
4919.575 Million cell updates/sec

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Perfect score: 63

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Scoring table: IDENTITY_NUC

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Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001as:*

5: Geneseq2001bs:*

6: Geneseq2002s:*

7: Geneseq2003as:*

8: Geneseq2003bs:*

9: Geneseq2003cs:*

10: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	63	100.0	397	3	Aaz94161 395 Nucle
3	63	100.0	397	3	Aa14719 Nucleotid
4	63	100.0	397	3	Aaz93077 Rous sarc
5	63	100.0	648	4	Aa43951 Rous sarc
6	63	100.0	2187	3	Aa14722 Nucleotid
7	63	100.0	2829	3	Aaz93333 Partial s
8	63	100.0	2878	3	Aaz93078 Partial s
9	63	100.0	3188	2	Aa06310 Sequence
10	63	100.0	3276	2	Aa06311 Sequence
11	63	100.0	3310	3	Aaz93331 Partial s
12	63	100.0	3311	3	Aaz93079 Partial s
13	63	100.0	3383	2	Aa06309 Sequence
14	63	100.0	3427	2	Aa06313 Sequence
15	63	100.0	3885	4	Aac89169 AGRSVPHYD
16	63	100.0	3979	2	Aa06312 Sequence
17	63	100.0	4059	2	Aa075974
18	63	100.0	4341	2	Aa062391
19	63	100.0	4341	6	Aa17704 Vector pv
20	63	100.0	4341	6	Abn83143 Plasmid p
21	63	100.0	4457	9	Ad35599 Bicistron
22	63	100.0	4487	3	Aa09085 AGRSV-bet
23	63	100.0	5653	2	Aat02998 RSV tar R

Aat76902	RSV tar R
Aa43814	PRLD3D4 c
Aa43813	PRLD3D3D4
Aa43812	PRLD3D2D3
Aa43869	Expressio
Aat12662	IL-4.Y124
Add35600	Tricistron
Add35601	Tetracist
Aaz45929	Nucleotid
Aa59078	Nucleotid
Aat84562	Plasmid p
Aat84561	Plasmid p
Aat87083	Plasmid p
Aat87084	Plasmid p
Aa04866	cDNA enco
Aa04865	cDNA enco
Aa05850	APP-REP 7
Aa05849	APP-REP 7
Ab157333	Vector p1
Aa53873	Expressio
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Aa53874	Expressio
Aa53875	Expressio
Aa53876	Expressio
Aa59077	Plasmid p
Ab94279	Nucleotid
Aa156865	DNA seque
Ab75125	Chromosom
Aa15269	DNA of ex
Aa156867	DNA seque
Aaz94163	Adenoviru
Aa156866	DNA seque
Aax02780	Vector pM
Ab159282	Nucleotid
Ab159283	Nucleotid
Ab159278	Nucleotid
Ab159280	Nucleotid
Ab159286	Nucleotid
Ab159276	Nucleotid
Ab159285	Nucleotid
Aat71261	ROUS sarc
Aa60824	Nucleotid
Aat2602	Luciferas
Aaz29699	Viral exp
Ab23249	Lac repre
Aa15665	Human res
Ab190071	Human pol
Aac92489	Fragment
Abk10062	Expressio
Aa09997	Bovine sc
Aa075973	pHIA-B7/b
Ab23250	Nucleotid
Ab159284	Nucleotid
Ab159277	Nucleotid
Aad28311	LSRNL vec
Aad28272	LSRNL vec
Ab159279	Nucleotid
Aac34589	A6 fragme
Aa03238	Marek's d
Ab159281	Nucleotid
Aat32735	Primer of
Aa070704	5' leader
Aa64166	Human cer
Aac86349	Linker us
Aac86350	Linker us
Aac27899	Edm2 vec
Aa71258	Proviral
Aa60821	Nucleotid
Aa01564	PHI diag
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Add35012	Mouse mit
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C 97 23.8 37.8 345 4 AAH73312 Human cer
 C 98 23.8 37.8 354 4 AAH71429 Human cer
 99 23.8 37.8 735 8 ADB82874 Human cdn
 100 23.8 37.8 759 8 ADB83122 Human cdn

ALIGNMENTS

RESULT 1
 AAF84457
 ID AAF84457 standard; DNA; 101 BP.
 XX AC AAF84457;
 XX AC AAF84457;
 DT 25-JUN-2001 (first entry)
 XX DE Rous sarcoma virus (RSV) promoter enhancer.
 XX XX Rous sarcoma virus; RSV; promoter enhancer; Pec promoter;
 XX KW chicken beta-actin promoter; recombinant vector; genetic vaccine;
 XX KW gene therapy; ds.
 XX OS Rous sarcoma virus.
 XX PN JP2001000188-A.
 XX PD 09-JAN-2001.
 XX PF 22-JUN-1999; 99JP-00174804.
 XX PR 22-JUN-1999; 99JP-00174804.
 XX PA (JAFG) NIPPON ZEON KK.
 XX DR WPI; 2001-285232/30.
 XX PT New DNA molecule for use as a promoter for preparing a recombinant
 XX PT containing the DNA which is used for preparing a vaccine.
 XX PS Example 1; Page 12; 15pp; Japanese.

XX CC The invention relates to a 5' and a 3' fragment of the chicken beta-actin
 CC promoter (AAF84452 and AAF84453, respectively), which exhibit promoter
 CC activity. The chicken beta-actin promoter fragments may be used to drive
 CC expression of a heterologous gene in a recombinant vector used as the
 CC active component of a genetic vaccine. The present sequence represents a
 CC Rous sarcoma virus (RSV) promoter enhancer used in an exemplification of
 CC the invention
 XX SQ Sequence 101 BP; 28 A; 26 C; 18 G; 29 T; 0 U; 0 Other;

Query Match 100.0%; Score 63; DB 4; Length 101;
 Best Local Similarity 100.0%; Pred. No. 1.4e-14;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCATTTCACCATTCACCATTCGTTGTCAC 60
 DB 32 TTTAAGTGGCTAGCTCGATACATAAAGCCATTTCACCATTCACCATTCGTTGTCAC 91
 QY 61 CTC 63
 DB 92 CTC 94

RESULT 2
 AA294161
 ID AA294161 standard; DNA; 397 BP.
 XX AC AA294161;
 XX AC AA294161;
 XX DT 19-JUN-2000 (first entry)
 XX XX Rous sarcoma virus.

DE 395 Nucleic acid Rous sarcoma virus promoter.
 XX XX Adenovirus; vector; RSV; promoter; prostate cancer; gene therapy;
 KW tumour suppressor gene; p16; ss.
 XX OS Rous sarcoma virus.
 XX PN WO200014211-A1.
 XX PD 16-MAR-2000.
 XX PF 02-SEP-1999; 99WO-US018833.
 XX PR 02-SEP-1998; 98US-00145729.
 XX PA (GENO-) GENOTHERAPEUTICS INC.
 XX PI Steiner MS, Lu Y;
 XX DR WPI; 2000-256967/22.
 XX PT Replication-deficient adenovirus type 5 expression vector, useful in gene
 PT therapy of prostate cancer, comprises a nucleic acid encoding p16 under
 PT the control of a Rous Sarcoma virus promoter.

XX PS Claim 1; Page 12; 118pp; English.
 XX CC The present sequence is that of 395 nucleic acid Rous sarcoma virus (RSV)
 CC promoter. A novel replication-deficient adenovirus type 5 expression
 CC vector of the invention, termed AdRSVP16 (see AA294163), has a deletion
 CC in an E1 and E3 region of the genome and contains a p16 tumour suppressor
 CC gene under the control of the RSV promoter. The adenoviral vector is used
 CC in the gene therapy of prostate cancer, in which p16 is frequently
 CC abnormal. Gene therapy is used to replace a missing, mutated or
 CC inactivated p16 tumour suppressor gene, thereby inhibiting the growth
 CC and/or progression of the tumour

XX SQ Sequence 397 BP; 108 A; 79 C; 110 G; 100 T; 0 U; 0 Other;
 Query Match 100.0%; Score 63; DB 3; Length 397;
 Best Local Similarity 100.0%; Pred. No. 1.9e-14;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCATTTCACCATTCACCATTCGTTGTCAC 60
 DB 334 TTTAAGTGGCTAGCTCGATACATAAAGCCATTTCACCATTCACCATTCGTTGTCAC 393
 QY 61 CTC 63
 DB 394 CTC 396

RESULT 3
 AAA14719
 ID AAA14719 standard; DNA; 397 BP.
 XX AC AAA14719;
 XX DT 08-AUG-2000 (first entry)
 XX DE Nucleotide sequence of the Rous Sarcoma virus promoter.
 XX KW Cellular cytotoxicity; tumor cell; expression vector; beta-lactamase;
 KW replication-deficient adenovirus type 5; suicide gene therapy;
 KW cancer cell; chemotherapy; beta-lactamase produg enzyme; produg rcm;
 KW anticancer; tumor; leukemia; breast cancer; Wilm's tumor;
 KW small cell lung carcinoma; Ewing's sarcoma; colon carcinoma;
 KW papillary adenocarcinoma; promoter; ss.

XX OS Rous sarcoma virus.
 XX PN WO200020608-A1.
 XX XX

PD 13-APR-2000.
 XX
 PF 01-OCT-1999; 99WO-US020908.
 XX
 PR 02-OCT-1998; 98US-00165321.
 XX
 PA (GENO-) GENOTHERAPEUTICS INC.
 XX
 PI Steiner MS;
 XX
 DR WPI; 2000-303788/26.
 XX
 XX
 PT Treating cancer using viral vectors which encode enzymes that convert
 PT inactive drugs to active cytotoxic agents, expression of the enzyme is
 PT tissue specific therefore targeting the effects of the drug to tumor
 PT cells.
 XX
 PS Disclosure; Page 13-14; 130pp; English.
 XX
 CC The specification describes a method for inducing cellular cytotoxicity
 CC in tumor cells using replication-deficient adenovirus type 5 expression
 CC vectors. The vectors comprise a sequence encoding a beta-lactamase under
 CC the control of a Rous Sarcoma virus in combination with a prodrug
 CC conjugated to a toxic agent. Tissue specific expression of the enzyme
 CC converts the inactive drugs into active cancer killing agents. The
 CC adenovirus genome has a deletion in an E1 and/or E3 region, and the beta-
 CC lactamase sequence is inserted within this region. The vectors are used
 CC for suicide gene therapy. This involves introducing genes into cancer
 CC cells that encode enzymes capable of converting inactive drugs into
 CC active cancer killing agents. If tissue specific promoters are coupled to
 CC the prodrug enzymes, then production of the prodrug will be tissue
 CC specific and targeted to the tumor. Therefore the cancer cells act as
 CC their own factories to activate chemotherapy agents and commit suicide.
 CC Beta-lactamase prodrug enzymes convert prodrug TCM into an active
 CC anticancer agent which is cytotoxic to cancer cells PPC-1. The method is
 CC used to treat patients with cancers of the brain, bladder or prostate. It
 CC may also be used to treat a range of other tumors such as leukemia,
 CC breast cancer, Wilms' tumor, small cell lung carcinoma, Ewing's sarcoma,
 CC colon carcinoma and papillary adenocarcinomas. The present sequence
 CC represents the Rous Sarcoma virus promoter, which was used to
 CC construct vectors of the invention
 XX
 SQ Sequence 397 BP; 108 A; 79 C; 110 G; 100 T; 0 U; 0 Other;

Query Match 100.0%; Score 63; DB 3; Length 397;
 Best Local Similarity 100.0%; Pred. No. 1.9e-14;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGGACCATTCACCAATGGTGTGCAC 60
 DB 334 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGGACCATTCACCAATGGTGTGCAC 393
 QY 61 CTC 63
 DB 394 CTC 396

RESULT 4
 AAZ93077
 ID AAZ93077 standard; DNA; 397 BP.
 XX
 AC AAZ93077;
 XX
 DT 04-JUL-2000 (first entry)
 XX
 DE Rous Sarcoma Virus promoter sequence.
 XX
 KW Adenovirus; vector; E1; E3; cytochrome; NADPH cytochrome reductase;
 KW Rous Sarcoma virus; RSV; chemotoxicity; transfection; sensitisation;
 KW prodrug; nicotinamide adenine dinucleotide phosphatase; ss.
 OS
 XX Rous sarcoma virus.
 XX

PN WO200014256-A1.
 XX
 PD 16-MAR-2000.
 XX
 PF 03-SEP-1999; 99WO-US018834.
 XX
 PR 04-SEP-1998; 98US-00148275.
 XX
 XX (GENO-) GENOTHERAPEUTICS INC.
 PA
 PI Steiner MS, Lu Y;
 XX
 DR WPI; 2000-257001/22.
 XX
 PT Replication-deficient adenovirus type 5 expression vectors used for gene
 PT therapy of cancer, especially prostate cancer, comprising an insertion of
 PT nucleic acid encoding cytochrome p450 genes.
 XX
 PS Claim 8; Page 18; 110pp; English.
 XX
 CC Replication-deficient adenovirus type 5 expression vectors comprise an
 CC adenovirus genome with a deletion in the E1 and E2 region of the genome
 CC and an insertion within the region under the control of a Rous Sarcoma
 CC Virus promoter can be used to induce chemotoxicity in tumour cells. Three
 CC such expression vectors are described, the inserted nucleic acids in each
 CC being the following: vector (I) has an insertion of a nucleic acid
 CC encoding a cytochrome 2C9 p450 and is designated Ad5RV2C9 (ATCC VR-
 CC 2628). Vector (II) has an insertion of a nucleic acid encoding a
 CC cytochrome 3A4 p450 and is designated Ad5RV3A4 (ATCC VR-2629). Vector
 CC (III) has an insertion of a nucleic acid encoding a nicotinamide adenine
 CC dinucleotide phosphatase (NADPH) cytochrome p450 reductase and is
 CC designated Ad5RVRED (ATCC VR-2630). The chemotoxicity of a tumor cell
 CC can be induced by administering (I) and (III) or (II) and (III) into the
 CC tumor cell (e.g. a prostate tumor cell) to selectively sensitize the cell
 CC to a prodrug and then administering the prodrug which kills the cell,
 CC inducing its chemotoxicity. The method uses gene-directed enzyme prodrug
 CC therapy to transfer a drug susceptibility gene to the tumor which
 CC activates a nontoxic prodrug intratumorally so the released drug can kill
 CC the tumor cells containing the drug susceptibility gene
 XX
 SQ Sequence 397 BP; 108 A; 79 C; 110 G; 100 T; 0 U; 0 Other;

Query Match 100.0%; Score 63; DB 3; Length 397;
 Best Local Similarity 100.0%; Pred. No. 1.9e-14;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGGACCATTCACCAATGGTGTGCAC 60
 DB 334 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGGACCATTCACCAATGGTGTGCAC 393
 QY 61 CTC 63
 DB 394 CTC 396

RESULT 5
 AAH43951
 ID AAH43951 standard; DNA; 648 BP.
 XX
 AC AAH43951;
 XX
 DT 06-SEP-2001 (first entry)
 XX
 DE Rous sarcoma virus promoter nucleotide sequence SEQ ID NO:1.
 XX
 KW Rous sarcoma virus; promoter; enhancer; RSV; primate; gene expression;
 KW transgene; genetic engineering; gene therapy; immunisation; ds.
 XX
 OS Rous sarcoma virus.
 XX
 PN WO200142444-A2.
 XX
 PD 14-JUN-2001.

XX PF 08-DEC-2000; 2000WO-US033256.
 XX PR 10-DEC-1999; 98US-0170019P.
 XX PA (ARIA-) ARIAD GENE THERAPEUTICS INC.
 XX PA (UYPE-) UNIV PENNSYLVANIA.
 XX PI Rivera V, Zoltick P, Wilson JM;
 XX DR WPI; 2001-381673/40.
 XX XX Genetically engineering a primate for expression of a desired gene,
 PT comprises introducing into the primate a transgene comprising Rous
 PT Sarcoma Virus (RSV) promoter and a nucleic acid sequence heterologous to
 PT RSV promoter.
 XX PS Claim 7; Page 44; 64pp; English.
 XX CC The present invention describes a method for genetically engineering a
 CC primate for expression of a desired gene comprising introducing into the
 CC primate a transgene comprising an Rous Sarcoma Virus (RSV) promoter and a
 CC nucleic acid sequence heterologous to RSV promoter. Also described is a
 CC primate cell (I) containing and capable of expressing a transgene
 CC comprising an RSV promoter operably linked to a recombinant nucleic acid
 CC encoding one or more fusion proteins, where the fusion proteins bind to a
 CC ligand and in the presence of the ligand modulate(s) the expression level
 CC of a target gene. The method can be used for high level expression of
 CC genes in primates or for engineering primate cells. It is useful for
 CC increasing the efficacy of many gene therapy strategies, and for
 CC increasing the efficacy of intracellular immunisation agents, molecules
 CC like ribozymes, antisense RNA, and dominant negative proteins, that act
 CC either stoichiometrically, or by competition. The method increases the
 CC efficacy of many gene therapy strategies by substantially elevating the
 CC expression of an exogenous therapeutic gene, and allowing expression to
 CC reach therapeutically effective levels. The present sequence represents a
 CC specifically claimed RSV enhancer/promoter nucleotide sequence from the
 CC present invention
 XX SQ Sequence 648 BP; 163 A; 135 C; 179 G; 171 T; 0 U; 0 Other;
 Query Match 100.0%; Score 63; DB 4; Length 648;
 Best Local Similarity 100.0%; Pred. No. 2.2e-14;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTAAGTGGCTAGCTCGATACATTAAGCCGATTTGACCATTCACCATTTGGTGGCAC 60
 Db 550 TTTAAGTGGCTAGCTCGATACATTAAGCCGATTTGACCATTCACCATTTGGTGGCAC 609
 QY 61 CTC 63
 Db 610 CTC 612
 RESULT 6
 ID AAA14722 standard; DNA; 2187 BP.
 XX AC AAA14722;
 XX DT 06-AUG-2003 (revised)
 XX DT 08-AUG-2000 (first entry)
 XX DE Nucleotide sequence of region A of vector Ad5RSVbeta-lactamase.
 XX KW Cellular cytotoxicity; tumor cell; expression vector; beta-lactamase;
 KW replication-deficient adenovirus type 5; suicide gene therapy;
 KW cancer cell; chemotherapy; beta-lactamase prodrug enzyme; prodrug TCM;
 KW anticancer; tumor; leukemia; breast cancer; Wilms' tumor;
 KW small cell lung carcinoma; Ewing's sarcoma; colon carcinoma;
 KW papillary adenocarcinoma; ss.
 XX OS Synthetic.

OS Rous sarcoma virus.
 OS Mastadenovirus.
 XX FN WO2000020608-A1.
 XX PD 13-APR-2000.
 XX PF 01-OCT-1999; 99WO-US020908.
 XX PR 02-OCT-1998; 98US-00165321.
 XX PA (GENO-) GENOTHERAPEUTICS INC.
 XX PI Steiner MS;
 XX DR WPI; 2000-303788/26.
 XX XX Treating cancer using viral vectors which encode enzymes that convert
 PT inactive drugs to active cytotoxic agents, expression of the enzyme is
 PT tissue specific therefore targeting the effects of the drug to tumor
 PT cells.
 XX PS Disclosure; Fig 10; 130pp; English.
 XX CC The specification describes a method for inducing cellular cytotoxicity
 CC in tumor cells using replication-deficient adenovirus type 5 expression
 CC vectors. The vectors comprise a sequence encoding a beta-lactamase under
 CC the control of a Rous Sarcoma Virus in combination with a prodrug
 CC conjugated to a toxic agent. Tissue specific expression of the enzyme
 CC converts the inactive drugs into active cancer killing agents. The
 CC adenovirus genome has a deletion in an E1 and/or E3 region, and the beta-
 CC lactamase sequence is inserted within this region. The vectors are used
 CC for suicide gene therapy. This involves introducing genes into cancer
 CC cells that encode enzymes capable of converting inactive drugs into
 CC active cancer killing agents. If tissue specific promoters are coupled to
 CC the prodrug enzymes, then production of the prodrug will be tissue
 CC specific and targeted to the tumor. Therefore the cancer cells act as
 CC their own factories to activate chemotherapy agents and commit suicide.
 CC Beta-lactamase prodrug enzymes convert prodrug TCM into an active
 CC anticancer agent which is cytotoxic to cancer cells PPC-1. The method is
 CC used to treat patients with cancers of the brain, bladder or prostate. It
 CC may also be used to treat a range of other tumors such as leukemia,
 CC breast cancer, Wilms' tumor, small cell lung carcinoma, Ewing's sarcoma,
 CC colon carcinoma and papillary adenocarcinomas. The present sequence
 CC represents region A of vector Ad5RSVbeta-lactamase, a vector of the
 CC invention. (Updated on 06-AUG-2003 to correct OS field.)
 XX SQ Sequence 2187 BP; 562 A; 477 C; 592 G; 556 T; 0 U; 0 Other;
 Query Match 100.0%; Score 63; DB 3; Length 2187;
 Best Local Similarity 100.0%; Pred. No. 2.9e-14;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTAAGTGGCTAGCTCGATACATTAAGCCGATTTGACCATTCACCATTTGGTGGCAC 60
 Db 742 TTTAAGTGGCTAGCTCGATACATTAAGCCGATTTGACCATTCACCATTTGGTGGCAC 801
 QY 61 CTC 63
 Db 802 CTC 804
 RESULT 7
 ID AAZ93333 standard; DNA; 2829 BP.
 XX AC AAZ93333;
 XX DT 04-JUL-2000 (first entry)
 XX DE Partial sequence of replication deficient adenoviral vector Ad5RSV2C9.
 XX KW Adenovirus; vector; E1; E3; cytochrome; NADPH cytochrome reductase;

KW Rous Sarcoma virus; BSV; chemotoxicity; transfection; sensitisation;
 KW prodrug; nicotinamide adenine dinucleotide phosphatase; ss.
 XX Synthetic.
 OS
 XX WO200014256-A1.
 XX
 XX 16-MAR-2000.
 XX
 XX 03-SEP-1999; 99WO-US018834.
 XX
 XX 04-SEP-1998; 98US-00148275.
 XX
 XX (GENO-) GENOTHERAPEUTICS INC.
 XX
 XX Steiner MS, Lu Y;
 XX
 XX WPI; 2000-257001/22.
 XX
 XX Replication-deficient adenovirus type 5 expression vectors used for gene
 PT therapy of cancer, especially prostate cancer, comprising an insertion of
 PT nucleic acid encoding cytochrome p450 genes.
 XX
 XX Claim 16; Fig 11A; 110pp; English.

XX Replication-deficient adenovirus type 5 expression vectors comprise an
 CC adenovirus genome with a deletion in the E1 and E2 region of the genome
 CC and an insertion within the region under the control of a Rous Sarcoma
 CC virus promoter can be used to induce chemotoxicity in tumour cells. Three
 CC such expression vectors are described, the inserted nucleic acids in each
 CC being the following: Vector (I) has an insertion of a nucleic acid
 CC encoding a cytochrome 2C9 p450 and is designated AdRSV2C9 (ATCC VR-
 CC 2628). Vector (II) has an insertion of a nucleic acid encoding a
 CC cytochrome 3A4 p450 and is designated AdRSV3A4 (ATCC VR-2629). Vector
 CC (III) has an insertion of a nucleic acid encoding a nicotinamide adenine
 CC dinucleotide phosphatase (NADPH) cytochrome p450 reductase and is
 CC designated AdRSVRED (ATCC VR-2630). The chemotoxicity of a tumor cell
 CC can be induced by administering (I) and (III) or (II) and (III) into the
 CC tumor cell (e.g. a prostate tumor cell) to selectively sensitise the cell
 CC to a prodrug and then administering the prodrug which kills the cell,
 CC inducing its chemotoxicity. The method uses gene-directed enzyme prodrug
 CC therapy to transfer a drug susceptibility gene to the tumor which
 CC activates a nontoxic prodrug intratumorally so the released drug can kill
 CC the tumor cells containing the drug susceptibility gene. This sequence is
 CC designated region A of the vector AdRSV2C9 and is the sequence of the
 CC cytochrome 2C9 p450
 XX
 XX Sequence 2829 BP; 748 A; 633 C; 707 G; 741 T; 0 U; 0 Other;

Query Match 100.0%; Score 63; DB 3; Length 2829;
 Best Local Similarity 100.0%; Pred. No. 3e-14;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
 Db 742 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
 QY 61 CTC 63
 Db 802 CTC 804

RESULT 8
 AAZ93078
 ID AAZ93078 standard; DNA; 2878 BP.
 XX
 XX AAZ93078;
 XX
 XX 04-JUL-2000 (first entry)
 DT
 XX Partial sequence of replication deficient adenoviral vector AdRSV3A4.
 DE
 XX Adenovirus; vector; E1; E3; cytochrome; NADPH cytochrome reductase;
 KW

KW Rous Sarcoma virus; RSV; chemotoxicity; transfection; sensitisation;
 KW prodrug; nicotinamide adenine dinucleotide phosphatase; ss.
 XX Synthetic.
 OS
 XX WO200014256-A1.
 XX
 XX 16-MAR-2000.
 XX
 XX 03-SEP-1999; 99WO-US018834.
 XX
 XX 04-SEP-1998; 98US-00148275.
 XX
 XX (GENO-) GENOTHERAPEUTICS INC.
 XX
 XX Steiner MS, Lu Y;
 XX
 XX WPI; 2000-257001/22.
 XX
 XX Replication-deficient adenovirus type 5 expression vectors used for gene
 PT therapy of cancer, especially prostate cancer, comprising an insertion of
 PT nucleic acid encoding cytochrome p450 genes.
 XX
 XX Claim 17; Fig 11B; 110pp; English.

XX Replication-deficient adenovirus type 5 expression vectors comprise an
 CC adenovirus genome with a deletion in the E1 and E2 region of the genome
 CC and an insertion within the region under the control of a Rous Sarcoma
 CC virus promoter can be used to induce chemotoxicity in tumour cells. Three
 CC such expression vectors are described, the inserted nucleic acids in each
 CC being the following: Vector (I) has an insertion of a nucleic acid
 CC encoding a cytochrome 2C9 p450 and is designated AdRSV2C9 (ATCC VR-
 CC 2628). Vector (II) has an insertion of a nucleic acid encoding a
 CC cytochrome 3A4 p450 and is designated AdRSV3A4 (ATCC VR-2629). Vector
 CC (III) has an insertion of a nucleic acid encoding a nicotinamide adenine
 CC dinucleotide phosphatase (NADPH) cytochrome p450 reductase and is
 CC designated AdRSVRED (ATCC VR-2630). The chemotoxicity of a tumor cell
 CC can be induced by administering (I) and (III) or (II) and (III) into the
 CC tumor cell (e.g. a prostate tumor cell) to selectively sensitise the cell
 CC to a prodrug and then administering the prodrug which kills the cell,
 CC inducing its chemotoxicity. The method uses gene-directed enzyme prodrug
 CC therapy to transfer a drug susceptibility gene to the tumor which
 CC activates a nontoxic prodrug intratumorally so the released drug can kill
 CC the tumor cells containing the drug susceptibility gene. This sequence is
 CC designated region A of the vector AdRSV3A4 and is the sequence of the
 CC cytochrome 3A4 p450
 XX
 XX Sequence 2878 BP; 786 A; 609 C; 710 G; 773 T; 0 U; 0 Other;

Query Match 100.0%; Score 63; DB 3; Length 2878;
 Best Local Similarity 100.0%; Pred. No. 3e-14;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
 Db 742 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
 QY 61 CTC 63
 Db 802 CTC 804

RESULT 9
 AAQ06310
 ID AAQ06310 standard; DNA; 3188 BP.
 XX
 XX AAQ06310;
 XX
 XX 25-MAR-2003 (revised)
 DT
 XX 29-JAN-1991 (first entry)
 DE
 XX Sequence of plasmid p79DBAM.
 XX

XW IFN-gamma receptor; autoimmune disease; multiple sclerosis;
XX hypersensitivity; ds.
OS Homo sapiens.

XX Key Location/Qualifiers

FT LTR 279..335

FT polyA_signal /*tag= a

FT 497..502

FT /*tag= b

XX EP393502-A.

XX 24-OCT-1990.

XX 11-APR-1990; 90EP-00106992.

XX 19-APR-1989; 89EP-00810295.

XX (HOFF) HOFFMANN-LA ROCHE AG.

XX Fountoulak M, Garotta G, Stuber D;

XX WPI; 1990-322042/43.

XX Soluble interferon-gamma receptors - for treating auto-immune diseases,
XX chronic inflammations, etc.

XX Disclosure; Fig 49; 174pp; English.

XX IFN-gamma is a therapeutically active agent in the treatment of
XX autoimmune disease, allograft transplant rejections, multiple sclerosis,
XX chronic inflammations and delayed hypersensitivity. It is also useful in
XX identifying IFN-gamma agonists and antagonists. See also AAQ06301.
XX (Updated on 25-MAR-2003 to correct PR field.)

XX Sequence 3188 BP; 797 A; 774 C; 882 G; 735 T; 0 U; 0 Other;

Query Match 100.0%; Score 63; DB 2; Length 3188;

Best Local Similarity 100.0%; Pred. No. 3.1e-14;

Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAAAGTCCTAGCTGATACAAATAAAGCGCATTTGACCATTCACCACTTGGTGTGCAC 60

Db 250 TTAAAGTCCTAGCTGATACAAATAAAGCGCATTTGACCATTCACCACTTGGTGTGCAC 309

QY 61 CTC 63

Db 310 CTC 312

RESULT 10

AAQ06311

ID AAQ06311 standard; DNA; 3276 BP.

XX AC AAQ06311;

XX 25-MAR-2003 (revised)

XX 29-JAN-1991 (first entry)

XX Sequence of plasmid p238BGL.

XX IFN-gamma receptor; autoimmune disease; multiple sclerosis;
XX hypersensitivity; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 243..426

FT /*tag= b

FT 243..405

FT /*tag= c

FT Sig-peptide /label= S.P.1

FT LTR 279..242

FT polyA_signal /*tag= a

FT 585..590

FT /*tag= d

XX EP393502-A.

XX 24-OCT-1990.

XX 11-APR-1990; 90EP-00106992.

XX 19-APR-1989; 89EP-00810295.

XX (HOFF) HOFFMANN-LA ROCHE AG.

XX Fountoulak M, Garotta G, Stuber D;

XX WPI; 1990-322042/43.

XX P-PSDB; AAR07066.

XX Soluble interferon-gamma receptors - for treating auto-immune diseases,
XX chronic inflammations, etc.

XX Disclosure; Fig 51; 174pp; English.

XX IFN-gamma is a therapeutically active agent in the treatment of
XX autoimmune disease, allograft transplant rejections, multiple sclerosis,
XX chronic inflammations and delayed hypersensitivity. It is also useful in
XX identifying IFN-gamma agonists and antagonists. See also AAQ06301.
XX (Updated on 25-MAR-2003 to correct PR field.)

XX Sequence 3276 BP; 814 A; 794 C; 914 G; 754 T; 0 U; 0 Other;

Query Match 100.0%; Score 63; DB 2; Length 3276;

Best Local Similarity 100.0%; Pred. No. 3.1e-14;

Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAAAGTCCTAGCTGATACAAATAAAGCGCATTTGACCATTCACCACTTGGTGTGCAC 60

Db 250 TTAAAGTCCTAGCTGATACAAATAAAGCGCATTTGACCATTCACCACTTGGTGTGCAC 309

QY 61 CTC 63

Db 310 CTC 312

RESULT 11

AAZ93331

ID AAZ93331 standard; DNA; 3310 BP.

XX AC AAZ93331;

XX 04-JUL-2000 (first entry)

XX Partial sequence of replication deficient adenoviral vector Ad5RSVRed.

XX Adenovirus; vector; E1; E3; cytochrome; NADPH cytochrome reductase;

XX Rous Sarcoma virus; RSV; chemotoxicity; transfection; sensitisation;

XX prodrug; nicotinamide adenine dinucleotide phosphatase; ss.

XX Synthetic.

XX WO2000014256-A1.

XX 16-MAR-2000.

XX 03-SEP-1999; 99WO-US018834.

XX 04-SEP-1998; 98US-00148275.

XX (GENO-) GENOTHERAPEUTICS INC.

XX Steiner MS, Lu Y;

XX DR WPI; 2000-257001/22.

XX XX Replication-deficient adenovirus type 5 expression vectors used for gene

PT therapy of cancer, especially prostate cancer, comprising an insertion of

PT nucleic acid encoding cytochrome p450 genes.

XX PS Disclosure; Fig 10; 110pp; English.

XX XX

CC Replication-deficient adenovirus type 5 expression vectors comprise an

CC adenovirus genome with a deletion in the E1 and E2 region of the genome

CC and an insertion within the region under the control of a Rous Sarcoma

CC Virus promoter can be used to induce chemotoxicity in tumour cells. Three

CC such expression vectors are described, the inserted nucleic acids in each

CC being the following: Vector (I) has an insertion of a nucleic acid

CC encoding a cytochrome 2C9 p450 and is designated Ad5RSV2C9 (ATCC VR-

CC 2628). Vector (II) has an insertion of a nucleic acid encoding a

CC cytochrome 3A4 p450 and is designated Ad5RSV3A4 (ATCC VR-2629). Vector

CC dinucleotide phosphatase (NADPH) cytochrome p450 reductase and is

CC designated Ad5RSVRED (ATCC VR-2630). The chemotoxicity of a tumor cell

CC can be induced by administering (I) and (III) or (II) and (III) into the

CC tumor cell (e.g. a prostate tumor cell) to selectively sensitize the cell

CC to a prodrug and then administering the prodrug which kills the cell,

CC inducing its chemotoxicity. The method uses gene-directed enzyme prodrug

CC therapy to transfer a drug susceptibility gene to the tumor which

CC activates a nontoxic prodrug intratumorally so the released drug can kill

CC the tumor cells containing the drug susceptibility gene. This sequence is

CC designated region A of the vector Ad5RSVRED

XX XX

SQ Sequence 3310 BP; 755 A; 881 C; 980 G; 694 T; 0 U; 0 Other;

Query Match 100.0%; Score 63; DB 3; Length 3310;

Best Local Similarity 100.0%; Pred. No. 3.1e-14;

Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCCTAGCTCGATACAAATAAGCCATTGACCATTCACCATTTGGTGTGCAC 60

|||||

Db 742 TTTAAGTCCCTAGCTCGATACAAATAAGCCATTGACCATTCACCATTTGGTGTGCAC 801

QY 61 CTC 63

|||

Db 802 CTC 804

RESULT 12

AAZ93079

ID AAZ93079 standard; DNA; 3311 BP.

XX AC AAZ93079;

XX XX

DT 04-JUL-2000 (first entry)

XX XX

DE Partial sequence of replication deficient adenoviral vector Ad5RSVRED.

XX Adenovirus; vector; E1; E3; cytochrome; NADPH cytochrome reductase;

KW Rous Sarcoma virus; RSV; chemotoxicity; transfection; sensitisation;

KW prodrug; nicotinamide adenine dinucleotide phosphatase; ss.

XX OS Synthetic.

XX XX

PN W0200014256-A1.

XX XX

PD 16-MAR-2000.

XX XX

PF 03-SEP-1999; 99WO-US018834.

XX XX

PR 04-SEP-1998; 98US-00148275.

XX XX

PA (GENO-) GENOTHERAPEUTICS INC.

XX XX

PI Steiner MS, Lu Y;

XX XX

DR WPI; 2000-257001/22.

XX XX Replication-deficient adenovirus type 5 expression vectors used for gene

PT therapy of cancer, especially prostate cancer, comprising an insertion of

PT nucleic acid encoding cytochrome p450 genes.

XX PS Claim 18; Fig 11C; 110pp; English.

XX XX

CC Replication-deficient adenovirus type 5 expression vectors comprise an

CC adenovirus genome with a deletion in the E1 and E2 region of the genome

CC and an insertion within the region under the control of a Rous Sarcoma

CC Virus promoter can be used to induce chemotoxicity in tumour cells. Three

CC such expression vectors are described, the inserted nucleic acids in each

CC being the following: Vector (I) has an insertion of a nucleic acid

CC encoding a cytochrome 2C9 p450 and is designated Ad5RSV2C9 (ATCC VR-

CC 2628). Vector (II) has an insertion of a nucleic acid encoding a

CC cytochrome 3A4 p450 and is designated Ad5RSV3A4 (ATCC VR-2629). Vector

CC dinucleotide phosphatase (NADPH) cytochrome p450 reductase and is

CC designated Ad5RSVRED (ATCC VR-2630). The chemotoxicity of a tumor cell

CC can be induced by administering (I) and (III) or (II) and (III) into the

CC tumor cell (e.g. a prostate tumor cell) to selectively sensitize the cell

CC to a prodrug and then administering the prodrug which kills the cell,

CC inducing its chemotoxicity. The method uses gene-directed enzyme prodrug

CC therapy to transfer a drug susceptibility gene to the tumor which

CC activates a nontoxic prodrug intratumorally so the released drug can kill

CC the tumor cells containing the drug susceptibility gene. This sequence is

CC designated region A of the vector Ad5RSVRED and is the sequence of the

CC cytochrome NADPH p450 reductase

XX XX

SQ Sequence 3311 BP; 755 A; 881 C; 981 G; 694 T; 0 U; 0 Other;

Query Match 100.0%; Score 63; DB 3; Length 3311;

Best Local Similarity 100.0%; Pred. No. 3.1e-14;

Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCCTAGCTCGATACAAATAAGCCATTGACCATTCACCATTTGGTGTGCAC 60

|||||

Db 742 TTTAAGTCCCTAGCTCGATACAAATAAGCCATTGACCATTCACCATTTGGTGTGCAC 801

QY 61 CTC 63

|||

Db 802 CTC 804

RESULT 13

AAQ06309

ID AAQ06309 standard; DNA; 3383 BP.

XX AC AAQ06309;

XX XX

DT 25-MAR-2003 (revised)

DT 29-JAN-1991 (first entry)

XX XX

DE Sequence of plasmid p76BGL.

XX XX

KW IFN-gamma receptor; autoimmune disease; multiple sclerosis;

KW hypersensitivity; ds.

XX XX

OS Homo sapiens.

XX XX

PH Key Location/Qualifiers

FT LTR 279..504

FT /*tag= a

FT CDS 505..540

FT /*tag= b

FT polyA_signal 692..697

FT /*tag= c

XX XX

PN EP393502-A.

XX XX

PD 24-OCT-1990.

XX XX

```

PF 11-APR-1990; 90EP-00106992.
XX
XX
PR 19-APR-1989; 89EP-00810295.
XX
XX (HOFF ) HOFFMANN-LA ROCHE AG.
XX
XX
PI Fountoulak M, Garotta G, Stuber D;
XX
XX WPI; 1990-322042/43.
DR
DR P-PSDB; AAR07065.
XX
XX Soluble interferon-gamma receptors - for treating auto-immune diseases,
PT chronic inflammations, etc.
XX
XX Disclosure; Fig 47; 174pp; English.
XX
XX IFN-gamma is a therapeutically active agent in the treatment of
CC autoimmune disease, allograft transplant rejections, multiple sclerosis,
CC chronic inflammations and delayed hypersensitivity. It is also useful in
CC identifying IFN-gamma agonists and antagonists. See also AAQ06301.
XX (Updated on 25-MAR-2003 to correct PR field.)
XX
XX Sequence 3383 BP; 838 A; 828 C; 929 G; 788 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 63; DB 2; Length 3383;
Best Local Similarity 100.0%; Pred. No. 3.1e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTAAGTCCTAGCTGATACATAAAGCGCATTTGACCATTCACCATTCGTTGTGCAC 60
DB 250 TTTAAGTCCTAGCTGATACATAAAGCGCATTTGACCATTCACCATTCGTTGTGCAC 309
QY 61 CTC 63
DB 310 CTC 312
RESULT 14
AAQ06313
ID AAQ06313 standard; DNA; 3427 BP.
XX
XX AAQ06313;
XX
XX 25-MAR-2003 (revised)
DT 29-JAN-1991 (first entry)
XX
XX Sequence of plasmid p267BGL.
XX
XX IFN-gamma receptor; autoimmune disease; multiple sclerosis;
KW hypersensitivity; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH 279..492
LTR /*tag= a
FT 493..585
CDS /*tag= b
FT /*tag= c
FT 493..564
FT /*tag= C
FT /label= S.P.2
FT polyA_signal 736..741
FT /*tag= d
XX
XX EP393502-A.
XX
XX 24-OCT-1990.
XX
XX 11-APR-1990; 90EP-00106992.
XX
XX 19-APR-1989; 89EP-00810295.
XX
XX (HOFF ) HOFFMANN-LA ROCHE AG.
XX

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XX
XX Fountoulak M, Garotta G, Stuber D;
XX
XX WPI; 1990-322042/43.
DR
DR P-PSDB; AAR07067.
XX
XX Soluble interferon-gamma receptors - for treating auto-immune diseases,
PT chronic inflammations, etc.
XX
XX Disclosure; Fig 59; 174pp; English.
XX
XX IFN-gamma is a therapeutically active agent in the treatment of
CC autoimmune disease, allograft transplant rejections, multiple sclerosis,
CC chronic inflammations and delayed hypersensitivity. It is also useful in
CC identifying IFN-gamma agonists and antagonists. See also AAQ06301.
XX (Updated on 25-MAR-2003 to correct PR field.)
XX
XX Sequence 3427 BP; 846 A; 840 C; 942 G; 799 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 63; DB 2; Length 3427;
Best Local Similarity 100.0%; Pred. No. 3.2e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTAAGTCCTAGCTGATACATAAAGCGCATTTGACCATTCACCATTCGTTGTGCAC 60
DB 250 TTTAAGTCCTAGCTGATACATAAAGCGCATTTGACCATTCACCATTCGTTGTGCAC 309
QY 61 CTC 63
DB 310 CTC 312
RESULT 15
AAC89169
ID AAC89169 standard; DNA; 3885 BP.
XX
XX AAC89169;
XX
XX 08-MAR-2001 (first entry)
DT
DE ADRSVpHYDE region A coding sequence.
XX
XX p-HYDE; cytostatic; gene therapy; apoptosis; leukaemia; prostate;
KW tumour suppressor gene; DNA repair; cancer; melanoma; lymphoma;
KW colorectal; pancreatic; breast; brain; gastric carcinoma; ds.
XX
XX Unidentified.
XX
XX WO2000071564-A2.
PN
XX 30-NOV-2000.
XX
XX 01-MAY-2000; 2000WO-US011456.
XX
XX 29-APR-1999; 99US-00302457.
PR 29-APR-1999; 99US-0131607P.
PR 08-FEB-2000; 2000US-00499817.
XX
XX (UUTE-) UNIV TENNESSEE RES CORP.
XX
XX Steiner MS, Wang C, Rinaldy A, Menon R;
PI
XX WPI; 2001-032016/04.
DR
XX New isolated nucleic acid encoding a mammalian p-Hyde protein of the p-
PT Hyde family is useful for treating cancer, e.g. prostate cancer.
XX
XX Disclosure; Fig 10; 171pp; English.
XX
XX The present sequence is region A of ADRSVpHYDE. ADRSVpHYDE is an
CC adenovirus vector expressing p-HYDE. p-HYDE induces susceptibility of a
CC cancer cell to cell death. The p-HYDE gene is associated with the
CC regression of tumour growth in vivo, the induction to susceptibility to
CC

```


CC apoptosis caused by UV or chemotherapy induced DNA damage and prevention
 CC of DNA repair with the upregulation of apoptosis as the result of UV
 CC damage and the failure to repair DNA. The present sequence may be used to
 CC treat cancer, preferably melanoma, lymphoma, leukaemia, prostate,
 CC colorectal, pancreatic, breast, brain or gastric carcinoma
 XX
 SQ Sequence 3885 BP; 847 A; 1039 C; 1063 G; 936 T; 0 U; 0 Other;
 Query Match 100.0%; Score 63; DB 4; Length 3885;
 Best Local Similarity 100.0%; Pred. No. 3.2e-14; Indels 0; Gaps 0;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTAAGTCCCTAGCTGATACATAAAGCCATTGACCAATTCACCAATGGTGTGCAC 60
 DB 742 TTTAAGTCCCTAGCTGATACATAAAGCCATTGACCAATTCACCAATGGTGTGCAC 801
 QY 61 CTC 63
 DB 802 CTC 804
 RESULT 16
 AAQ06312
 ID AAQ06312 standard; DNA; 3979 BP.
 XX
 AC AAQ06312;
 XX
 DT 25-MAR-2003 (revised)
 DT 29-JAN-1991 (first entry)
 XX
 DE Sequence of plasmid p2645GL.
 XX
 KW IFN-gamma receptor; autoimmune disease; multiple sclerosis;
 KW hypersensitivity; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 243..426
 FT /tag= b
 FT Sig-peptide 243..405
 FT /tag= c
 FT LTR 279..242
 FT /label= S.P.1
 FT /tag= a
 FT polyA_signal 1288..1292
 FT /tag= d
 XX
 PN EP393502-A.
 XX
 PD 24-OCT-1990.
 XX
 PF 11-APR-1990; 90EP-00106992.
 XX
 PR 19-APR-1989; 89EP-00810295.
 XX
 PA (HOFF) HOFFMANN-LA ROCHE AG.
 XX
 PI Fountoulak M, Garotta G, Stuber D;
 XX
 DR WPI; 1990-322042/43.
 DR P-PSDB; AAQ07066.
 XX
 FT Soluble interferon-gamma receptors - for treating auto-immune diseases,
 FT chronic inflammations, etc.
 XX
 PS Disclosure; Fig 55; 174pp; English.
 XX
 CC IFN-gamma is a therapeutically active agent in the treatment of
 CC autoimmune disease, allograft transplant rejections, multiple sclerosis,
 CC chronic inflammations and delayed hypersensitivity. It is also useful in
 CC identifying IFN-gamma agonists and antagonists. See also AAQ06301.
 CC (Updated on 25-MAR-2003 to correct PR field.)
 XX

XX
 SQ Sequence 3979 BP; 947 A; 987 C; 1113 G; 932 T; 0 U; 0 Other;
 Query Match 100.0%; Score 63; DB 2; Length 3979;
 Best Local Similarity 100.0%; Pred. No. 3.3e-14; Indels 0; Gaps 0;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTAAGTCCCTAGCTGATACATAAAGCCATTGACCAATTCACCAATGGTGTGCAC 60
 DB 250 TTTAAGTCCCTAGCTGATACATAAAGCCATTGACCAATTCACCAATGGTGTGCAC 309
 QY 61 CTC 63
 DB 310 CTC 312
 RESULT 17
 AAQ75974/c
 ID AAQ75974 standard; cDNA; 4059 BP.
 XX
 AC AAQ75974;
 XX
 DT 25-MAR-2003 (revised)
 DT 23-AUG-1995 (first entry)
 XX
 DE pHLA-B7 expression vector.
 XX
 XX expression vector; pHLA-B7; heavy human HLA-B7; bicistronic mRNA;
 KW light beta-2 microglobulin; class I major histocompatibility complex;
 KW MHC; human leukocyte antigen; HLA; covalently closed circular DNA; ds.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT misc_feature 1..354
 FT /tag= a
 FT /note= "pBR322 backbone contg. bacterial origin of
 FT replication"
 FT CDS 355..1170
 FT /tag= b
 FT /note= "kanamycin resistance gene open reading frame; the
 FT gene is taken from the transposable element Tn903"
 FT polyA_signal complement(1410..1177)
 FT /tag= c
 FT /note= "SV40 polyA signal sequence"
 FT intron complement(1412..11560)
 FT /tag= d
 FT /note= "SV40 small t intron"
 FT 3'UTR complement(1561..1794)
 FT /tag= e
 FT /note= "3' untranslated region of HLA-B7 heavy chain
 FT mRNA"
 FT CDS complement(1795..2880)
 FT /tag= f
 FT /note= "HLA-B7 open reading frame"
 FT LTR complement(2886..3415)
 FT /tag= g
 FT /note= "Rous sarcoma virus 3' LTR promoter region"
 FT misc_feature 3416..4059
 FT /tag= h
 FT /note= "pBR322 backbone"
 XX
 PN MO9429469-A2.
 XX
 PD 22-DEC-1994.
 XX
 PF 27-MAY-1994; 94WO-US006069.
 XX
 PR 07-JUN-1993; 93US-00074344.
 XX
 PA (VICA-) VICAL INC.
 PA (UNMI) UNIV MICHIGAN.
 XX

PI Nabel GJ, Nabel EG, Lew D, Marquet M;
 XX WPI; 1995-036494/05.
 XX
 XX New vectors for gene therapy, partic for tumours - comprising genetic
 FT material encoding one or more cistron(s) which express immunogenic or
 FT therapeutic peptide(s).
 XX
 XX Claim 9; Page 42-43; 50pp; English.
 XX
 XX This HLA-B7 antigen encoding plasmid was developed to incorporate many
 CC advantageous features, eg. the kanamycin resistance gene. The
 CC eradication of two open reading frames encoding portions of SV40 viral
 CC proteins lowers the risk of tumorigenicity. The vector may also operate
 CC as a cassette into which cistrons may be inserted and removed at will for
 CC the transcription and subsequent translation of peptides of interest. The
 CC vector is used partic. for the treatment of neoplastic disease, eg.
 CC melanoma, and provides enhanced gene delivery and expression in vivo.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 4059 BP; 975 A; 1051 C; 1033 G; 1000 T; 0 U; 0 Other;
 Query Match 100.0%; Score 63; DB 2; Length 4059;
 Best Local Similarity 100.0%; Pred. No. 3.3e-14;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTAAGTGCCTAGCTCGATACATAAAGCGCCATTGACCATTCACACATTTGGTGTGCAC 60
 Db 2954 TTTAAGTGCCTAGCTCGATACATAAAGCGCCATTGACCATTCACACATTTGGTGTGCAC 2895
 QY 61 CTC 63
 Db 2894 CTC 2892
 RESULT 18
 AAQ62391
 ID AAQ62391 standard; DNA; 4341 BP.
 XX
 AC AAQ62391;
 XX
 DT 25-MAR-2003 (revised)
 DT 18-NOV-1994 (first entry)
 XX
 DE Vector pVAC1.
 XX
 XX Vector; pVAC1; pRC/RSV; leader sequence; termination signal;
 KW fusion protein; pSfi/Not.Tag1; pElB leader; human; immunoglobulin; VH1;
 KW single chain; Fv; murine antibody; retroviral; envelope; plasmid;
 KW vaccine; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT misc_RNA complement(1..775)
 FT /*tag= c
 FT /note= "Claim 9"
 FT misc_RNA 606..780
 FT /*tag= b
 FT /note= "Claim 8"
 FT misc_RNA 606..716
 FT /*tag= a
 FT /note= "Claim 7"
 FT
 XX
 XX WO9408008-A1.
 XX
 XX 14-APR-1994.
 XX
 XX 04-OCT-1993; 93WO-GB002054.
 XX
 XX 02-OCT-1992; 92GB-00020808.
 XX
 XX (MEDI-) MEDICAL RES COUNCIL.

XX Hawkins RE, Russell SJ, Stevenson FK, Winter GP;
 PI WPI; 1994-135575/16.
 XX
 XX Modulating immune response to a disease marker - by administering a
 FT vector which expresses the disease marker to interact with the immune
 FT system.
 XX
 XX Claim 10; Fig 7; 77pp; English.
 XX
 XX This sequence represents the vector pVAC1. This vector is based on the
 CC commercially available vector pRC/RSV. Leader sequences and termination
 CC signals were introduced into the vector to allow for production of fusion
 CC proteins. The vector, pSfi/Not.Tag1, was modified to replace the pElB
 CC leader with the human immunoglobulin VH1 leader sequence that permits the
 CC encoding of an Sfil cloning site without modification of the amino acid
 CC sequence. This fragment was then cloned as an EcoRI/Blunt-HindIII
 CC fragment into NotI/Blunt- HindIII cut vector pRC/RSV to give pVAC1. The
 CC single chain Fv for an individual patient can be inserted within the VH1
 CC leader sequence. This plasmid when encoding a single chain murine
 CC antibody/retroviral envelope fusion protein can be used as a plasmid
 CC vaccine and it induces a strong humoral response to the antibody moiety
 CC in BALB/c mice. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 4341 BP; 1032 A; 1099 C; 1091 G; 1119 T; 0 U; 0 Other;
 Query Match 100.0%; Score 63; DB 2; Length 4341;
 Best Local Similarity 100.0%; Pred. No. 3.3e-14;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTAAGTGCCTAGCTCGATACATAAAGCGCCATTGACCATTCACACATTTGGTGTGCAC 60
 Db 542 TTTAAGTGCCTAGCTCGATACATAAAGCGCCATTGACCATTCACACATTTGGTGTGCAC 601
 QY 61 CTC 63
 Db 602 CTC 604
 RESULT 19
 AAS17704
 ID AAS17704 standard; DNA; 4341 BP.
 XX
 AC AAS17704;
 XX
 DT 12-MAR-2002 (first entry)
 DE Vector pVAC1 encoding a DNA vaccine.
 XX
 XX Cytostatic; vaccine; tetanus toxin; FrC; tumour; CTL; PCR primer; pVAC1;
 KW ds.
 XX
 XX Clostridium tetani.
 OS Homo sapiens.
 OS Synthetic.
 OS Cauliflower mosaic virus.
 XX
 PN WO200179510-A1.
 XX
 XX 25-OCT-2001.
 XX
 XX 17-APR-2001; 2001WO-GB001719.
 XX
 XX 17-APR-2000; 2000GB-00009470.
 XX
 XX (CANC-) CANCER RES VENTURES LTD.
 XX
 XX Rice J, Stevenson F;
 XX WPI; 2002-066370/09.
 XX
 XX Nucleic acid construct, useful to immunize against various diseases

PT including cancer, expresses the first domain of tetanus toxin Frc fused
XX to a disease peptide antigen to provide a vaccine.
PS Disclosure; Fig 4; 7lpp; English.
XX
CC The invention relates to a nucleic acid construct for delivery into
CC living cells in vivo, to induce an immune response to a disease peptide
CC antigen, where the construct directs expression of a fusion protein
CC comprising the peptide antigen and the first domain of Frc. Also included
CC are a nucleic acid vector comprising the above construct, a host cell
CC comprising the above construct or vector and a method of producing a
CC nucleic acid construct for inducing an immune response. The method
CC comprises identifying a nucleic acid sequence encoding a disease peptide
CC antigen comprising epitopes characteristic of the disease, cloning the
CC nucleic acid sequence, introducing the cloned nucleic acid into a vector
CC which allows the antigen to be expressed as a fusion with a first domain
CC Frc from tetanus toxin, and optionally isolating the construct from the
CC vector. The construct or vector is used as a vaccine to induce an immune
CC response, particularly to tumour antigens. The present sequence is vector
CC pVAC1 which encodes a vaccine of the invention
XX
SQ Sequence 4341 BP; 1033 A; 1099 C; 1090 G; 1119 T; 0 U; 0 Other;
Query Match 100.0%; Score 63; DB 6; Length 4341;
Best Local Similarity 100.0%; Pred. No. 3.3e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTAAGTCCTAGCTCGATACATAAAGCGCCATTTCACCATTCACCATTTGGTGTGCAC 60
Db |||||
542 TTTAAGTCCTAGCTCGATACATAAAGCGCCATTTCACCATTCACCATTTGGTGTGCAC 601
QY 61 CTC 63
Db |||
602 CTC 604
RESULT 20
ABN83143
ID ABN83143 standard; DNA; 4341 BP.
XX
AC ABN83143;
XX
DT 10-SEP-2002 (first entry)
XX
DE Plasmid pVAC1 complete sequence.
XX
KW Immune response; plant viral coat protein; pVAC1; cytostatic; virucide;
KW cancer; B cell malignancy; ds.
XX
OS Synthetic.
XX
FN WO200240513-A2.
XX
PD 23-MAY-2002.
XX
PF 20-NOV-2001; 2001WO-GB005142.
XX
PR 20-NOV-2000; 2000GB-00028319.
XX
PA (CANC-) CANCER RES VENTURES LTD.
XX
PI Savelyeva N, Stevenson F;
XX
DR WPI; 2002-500202/53.
XX
PT Nucleic acid construct for delivery into living cells as a vaccine,
PT useful for treating e.g. cancer, directs the expression of a fusion
PT protein comprising an antigen and an adjuvant sequence derived from a
PT plant viral coat protein.
XX
PS Example 3; Fig 7; 84pp; English.
XX
CC The invention relates to a novel nucleic acid construct for inducing an

CC immune response in vivo to an antigen, capable of directing the
CC expression of a fusion protein that comprises an antigen and an adjuvant
CC sequence derived from a plant viral coat protein. The construct of the
CC invention has cytostatic and virucide activity. The nucleic acid
CC construct is useful for inducing an immune response in a patient, for
CC vaccinating a patient against an infectious disease caused by an antigen
CC derived from a pathogen e.g. a virus, for treating a cancer patient or a
CC patient with a predisposition to cancer and for treating a patient having
CC a B cell malignancy, where the construct is encapsidated, and optionally,
CC a second nucleic acid sequence encoding a further immunomodulatory
CC polypeptide is administered to the patient. The construct is also useful
CC in medical treatment, and in the preparation of a vaccine for treating or
CC preventing a disease state associated with the antigen. The sequence
CC shows the complete sequence of vector pVAC1
XX
SQ Sequence 4341 BP; 1033 A; 1099 C; 1090 G; 1119 T; 0 U; 0 Other;
Query Match 100.0%; Score 63; DB 6; Length 4341;
Best Local Similarity 100.0%; Pred. No. 3.3e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTAAGTCCTAGCTCGATACATAAAGCGCCATTTCACCATTCACCATTTGGTGTGCAC 60
Db |||||
542 TTTAAGTCCTAGCTCGATACATAAAGCGCCATTTCACCATTCACCATTTGGTGTGCAC 601
QY 61 CTC 63
Db |||
602 CTC 604
RESULT 21
ADD35599
ID ADD35599 standard; DNA; 4457 BP.
XX
AC ADD35599;
XX
DT 15-JAN-2004 (first entry)
XX
DE Bicistronic eukaryotic expression vector Pl178.
XX
KW Multicistronic eukaryotic expression vector; multiple protein expression;
KW simultaneous expression; viral internal ribosomal entry site; viral IRES;
KW chain terminator; transcription pause site; gene transfer;
KW DNA immunisation; gene therapy; Pl178; kanamycin resistance gene;
KW Rous sarcoma virus; RSV promoter; rabbit beta-globin intron;
KW hepatitis C virus; HCV IRES; mRGS terminator; cyclic; circular; ds.
XX
OS Chimeric.
OS Synthetic.
OS Rous sarcoma virus.
OS Oryctolagus cuniculus.
OS Hepatitis C virus.
OS Escherichia coli.
XX
PN WO2003031630-A1.
XX
PD 17-APR-2003.
XX
PF 10-OCT-2002; 2002WO-IT000646.
XX
PR 12-OCT-2001; 2001IT-MI002110.
XX
PA (KERY-) KERYOS SPA.
XX
PI Fazio V, Rinaldi M, Sonzogni L, Tonon G, Orsini G;
XX
DR WPI; 2003-393446/37.
XX
PT New multicistronic recombinant plasmid vectors expressing two to our
PT genes simultaneously, useful in various biotechnological applications,
PT such as gene transfer, gene therapy and in DNA immunization.
XX
PS Claim 18; SEQ ID NO 2; 52pp; English.

XX The invention relates to multicistronic eukaryotic expression vectors for
 CC the expression of at least two proteins of interest which may be
 CC identical or different. The vectors comprise at least one eukaryotic
 CC expression cassette having a promoter/enhancer sequence, an intron
 CC sequence, a cloning site, a viral internal ribosomal entry site (IRES)
 CC and a chain terminator. The vectors may additionally contain a
 CC transcription pause site downstream of the chain terminator. The
 CC invention also encompasses eukaryotic host cells comprising a vector of
 CC the invention, and the recombinant expression of two or more eukaryotic
 CC proteins using host cells transformed with a vector of the invention.
 CC The vectors are useful in various biotechnological applications in which
 CC the simultaneous expression of two or more genes is necessary, such as
 CC gene transfer protocols, DNA immunisation, or for the expression of
 CC different molecules in the same cell. They may also be used in gene
 CC therapy. The present sequence represents a specifically claimed vector
 CC designated PL178, which comprises a Rous sarcoma virus (RSV) promoter,
 CC rabbit beta-globin intron, the hepatitis C virus (HCV) IRES, and a rabbit
 CC beta-globin gene mR3B terminator as well as a kanamycin resistance gene.
 XX
 SQ Sequence 4457 BP; 1095 A; 1027 C; 1123 G; 1212 T; 0 U; 0 Other;

Query Match 100.0%; Score 63; DB 9; Length 4457;
 Best Local Similarity 100.0%; Pred. No. 3.3e-14;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTAAGTCCTAGCTCGATACAAATAAAGCGCATTTGACCATTCACCACTTGGTGTGCAC 60
 DB 918 TTTAAGTCCTAGCTCGATACAAATAAAGCGCATTTGACCATTCACCACTTGGTGTGCAC 977
 QY 61 CTC 63
 DB 978 CTC 980

RESULT 22
 AAA09085
 ID AAA09085 standard; DNA; 4487 BP.
 XX
 AC AAA09085;
 DT 15-SEP-2003 (revised)
 DT 06-AUG-2003 (revised)
 DT 10-AUG-2000 (first entry)
 XX
 DE ADRSV-beta-galactosidase vector region A.
 XX
 KW Region A; replication-deficient; vector; lacZ; beta-galactosidase;
 KW Rous Sarcoma Virus; RSV; promoter; cytotoxicity; cytostatic; pro-drug;
 KW prostate cancer; gene therapy; ss.
 XX
 OS Human adenovirus type 5.
 OS Rous sarcoma virus.
 OS Escherichia coli.
 OS Chimeric.
 XX
 FN WO2000020038-A1.
 XX
 PD 13-APR-2000.
 XX
 PF 01-OCT-1999; 99WO-US020907.
 XX
 PR 02-OCT-1998; 98US-00165730.
 XX
 PA (GENO-) GENOTHERAPEUTICS INC.
 XX
 PI Steiner MS;
 XX
 DR WPI; 2000-303646/26.
 XX
 PT Inducing cellular cytotoxicity of tumor cell comprises introducing
 PT replication-deficient adenovirus type 5 expression vector containing gene
 PT encoding for enzyme having ability to convert nontoxic prodrug into

PT cancer killing drug.
 XX
 PS Claim 4; Fig 18B; 178pp; English.
 XX
 CC This sequence comprises Region A of a replication-deficient adenovirus
 CC type 5 vector containing a lacZ gene (encoding beta-galactosidase (beta-
 CC gal)) under the control of the Rous Sarcoma Virus (RSV) promoter.
 CC Inducing cellular cytotoxicity of a tumor cell comprises introducing a
 CC replication-deficient adenovirus type 5 expression vector comprising a
 CC gene that encodes for an enzyme that has the ability to convert a non-
 CC toxic pro-drug into a cancer killing drug which then destroys cancer
 CC cells. The adenovirus genome preferably has a deletion in an E1 and E3
 CC region and an insertion within the region of a nucleic acid encoding
 CC Escherichia coli beta-gal under the control of a promoter. The pro-drug
 CC active site is masked by beta-gal. Functional beta-gal is expressed from
 CC the vector so as to activate the pro-drug into an agent toxic to the
 CC cells. Beta-gal can be under the control of an RSV, probasin (PB),
 CC Prostate Specific Antigen (PSA) or Mouse Mammary Tumor Virus (MMTV)
 CC promoter. The vectors provide a novel way to treat prostate cancer by
 CC gene therapy. (Updated on 06-AUG-2003 to correct OS field.) (Updated on
 CC 15-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 4487 BP; 1031 A; 1148 C; 1288 G; 1020 T; 0 U; 0 Other;

Query Match 100.0%; Score 63; DB 3; Length 4487;
 Best Local Similarity 100.0%; Pred. No. 3.4e-14;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACAAATAAAGCGCATTTGACCATTCACCACTTGGTGTGCAC 60
 DB 742 TTTAAGTCCTAGCTCGATACAAATAAAGCGCATTTGACCATTCACCACTTGGTGTGCAC 801
 QY 61 CTC 63
 DB 802 CTC 804

RESULT 23
 AA020998
 ID AA020998 standard; DNA; 5653 BP.
 XX
 AC AA020998;
 XX
 DT 24-MAR-1996 (first entry)
 XX
 DE RSV tar Rev M10 expression plasmid pRSVtarRevM10.
 XX
 KW Plasmid pRSVtarRevM10; particle-mediated gene transfer; cyclic;
 KW particle acceleration; HIV virus infection; gene therapy; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT misc_feature 1..36
 FT /tag= a
 FT /note= "pBR322 vector sequence"
 FT enhancer 37..610
 FT /tag= b
 FT /note= "RSV enhancer"
 FT promoter 611..699
 FT /tag= c
 FT /label= tar
 FT /note= "HIV promoter tat responsive element"
 FT mat_peptide 700..1129
 FT /tag= d
 FT /note= "Rev M10 open reading frame"
 FT polyA_signal 1243
 FT /tag= e
 FT /note= "cattle somatotropin poly(A) site"
 FT promoter 1993..2300
 FT /tag= f
 FT /note= "pSVneo promoter"
 FT misc_feature 2346

```

FT      /*tag= g
FT      /label= kanamycin_resistance_gene
FT      /note= "pSV2 neo selectable marker gene"
FT      3360
FT      polyA_signal
FT      /*tag= h
FT      /note= "pSV2 neo"
FT      3459..5653
FT      /*tag= i
FT      /note= "plasmid pUC ori/amp sequence"
FT
XX      WO9529703-A1.
XX
XX      09-NOV-1995.
XX
XX      01-MAY-1995; 95WO-US005024.
XX
XX      29-APR-1994; 94US-00235277.
XX
XX      (NABE/) NABEL G J.
XX      (WOFF/) WOFFENDIN C.
XX      (YANG/) YANG N.
XX      (SHEE/) SHEEHY M J.
XX
XX      Nabel GJ, Woffendin C, Yang N, Sheehy MJ;
XX      WPI; 1995-403807/51.
XX
XX      Particle-mediated gene transfer - in T cells, monocytes, macrophage(s),
XX      dendrites or haematopoietic stem cells, partic. for treating HIV
XX      infection.
XX      Disclosure; Fig 11a-11e; 96pp; English.
XX
XX      Expression plasmid pRSVtRevM10 contains the Rev M10 HIV protective gene
XX      (a dominant-negative inhibition gene) under the control of the Tat
XX      sequence (HIV promoter -18 to -72), i.e. gene expression is activated by
XX      Tat. The plasmid also contains the kanamycin- resistance selectable
XX      marker gene. The plasmid is used in a particle-mediated gene transfer
XX      process for Rev M10 gene expression in T-cells (preferably), monocytes,
XX      macrophages, haematopoietic stem cells or dendrites. The gold
XX      microparticle acceleration process results in stable incorporation of
XX      foreign genes in the cells. This method is used to treat HIV infection.
XX      Rev M10 transduced cells are resistant to HIV challenge. The method may
XX      be applied to the transfer of other therapeutic genes in a gene therapy
XX      process
XX
XX      Sequence 5653 BP; 1328 A; 1428 C; 1478 G; 1419 T; 0 U; 0 Other;
XX
XX      Query Match 100.0%; Score 63; DB 2; Length 5653;
XX      Best Local Similarity 100.0%; Pred. No. 3.5e-14;
XX      Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      QY 1 TTTAAGTGGCTAGCTCGATACATATAAGCCATTTCACCATTCACCATTTGGTGGCAC 60
XX      |||||
XX      Db 542 TTTAAGTGGCTAGCTCGATACATATAAGCCATTTCACCATTCACCATTTGGTGGCAC 601
XX      |||||
XX      QY 61 CTC 63
XX      |||
XX      Db 602 CTC 604

RESULT 24
AAT76802
ID AAT76802 standard; DNA; 5653 BP.
XX
XX      AC AAT76802;
XX
XX      18-NOV-1997 (first entry)
XX
XX      RSV tar Rev m10 retroviral vector DNA sequence.
XX
XX      inhibit; Human Immunodeficiency Virus; HIV; gene expression;
XX      transcription activation region; TAR; negative transdominant mutant;
XX

```

```

KW      Rev M10; mutant; nuclear protein; viral regulatory protein; tat;
KW      RSV tar Rev M10 plasmid; Rous sarcoma virus; RSV; ds.
XX
XX      Synthetic.
XX
XX      Key
XX      enhancer
XX      Location/Qualifiers
XX      37..1129
XX      /*tag= b
XX      /note= "expression control sequence, contains Rous
XX      Sarcoma Virus enhancer and Rev M10 gene"
XX      700..1129
XX      /*tag= a
XX      /note= "Rev M10 gene"
XX
XX      US5650306-A.
XX
XX      22-JUL-1997.
XX
XX      07-JUN-1993; 93US-00073836.
XX
XX      07-JUN-1993; 93US-00073836.
XX
XX      (UNMI ) UNIV MICHIGAN.
XX
XX      Woffendin C, Liu J, Nabel GJ, Yang Z;
XX      WPI; 1997-384672/35.
XX
XX      Recombinant nucleic acid for inhibiting HIV gene expression - comprises
XX      expression control sequence and transcription activation region linked to
XX      rev negative trans:dominant mutant gene.
XX
XX      Claim 7; Fig 7; 35pp; English.
XX
XX      Recombinant nucleic acid molecules for the improved expression of genes
XX      which inhibit Human Immunodeficiency Virus (HIV) gene expression are
XX      claimed, which comprise an expression control sequence and a
XX      transcription activation region (TAR) sequence, operatively linked to a
XX      negative transdominant mutant gene (a protective gene), where the
XX      negative transdominant mutant gene is a mutant of rev. Rev is an 18 kDa
XX      nuclear viral regulatory protein in HIV gene expression which controls
XX      export of viral RNA from the nucleus to the cytoplasm of infected cells.
XX      The TAR sequence which is found in the HIV genome controls the regulatory
XX      activity of the tat protein. The TAR sequence is linked to the protective
XX      gene, and therefore controls its expression. This sequence is a preferred
XX      recombinant nucleic acid vector, designated RSV tar Rev M10 plasmid
XX
XX      Sequence 5653 BP; 1326 A; 1429 C; 1478 G; 1420 T; 0 U; 0 Other;
XX
XX      Query Match 100.0%; Score 63; DB 2; Length 5653;
XX      Best Local Similarity 100.0%; Pred. No. 3.5e-14;
XX      Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      QY 1 TTTAAGTGGCTAGCTCGATACATATAAGCCATTTCACCATTCACCATTTGGTGGCAC 60
XX      |||||
XX      Db 542 TTTAAGTGGCTAGCTCGATACATATAAGCCATTTCACCATTCACCATTTGGTGGCAC 601
XX      |||||
XX      QY 61 CTC 63
XX      |||
XX      Db 602 CTC 604

RESULT 25
AAQ43814
ID AAQ43814 standard; DNA; 5750 BP.
XX
XX      AC AAQ43814;
XX
XX      25-MAR-2003 (revised)
XX      20-OCT-1993 (first entry)
XX
XX      PRLD3D4 construct.
XX

```

KW Epidermal growth factor receptor truncate protein; EGF; binding sites;
 KW adsorptive agents; mammalian cell growth abnormality; detection; growth;
 KW reproduction; signal transmission; ds.
 XX
 OS Synthetic.
 XX
 XX
 FH Key Location/Qualifiers
 FT misc_feature 1077..1079
 FT /*tag= a
 FT /note= "codon ARA encodes Ile"
 XX
 PN US5218090-A.
 XX
 PD 08-JUN-1993.
 XX
 PF 26-OCT-1990; 90US-00604728.
 XX
 PR 12-JUN-1990; 90US-00536896.
 XX
 PA (WARN) WARNER LAMBERT CO.
 XX
 PI Connors RW;
 XX
 DR WPI; 1993-196297/24.
 DR P-PSDB; AAR38211.
 XX
 PT New epidermal growth factor receptor truncate proteins - which bind
 PT ligands of EGF receptor without transmitting signal for growth or
 PT reproduction.
 XX
 PS Disclosure; Fig 9; 42pp; English.
 CC The sequence is that of the pRLD3D4 construct which encodes the epidermal
 CC growth factor (EGF) receptor truncate protein L03D4 having EGF binding
 CC sites. The protein binds ligands of the EGF receptor without transmitting
 CC a signal for the growth and reproduction of a cell. It can be used as an
 CC adsorptive agent for any moieties that bind the EGF receptor as the
 CC portal of entry to a cell. It competes with the EGF receptor present on
 CC the cell surface for the binding of ligands and thereby inhibits the
 CC action of the ligands or prevents the entry of viruses into cells. It can
 CC also be used as for the EGF receptor itself, such as in the detection of
 CC abnormalities in mammalian cell growth. It is also useful for prepreg.
 CC agonists or agonists. The features table indicate a discrepancy between
 CC the L03D4 protein sequence given in the specification and that which the
 CC pRLD3D4 DNA sequence given in the specification would encode. (Updated on
 CC 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 5750 BP; 1367 A; 1479 C; 1536 G; 1367 T; 0 U; 1 Other;
 Query Match 100.0%; Score 63; DB 2; Length 5750;
 Best Local Similarity 100.0%; Pred. No. 3.5e-14;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTAAGTCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGGCAC 60
 Db 542 TTTAAGTCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGGCAC 601
 QY 61 CTC 63
 Db 602 CTC 604
 RESULT 26
 ID AAQ43813
 AC AAQ43813;
 XX
 XX 25-MAR-2003 (revised)
 DT 20-OCT-1993 (first entry)
 XX
 XX pRLD2D3D4 construct.
 DE

XX
 KW Epidermal growth factor receptor truncate protein; EGF; binding sites;
 KW adsorptive agents; mammalian cell growth abnormality; detection; growth;
 KW reproduction; signal transmission; ds.
 XX
 OS Synthetic.
 XX
 XX
 FH Key Location/Qualifiers
 FT CDS 665..2193
 FT /*tag= a
 FT /codon= 707-708 CG encodes Ile
 FT /note= "encodes LD2D3D4"
 FT misc_feature 1519..1521
 FT /*tag= b
 FT /note= "codon ARA encodes Ile"
 XX
 PN US5218090-A.
 XX
 PD 08-JUN-1993.
 XX
 PF 26-OCT-1990; 90US-00604728.
 XX
 PR 12-JUN-1990; 90US-00536896.
 XX
 PA (WARN) WARNER LAMBERT CO.
 XX
 PI Connors RW;
 XX
 DR WPI; 1993-196297/24.
 DR P-PSDB; AAR38210.
 XX
 PT New epidermal growth factor receptor truncate proteins - which bind
 PT ligands of EGF receptor without transmitting signal for growth or
 PT reproduction.
 XX
 PS Disclosure; Fig 6; 42pp; English.
 CC The sequence is that of the pRLD2D3D4 construct which encodes the
 CC epidermal growth factor (EGF) receptor truncate protein LD2D3D4 having
 CC EGF binding sites. The protein binds ligands of the EGF receptor without
 CC transmitting a signal for the growth and reproduction of a cell. It can
 CC be used as an adsorptive agent for any moieties that bind the EGF
 CC receptor as the portal of entry to a cell. It competes with the EGF
 CC receptor present on the cell surface for the binding of ligands and
 CC thereby inhibits the action of the ligands or prevents the entry of
 CC viruses into cells. It can also be used as for the EGF receptor itself,
 CC such as in the detection of abnormalities in mammalian cell growth. It is
 CC also useful for prepreg. novel receptors for efficient detection of ligands
 CC and their anti-agonists or agonists. The features table indicates the
 CC discrepancies between the LD2D3D4 protein sequence given in the
 CC specification and that which the pRLD2D3D4 DNA sequence given in the
 CC specification would encode. (Updated on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 6207 BP; 1474 A; 1620 C; 1670 G; 1442 T; 0 U; 1 Other;
 Query Match 100.0%; Score 63; DB 2; Length 6207;
 Best Local Similarity 100.0%; Pred. No. 3.6e-14;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTAAGTCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGGCAC 60
 Db 542 TTTAAGTCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGGCAC 601
 QY 61 CTC 63
 Db 602 CTC 604
 RESULT 27
 ID AAQ43812
 AC AAQ43812 standard; DNA; 6274 BP.
 XX
 XX AAQ43812;
 AC

```

XX 25-MAR-2003 (revised)
DT 20-OCT-1993 (first entry)
XX
XX pRLD1D2D3_ApaI construct.
DE
XX Epidermal growth factor receptor truncate protein; EGF; growth;
KW binding sites; adsorptive agents; mammalian cell growth abnormality;
KW detection; reproduction; signal transmission; pRLD1D2D3ApaI; ds.
XX
XX Synthetic.
OS
XX Key Location/Qualifiers
FH 665..2253
FT /*tag= a
FT /codon= 707-708 CG encodes Ile
FT /*note= "encodes LRD1D2D3ApaI"
FT misc_feature 1939..1941
FT /*tag= b
FT /*note= "codon AYA encodes Ile"
XX
XX US5218090-A.
PN
XX
XX 08-JUN-1993.
PD
XX
XX 26-OCT-1990; 90US-00604728.
PF
XX
XX 12-JUN-1990; 90US-00536896.
PR
XX
XX (WARN ) WARNER LAMBERT CO.
PA
XX
XX Connors RW;
PI
XX
XX WPI; 1993-196297/24.
DR
XX P-PSDB; AAR38209.
DR
XX
XX New epidermal growth factor receptor truncate proteins - which bind
PT ligands of EGF receptor without transmitting signal for growth or
PT reproduction.
XX
XX Disclosure; Fig 3; 42pp; English.
XX
XX The sequence is that of the pRLD1D2D3 construct which encodes the
CC epidermal growth factor (EGF) receptor truncate protein LRD1D2D3ApaI,
CC having EGF binding sites. The protein binds ligands of the EGF receptor
CC without transmitting a signal for the growth and reproduction of a cell.
CC It can be used as an adsorptive agent for any moieties that bind the EGF
CC receptor as the portal of entry to a cell. It competes with the EGF
CC receptor present on the cell surface for the binding of ligands and
CC thereby inhibits the action of the ligands or prevents the entry of
CC viruses into cells. It can also be used as for the EGF receptor itself,
CC such as in the detection of abnormalities in mammalian cell growth. It is
CC also useful for prep. novel receptors for efficient detection of ligands
CC and their anti-agonists or agonists. The features table indicates the
CC discrepancies between the LRD1D2D3 protein sequence given in the
CC specification and that which the pRLD1D2D3 DNA sequence given in the
CC specification would encode. (Updated on 25-MAR-2003 to correct PF field.)
XX
XX Sequence 6274 BP; 1506 A; 1610 C; 1664 G; 1493 T; 0 U; 1 Other;
SQ
Query Match 100.0%; Score 63; DB 2; Length 6274;
Best Local Similarity 100.0%; Pred. No. 3.6e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTAAGTCCTAGCTCGATACATTAACGCCATTGACCATTCACCATTTGGTGTGCAC 60
|||||
Db 542 TTTAAGTCCTAGCTCGATACATTAACGCCATTGACCATTCACCATTTGGTGTGCAC 601
|||||

Qy 61 CTC 63
Db 602 CTC 604

```

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RESULT 28
AAAS3869
ID AAAS3869 standard; DNA; 6838 BP.
XX
XX AAAS3869;
AC
XX 03-JAN-2001 (first entry)
DT
XX Expression vector pRIG-1.
DE
XX
XX Vector; endogenous gene; activation; over-expression; erythropoietin;
KW growth hormone; drug discovery; granulocyte colony stimulating factor;
KW ds.
XX
XX Synthetic.
OS
XX WO200049162-A2.
FN
XX 24-AUG-2000.
PD
XX
XX 22-FEB-2000; 2000WO-US004429.
PF
XX
XX 19-FEB-1999; 99US-00253022.
PR
XX 08-MAR-1999; 99US-00263814.
PR
XX 26-MAR-1999; 99US-00276820.
XX
XX (ATHE-) ATHERSYS INC.
XX
XX Harrington JU, Sherf B, Rundlett S;
PI
XX
XX WPI; 2000-549276/50.
DR
XX
XX Non-targeted activation of endogenous genes, e.g. for the production of
PT erythropoietin, growth hormone or granulocyte-colony stimulating factor
PT proteins and for drug discovery.
XX
XX Example 1; Fig 14; 240pp; English.
XX
XX New methods, vectors and cells are described for non-targeted activation
CC and over-expression of endogenous genes. The vector constructs comprise
CC transcriptional regulatory sequences (TRS) and unpaired splice donor
CC sequences (USDS), preferably the vectors comprise (in sequential order) a
CC TRS, an USDS, a rare cutting restriction site (RCRS) and a linearization
CC site (LS) with a second TRS linked to a selectable marker (SM) lacking a
CC polyadenylation signal. The methods, vectors and cells comprising the
CC vectors may be used for the non-targeted activation and over-expression
CC of endogenous genes, e.g. for the production of proteins (including
CC erythropoietin, growth hormone or granulocyte-colony stimulating factor)
CC and drug discovery. The advantage of these methods are that endogenous
CC genes including those associated with human disease and development, may
CC be activated and isolated without prior knowledge of the sequence
CC structure, function or expression profile of the genes being known
XX
XX Sequence 6838 BP; 1679 A; 1669 C; 1709 G; 1781 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 63; DB 3; Length 6838;
Best Local Similarity 100.0%; Pred. No. 3.7e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTAAGTCCTAGCTCGATACATTAACGCCATTGACCATTCACCATTTGGTGTGCAC 60
|||||
Db 1761 TTTAAGTCCTAGCTCGATACATTAACGCCATTGACCATTCACCATTTGGTGTGCAC 1820
|||||

Qy 61 CTC 63
Db 1821 CTC 1823

```

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RESULT 29
AAT12662
ID AAT12662 standard; cDNA; 6926 BP.
XX
XX AAT12662;
AC

```

XX 09-MAY-1996 (first entry)
 XX
 XX IL-4.Y124D/IgG1 fusion DNA in vector pDB951.
 DE
 XX Interleukin-4; interleukin-13; antagonist; IL-4; IL-13; immunoglobulin;
 KW IgG; constant domain; allergy; autoimmune disease; chronic infection;
 KW IL4.Y124D/IgG1; fusion protein; therapy; vector; COSFclink; pDB951; ss.
 XX
 OS Synthetic.
 XX
 XX WO9604388-A1.
 PN
 XX 15-FEB-1996.
 XX
 XX 28-JUL-1995; 95WO-EP003036.
 PF
 XX 29-JUL-1994; 94GB-00015379.
 PR
 XX 06-JUN-1995; 95US-00468297.
 PR
 XX (SMIK) SMITHKLINE BEECHAM PLC.
 PA
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA
 XX Browne MJ, Murphy KB, Chapman CG, Clinkenbeard HE, Young PR;
 PI Shatzman AB;
 PI
 XX WPI; 1996-129404/13.
 DR
 XX
 XX New soluble protein antagonists of interleukin-4 and interleukin-13 -
 PT comprise IL-4 mutant fused to Ig constant domain, useful in treating e.g.
 PT allergy, autoimmune disease or chronic infection.
 PT
 XX Example 1; Page 23-25; 35pp; English.
 PS
 XX Vector plasmid pDB951 (AA12662) is derived from the COSFclink vector
 CC (AA12661) and contains a fusion gene (AA12658) coding for a human
 CC interleukin-4(Y124D) mutant-human IgG4 constant region fusion protein
 CC (AA790920). HeLa cells transfected by the vector produce soluble fusion
 CC protein showing IL-4 antagonist activity
 CC
 XX Sequence 6926 BP; 1890 A; 1698 C; 1679 G; 1659 T; 0 U; 0 Other;
 SQ
 Query Match 100.0%; Score 63; DB 2; Length 6926;
 Best Local Similarity 100.0%; Pred. No. 3.7e-14;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTAAGTCCTAGCTCGATACATAAAGCCATTTCACCATTCACCATTCGTTGTGCAC 60
 Db 709 TTTAAGTCCTAGCTCGATACATAAAGCCATTTCACCATTCACCATTCGTTGTGCAC 768
 QY 61 CTC 63
 Db 769 CTC 771
 RESULT 30
 ADD35600/c
 ID ADD35600 standard; DNA; 7086 BP.
 XX
 AC ADD35600;
 XX
 XX 15-JAN-2004 (first entry)
 DT
 XX Tricistronic eukaryotic expression vector PL249.
 DE
 XX Multicistronic eukaryotic expression vector; multiple protein expression;
 KW simultaneous expression; viral internal ribosomal entry site; viral IRES;
 KW chain terminator; transcription pause site; gene transfer;
 KW DNA immunisation; gene therapy; PL190; kanamycin resistance gene;
 KW cytomegalovirus; CMV promoter/enhancer; CMV intron A;
 KW encephalomyocarditis virus; EMCV IRES; SV40 polyadenylation site;
 KW Rous sarcoma virus; RSV promoter; rabbit beta-globin intron;
 KW MRGS terminator; cyclic; circular; ds.

XX Chimeric.
 OS Synthetic.
 OS Human herpesvirus 5.
 OS Encephalomyocarditis virus.
 OS Simian virus 40.
 OS Rous sarcoma virus.
 OS Oryctolagus cuniculus.
 OS Escherichia coli.
 XX
 PN WO2003031630-A1.
 XX
 XX 17-APR-2003.
 PD
 XX 10-OCT-2002; 2002WO-IT000646.
 PF
 XX 12-OCT-2001; 2001IT-MI002110.
 PR
 XX (KERY-) KERYOS SPA.
 XX
 XX Fazio V, Rinaldi M, Sonzogni L, Tonon G, Orsini G;
 PI WPI; 2003-393446/37.
 DR
 XX New multicistronic recombinant plasmid vectors expressing two to our
 PT genes simultaneously, useful in various biotechnological applications,
 PT such as gene transfer, gene therapy and in DNA immunization.
 PT
 XX Claim 18; SEQ ID NO 3; 52pp; English.
 PS
 XX The invention relates to multicistronic eukaryotic expression vectors for
 CC the expression of at least two proteins of interest which may be
 CC identical or different. The vectors comprise at least one eukaryotic
 CC expression cassette having a promoter/enhancer sequence, an intron
 CC sequence, a cloning site, a viral internal ribosomal entry site (IRES)
 CC and a chain terminator. The vectors may additionally contain a
 CC transcription pause site downstream of the chain terminator. The
 CC invention also encompasses eukaryotic host cells comprising a vector of
 CC the invention, and the recombinant expression of two or more eukaryotic
 CC proteins using host cells transformed with a vector of the invention.
 CC The vectors are useful in various biotechnological applications in which
 CC the simultaneous expression of two or more genes is necessary, such as
 CC gene transfer protocols, DNA immunisation, or for the expression of
 CC different molecules in the same cell. They may also be used in gene
 CC therapy. The present sequence represents a specifically claimed vector
 CC designated PL249, which comprises a cytomegalovirus (CMV)
 CC promoter/enhancer, CMV intron A, the encephalomyocarditis virus (EMCV)
 CC IRES, an SV40 polyadenylation site, a transcription pause site, a Rous
 CC sarcoma virus (RSV) promoter, rabbit beta-globin intron, and a rabbit
 CC beta-globin gene MRGS terminator as well as a kanamycin resistance gene.
 XX
 SQ Sequence 7086 BP; 1870 A; 1699 C; 1753 G; 1764 T; 0 U; 0 Other;
 Query Match 100.0%; Score 63; DB 9; Length 7086;
 Best Local Similarity 100.0%; Pred. No. 3.7e-14;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTAAGTCCTAGCTCGATACATAAAGCCATTTCACCATTCACCATTCGTTGTGCAC 60
 Db 1595 TTTAAGTCCTAGCTCGATACATAAAGCCATTTCACCATTCGTTGTGCAC 1536
 QY 61 CTC 63
 Db 1535 CTC 1533
 RESULT 31
 ADD35601/c
 ID ADD35601 standard; DNA; 7334 BP.
 XX
 AC ADD35601;
 XX
 XX 15-JAN-2004 (first entry)
 DT

XX Tetracistronic eukaryotic expression vector PL250.

DE Multicistronic eukaryotic expression vector; multiple protein expression;
 XX simultaneous expression; viral internal ribosomal entry site; viral IRES;
 KW chain terminator; transcription pause site; gene transfer;
 KW DNA immunisation; gene therapy; PL190; kanamycin resistance gene;
 KW cytomegalovirus; CMV promoter/enhancer; CMV intron A;
 KW encephalomyocarditis virus; EMCV IRES; SV40 polyadenylation site;
 KW Rous sarcoma virus; RSV promoter; rabbit beta-globin intron;
 KW hepatitis C virus; HCV IRES; MRGB terminator; cyclic; circular; ds.
 XX
 OS Chimeric.
 OS Synthetic.
 OS Human herpesvirus 5.
 OS Encephalomyocarditis virus.
 OS Simian virus 40.
 OS Rous sarcoma virus.
 OS Oryctolagus cuniculus.
 OS Hepatitis C virus.
 OS Escherichia coli.
 XX WO2003031630-A1.
 XX
 XX 17-APR-2003.
 XX
 XX 10-OCT-2002; 2002WO-IT000646.
 XX
 XX 12-OCT-2001; 2001IT-MI002110.
 XX (KERY-) KERYOS SPA.
 XX
 XX Fazio V, Rinaldi M, Sonzogni L, Tonon G, Orsini G;
 XX WPI; 2003-393446/37.
 DR
 XX
 XX New multicistronic recombinant plasmid vectors expressing two to our
 PT genes simultaneously, useful in various biotechnological applications,
 PT such as gene transfer, gene therapy and in DNA immunization.
 XX
 XX Claim 18; SEQ ID NO 4; 52pp; English.

XX The invention relates to multicistronic eukaryotic expression vectors for
 CC the expression of at least two proteins of interest which may be
 CC identical or different. The vectors comprise at least one eukaryotic
 CC expression cassette having a promoter/enhancer sequence, an intron
 CC sequence, a cloning site, a viral internal ribosomal entry site (IRES)
 CC and a chain terminator. The vectors may additionally contain a
 CC transcription pause site downstream of the chain terminator. The
 CC invention also encompasses eukaryotic host cells comprising a vector of
 CC the invention, and the recombinant expression of two or more eukaryotic
 CC proteins using host cells transformed with a vector of the invention.
 CC The vectors are useful in various biotechnological applications in which
 CC the simultaneous expression of two or more genes is necessary, such as
 CC gene transfer protocols, DNA immunisation, or for the expression of
 CC different molecules in the same cell. They may also be used in gene
 CC therapy. The present sequence represents a specifically claimed vector
 CC designated PL250, which comprises a cytomegalovirus (CMV)
 CC promoter/enhancer, CMV intron A, the encephalomyocarditis virus (EMCV)
 CC IRES, an SV40 polyadenylation site, a transcription pause site, a Rous
 CC sarcoma virus (RSV) promoter, rabbit beta-globin intron, the hepatitis C
 CC virus (HCV) IRES, and a rabbit beta-globin gene MRGB terminator as well
 CC as a kanamycin resistance gene.

XX
 SQ Sequence 7334 BP; 1922 A; 1775 C; 1825 G; 1812 T; 0 U; 0 Other;

Query Match 100.0%; Score 63; DB 9; Length 7334;
 Best Local Similarity 100.0%; Pred. No. 3.7e-14;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACATAAAGCCGATTCACCATTCACCATTTGGTGGAC 60
 |||||
 DB 1839 TTTAAGTCCTAGCTCGATACATAAAGCCGATTCACCATTCACCATTTGGTGGAC 1780

QY 61 CTC 63
 ||||
 DB 1779 CTC 1777

RESULT 32
 AAZ45929
 ID AAZ45929 standard; DNA; 7492 BP.
 XX AC AAZ45929;
 XX
 DT 25-APR-2000 (first entry)
 XX
 DE Nucleotide sequence of the vector p43C-AT-IN.
 XX
 KW Viral vector; p43C-AT-IN; alpha-1-antitrypsin; gene therapy; diabetes;
 KW alpha-1-antitrypsin deficiency; haemophilia; neurological disorder;
 KW adenosine deaminase deficiency; autoimmune disease; interleukin-2;
 KW immunodeficiency disease; infection; cytokine; circular; cancer; ss.
 XX
 OS Synthetic.
 OS Adeno-associated virus.
 OS Homo sapiens.
 XX
 XX WO9955564-A1.
 XX
 XX 04-NOV-1999.
 XX
 XX 23-APR-1999; 99WO-US008921.
 XX
 XX 24-APR-1998; 98US-0083025P.
 XX
 XX (UYFL) UNIV FLORIDA.
 XX
 XX Flotte TR, Song S, Byrnes BJ, Morgan M;
 WPI; 2000-147020/13.
 XX
 XX Recombinant viral vector useful in the gene therapy of alpha-1-
 PT antitrypsin deficiency and also in hemophilia and diabetes.
 XX
 XX Claim 32; Fig 19A-C; 85pp; English.

XX The present sequence represents a recombinant viral vector, designated
 CC p43C-AT-IN, which encodes human alpha-1-antitrypsin protein, and which is
 CC derived from vector p43C-AT by insertion of intron II sequence of the
 CC human alpha-1-antitrypsin gene into the human alpha-1-antitrypsin cDNA.
 CC The vector is exemplary of the vectors of the invention which comprise a
 CC polynucleotide encoding a protein, and are used for gene therapy to
 CC correct genetic disorders related to expression of a protein of interest.
 CC The vectors of the invention are based on Adeno associated virus (AAV).
 CC The vectors comprise AAV inverted terminal repeats and constitutive or
 CC regulatable promoters for driving high levels of gene expression. Vectors
 CC encoding alpha-1-antitrypsin protein or a biologically active fragment or
 CC variant are administered to mammalian cells (preferably myofibers, or
 CC myoblasts, hepatocytes or lung cells) for treating alpha-1-antitrypsin
 CC deficiency or ameliorating a condition resulting from a defective
 CC protein. The vectors can also be useful for genetic therapy of other
 CC conditions such as hemophilia, adenosine deaminase deficiency, diabetes,
 CC cancer, autoimmune diseases, neurological disorders, immunodeficiency
 CC diseases and bacterial or viral infections by the infusion of protein or
 CC a cytokine such as interleukin-2

XX
 SQ Sequence 7492 BP; 1920 A; 1904 C; 1825 G; 1843 T; 0 U; 0 Other;

Query Match 100.0%; Score 63; DB 3; Length 7492;
 Best Local Similarity 100.0%; Pred. No. 3.8e-14;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACATAAAGCCGATTCACCATTCACCATTTGGTGGAC 60
 |||||
 DB 27 TTTAAGTCCTAGCTCGATACATAAAGCCGATTCACCATTCACCATTTGGTGGAC 86

QY 61 CTC 63
 DB 87 CTC 89

RESULT 33
 AAA59078
 ID AAA59078 standard; DNA; 8238 BP.
 XX
 AC AAA59078;
 XX
 DT 07-NOV-2000 (first entry)
 XX
 DE Nucleotide sequence of a plasmid.
 XX
 KW Adenovirus; tripartite leader; adenovirus vector particle; gene delivery;
 KW ss.
 XX
 OS Synthetic.
 XX
 PN WO200042208-A1.
 XX
 PD 20-JUL-2000.
 XX
 PF 14-JAN-2000; 2000WO-EP000265.
 XX
 PR 14-JAN-1999; 99US-0115920P.
 XX
 PA (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GRS MEH.
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Nemerow GR, Von Seggern DJ, Hallenbeck PL, Stevenson SC;
 PI Skripchenko Y;
 PI
 PI WPI; 2000-476068/41.
 DR
 XX
 PT New nucleic acid comprising an adenovirus tripartite leader nucleotide
 PT for producing high-capacity and targeted vectors for adenovirus-based
 PT gene therapy.
 XX
 PS Disclosure; Page 195-198; 212pp; English.
 XX
 CC The specification describes a nucleic acid molecule comprising an
 CC adenovirus (AV) tripartite leader (TPL) nucleotide with a sequence
 CC comprising two different TPL exons or three same or different TPL exons.
 CC The nucleic acid is used to produce an adenovirus vector particle,
 CC deliver an exogenous gene to a target cell, pseudotype recombinant viral
 CC vectors, target an adenovirus vector to a cell, produce a modified
 CC adenovirus, deliver a heterologous gene to an animal and produce a
 CC gutless adenoviral vector particle. The present sequence represents a
 CC plasmid, which is used in the course of the invention
 XX
 SQ Sequence 8238 BP; 1762 A; 2156 C; 2340 G; 1980 T; 0 U; 0 Other;
 Query Match 100.0%; Score 63; DB 3; Length 8238;
 Best Local Similarity 100.0%; Pred. No. 3.8e-14;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTAAGTCCTAGCTCGATACAAATAAGCGCATTTGACCATTCACCACTGTTGTGCAC 60
 DB 742 TTTAAGTCCTAGCTCGATACAAATAAGCGCATTTGACCATTCACCACTGTTGTGCAC 801
 QY 61 CTC 63
 DB 802 CTC 804

RESULT 34
 AAT84562
 ID AAT84562 standard; cDNA; 8591 BP.
 XX

AC AAT84562;
 XX
 DT 25-MAR-2003 (revised)
 DT 15-DEC-1997 (first entry)
 XX
 DE Plasmid pCLL621 encoding amyloid precursor protein APP-REP 751.
 XX
 KW Amyloid precursor protein; APP; beta-amyloid protein; BAP; substrate;
 KW mucin; secretase; Alzheimer's disease; human; APP-REP 751; pCLL621; ds;
 KW cyclic.
 XX
 OS Homo; sapiens.
 OS Synthetic.
 OS Chimeric.
 XX
 PH Key Location/Qualifiers
 FT CDS 2393..3856
 FT /*tag= a
 XX
 PN US5652092-A.
 XX
 PD 29-JUL-1997.
 XX
 PF 05-JUN-1995; 95US-00462859.
 XX
 PR 01-MAY-1992; 92US-00877675.
 PR 20-SEP-1993; 93US-00123659.
 XX
 PA (AMCY) AMERICAN CYANAMID CO.
 XX
 PI Jacobsen JS, Vitek MP;
 XX
 DR WPI; 1997-392937/36.
 DR P-PSDB; AAW26394.
 XX
 PT Screening for compounds which reduce beta-amyloid protein formation -
 PT using cells which express a construct encoding a marker and an amyloid
 PT precursor mutain derived from APP isoforms.
 XX
 PS Disclosure; Fig 8; 84pp; English.
 XX
 CC Plasmid pCLL621 (AAT84562), desposited in E. coli as ATCC 69406, codes
 CC for an amyloid precursor protein (APP) substrate, designated APP-REP 751
 CC (see AAW26394), that has a 276-amino acid deletion of the native APP and
 CC carries a Substance P epitope marker on the N-terminal side of the beta-
 CC amyloid protein (BAP) domain. APP-REP 751 can be used in a claimed method
 CC for screening for a compound which reduces the formation of beta-amyloid
 CC protein, determined by measuring the amount of marker in a medium
 CC containing transfected cells. The method is used to detect compounds
 CC which inhibit the activity of proteolytic enzymes which cleave APP to
 CC generate BAP fragments. Such compounds can be used in the treatment of
 CC e.g. Alzheimer's disease. The deletion of a 276 amino acid portion of APP
 CC distinguishes the construct from endogenously expressed APP, and
 CC beneficially increases the resolution of APP-REP fragments resulting from
 CC the proteolytic cleavage by secretase or other amyloidogenic, BAP-
 CC generating cleavage events. (Updated on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 8591 BP; 2225 A; 2038 C; 2247 G; 2081 T; 0 U; 0 Other;
 Query Match 100.0%; Score 63; DB 2; Length 8591;
 Best Local Similarity 100.0%; Pred. No. 3.9e-14;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTAAGTCCTAGCTCGATACAAATAAGCGCATTTGACCATTCACCACTGTTGTGCAC 60
 DB 5177 TTTAAGTCCTAGCTCGATACAAATAAGCGCATTTGACCATTCACCACTGTTGTGCAC 5236
 QY 61 CTC 63
 DB 5237 CTC 5239

RESULT 35

AT84561
ID AAT84561 standard; cDNA; 8591 BP.
XX
AC AAT84561;
XX
DT 25-MAR-2003 (revised)
DT 15-DEC-1997 (first entry)
XX
DE Plasmid pCLL602 encoding amyloid precursor protein APP-REP 751.
XX
XX Amyloid precursor protein; APP; beta-amyloid protein; BAP; substrate;
KW muten; secretase; Alzheimer's disease; human; APP-REP 751; pCLL602; ds;
KW cyclic.
XX
XX Homo sapiens.
OS Synthetic.
OS Chimeric.
XX
XX Key Location/Qualifiers
FH CDS 2393..3871
FT /*tag= a
FT
XX
XX US5652092-A.
FN
XX 29-JUL-1997.
PD
XX 05-JUN-1995; 95US-00462859.
XX
XX 01-MAY-1992; 92US-00877675.
PR 20-SEP-1993; 93US-00123659.
XX
XX (AMCY) AMERICAN CYANAMID CO.
PA
XX Jacobeen JS, Vitek MP;
PI
XX WPI; 1997-392937/36.
DR P-PSDB; AAW26393.
XX
XX Screening for compounds which reduce beta-amyloid protein formation -
PT using cells which express a construct encoding a marker and an amyloid
PT precursor muten derived from APP isoforms.
XX
XX Disclosure; Fig 7; 84pp; English.
XX
XX Plasmid pCLL602 (AAT84561), deposited in E. coli as ATCC 69405, codes
CC for an amyloid precursor protein (APP) substrate, designated APP-REP 751
CC (see AAW26393), that has a 276-amino acid deletion of the native APP and
CC carries Substance P and Met-enkephalin epitope markers placed,
CC respectively, on the N-terminal and C-terminal sites of the beta-amyloid
CC protein (BAP) domain. APP-REP 751 can be used in a claimed method for
CC screening for a compound which reduces the formation of beta-amyloid
CC protein, determined by measuring the amount of marker in a medium
CC containing transfected cells. The method is used to detect compounds
CC which inhibit the activity of proteolytic enzymes which cleave APP to
CC generate BAP fragments. Such compounds can be used in the treatment of
CC e.g. Alzheimer's disease. The deletion of a 276 amino acid portion of APP
CC distinguishes the construct from endogenously expressed APP, and
CC beneficially increases the resolution of APP-REP fragments resulting from
CC the proteolytic cleavage by secretase or other amyloidogenic, BAP-
XX generating cleavage events. (Updated on 25-MAR-2003 to correct PF field.)
SQ Sequence 8591 BP; 2225 A; 2038 C; 2247 G; 2081 T; 0 U; 0 Other;
Query Match 100.0%; Score 63; DB 2; Length 8591;
Best Local Similarity 100.0%; Pred. No. 3.9e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTAAGTGCTAGCTCGATCAATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
Db 5177 TTTAAGTGCTAGCTCGATCAATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 5236
QY 61 CTC 63
|||

Db 5237 CTC 5239
RESULT 36
AAT87083
ID AAT87083 standard; cDNA; 8591 BP.
XX
AC AAT87083;
XX
DT 25-MAR-2003 (revised)
DT 06-JAN-1998 (first entry)
XX
DE Plasmid pCLL602 encoding amyloid precursor protein APP-REP 751.
XX
XX Amyloid precursor protein; APP; beta-amyloid protein; BAP; substrate;
KW muten; secretase; Alzheimer's disease; human; APP-REP 751; pCLL602; ds;
KW cyclic.
XX
XX Homo sapiens.
OS Synthetic.
OS Chimeric.
XX
XX Key Location/Qualifiers
FH CDS 2393..3871
FT /*tag= a
FT
XX
XX US5656477-A.
FN
XX 12-AUG-1997.
PD
XX 20-SEP-1993; 93US-00123659.
PR 01-MAY-1992; 92US-00877675.
XX
XX (AMCY) AMERICAN CYANAMID CO.
PA
XX Jacobeen JS, Vitek MP;
PI
XX WPI; 1997-414594/38.
DR P-PSDB; AAW26509.
XX
XX Nucleic acid encoding amyloid precursor muten(s) - comprising reporter
PT gene and coding sequence, for identifying compounds which modify the
PT activity of proteolytic enzymes which cleave APP.
XX
XX Disclosure; Fig 7; 84pp; English.
XX
XX Plasmid pCLL602 (AAT87083), deposited in E. coli as ATCC 69405, codes
CC for an amyloid precursor protein (APP) substrate, designated APP-REP 751
CC (see AAW26509), that has a 276-amino acid deletion of the native APP and
CC carries Substance P and Met-enkephalin epitope markers placed,
CC respectively, on the N-terminal and C-terminal sites of the beta-amyloid
CC protein (BAP) domain. APP-REP 751 can be used in a claimed method for
CC screening for a compound which reduces the formation of beta-amyloid
CC protein, determined by measuring the amount of marker in a medium
CC containing transfected cells. The method is used to detect compounds
CC which inhibit the activity of proteolytic enzymes which cleave APP to
CC generate BAP fragments. Such compounds can be used in the treatment of
CC e.g. Alzheimer's disease. The deletion of a 276 amino acid portion of APP
CC distinguishes the construct from endogenously expressed APP, and
CC beneficially increases the resolution of APP-REP fragments resulting from
CC the proteolytic cleavage by secretase or other amyloidogenic, BAP-
XX generating cleavage events. (Updated on 25-MAR-2003 to correct PF field.)
SQ Sequence 8591 BP; 2225 A; 2038 C; 2247 G; 2081 T; 0 U; 0 Other;
Query Match 100.0%; Score 63; DB 2; Length 8591;
Best Local Similarity 100.0%; Pred. No. 3.9e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTAAGTGCTAGCTCGATCAATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
Db 5177 TTTAAGTGCTAGCTCGATCAATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 5236
QY 61 CTC 63
|||

QY 61 CTC 63
DB 5237 CTC 5239

RESULT 37
AAT87084
ID AAT87084 standard; cDNA; 8591 BP.
XX AC AAT87084;
XX 25-MAR-2003 (revised)
DT 06-JAN-1998 (first entry)
XX Plasmid pCLL621 encoding amyloid precursor protein APP-REP 751.
DE
XX Amyloid precursor protein; APP; beta-amyloid protein; BAP; substrate;
KW mutin; secretase; Alzheimer's disease; human; APP-REP 751; pCLL621; ds;
KW cyclic.
XX Homo sapiens.
OS Synthetic.
OS Chimeric.
XX
XX Key Location/Qualifiers
FH Key 2393..3856
FT CDS /*tag= a
FT
XX US5656477-A.
XX
XX 12-AUG-1997.
XX
XX 20-SEP-1993; 93US-00123659.
XX
XX 01-MAY-1992; 92US-00877675.
XX (AMCY) AMERICAN CYANAMID CO.
XX
XX Jacobsen JS, Vitek MP;
XX WPI; 1997-414594/38.
DR P-PSDB; AAW26510.
XX
XX Nucleic acid encoding amyloid precursor mutin(s) - comprising reporter
PT gene and coding sequence, for identifying compounds which modify the
PT activity of proteolytic enzymes which cleave APP.
XX
XX Disclosure; Fig 8; 84pp; English.
XX
XX Plasmid pCLL621 (AAT87084), deposited in E. coli as ATCC 69406, codes
CC for an amyloid precursor protein (APP) substrate, designated APP-REP 751
CC (see AAW26510) that has a 276-amino acid deletion of the native APP and
CC carries a Substance P epitope marker on the N-terminal side of the beta-
CC amyloid protein (BAP) domain. APP-REP 751 can be used in a claimed method
CC for screening for a compound which reduces the formation of beta-amyloid
CC protein, determined by measuring the amount of marker in a medium
CC containing transfected cells. The method is used to detect compounds
CC which inhibit the activity of proteolytic enzymes which cleave APP to
CC generate BAP fragments. Such compounds can be used in the treatment of
CC e.g. Alzheimer's disease. The deletion of a 276 amino acid portion of APP
CC distinguishes the construct from endogenously expressed APP, and
CC beneficially increases the resolution of APP-REP fragments resulting from
CC the proteolytic cleavage by secretase or other amyloidogenic, BAP-
CC generating cleavage events. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 8591 BP; 2225 A; 2038 C; 2247 G; 2081 T; 0 U; 0 Other;
Query Match 100.0%; Score 63; DB 2; Length 8591;
Best Local Similarity 100.0%; Pred. No. 3.9e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTAAGTCCTAGCTGATACATTAACGCCATTGACCATTCACACATTGGTGTGCAC 5236

DB 5177 TTTAAGTCCTAGCTGATACATTAACGCCATTGACCATTCACACATTGGTGTGCAC 5236
QY 61 CTC 63
DB 5237 CTC 5239

RESULT 38
AAV04866
ID AAV04866 standard; DNA; 8591 BP.
XX
XX AAV04866;
XX
XX 01-MAY-1998 (first entry)
XX cDNA encoding amyloid precursor protein mutant APP-ARP 751.
DE
XX Beta-amyloid peptide; BAP; extracellular BAP plaque;
KW cerebrovascular deposit; Alzheimers disease; Downs syndrome;
KW amyloid precursor protein; APP; secretase; BAP aggregation;
KW abnormal proteolytic cleavage; ds.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Key 2393..3856
FT CDS /*tag= a
FT
XX US5703209-A.
XX
XX 30-DEC-1997.
XX
XX 05-JUN-1995; 95US-00464248.
XX
XX 01-MAY-1992; 92US-00877675.
XX 20-SEP-1993; 93US-00123659.
XX (AMCY) AMERICAN CYANAMID CO.
XX
XX Jacobsen JS, Vitek MP;
XX WPI; 1998-076482/07.
DR P-PSDB; AAW42979.
XX
XX Amyloid precursor protein fusion polypeptides - comprising APP fragment
PT and marker, useful for research and drug screening.
XX
XX Disclosure; Fig 8A-Q; 84pp; English.
XX
XX The present sequence encodes an amyloid precursor protein (APP), which
CC has a deletion of 276 amino acids to within 15 amino acids of the beta-
CC amyloid peptide (BAP) domain. The protein also contains the Abnormal
CC accumulation of extracellular BAP in plaques and cerebrovascular deposits
CC is characteristic in brains of individuals suffering from Alzheimers
CC disease and Downs syndrome. BAP is a poorly soluble, self-aggregating
CC protein which is derived from a larger amyloid precursor protein (APP).
CC APP is expressed as an integral membrane protein, and is cleaved by
CC secretase, between BAP 16lys and 17leu. Cleavage at this site precludes
CC amyloidogenesis and results in the release of the amino-terminal APP
CC fragment. Three major isoforms of APP exist: APP-695, APP-751 and APP-
CC 770. These isoforms are derived by alternative splicing. APP-REP 751 is
CC constructed by ligating restriction fragments representing N- and C-
CC terminal APP-751 cDNA and substrate P reporter epitope sequences. APP
CC can be used as a substrate for studying abnormal proteolytic cleavage
CC which results in the release of BAP, and also to screen for drugs that
CC will inhibit such cleavage
XX
SQ Sequence 8591 BP; 2225 A; 2038 C; 2247 G; 2081 T; 0 U; 0 Other;
Query Match 100.0%; Score 63; DB 2; Length 8591;
Best Local Similarity 100.0%; Pred. No. 3.9e-14;
Query Match 100.0%; Score 63; DB 2; Length 8591;
Best Local Similarity 100.0%; Pred. No. 3.9e-14;

Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCCATTTGACCATTCACCATTTGGTGGCAC 60
 |||||
 Db 5177 TTTAAGTGGCTAGCTCGATACATAAAGCCCATTTGACCATTCACCATTTGGTGGCAC 5236

QY 61 CTC 63
 |||||

Db 5237 CTC 5239

RESULT 39
 AAV04865
 ID AAV04865 standard; DNA; 8591 BP.
 XX
 AC AAV04865;
 XX
 XX 01-MAY-1998 (first entry)
 XX cDNA encoding amyloid precursor protein mutant APP-APP 751.
 XX
 XX Beta-amyloid peptide; BAP; extracellular BAP plaque;
 KW cerebrovascular deposit; Alzheimer's disease; Downs syndrome;
 KW amyloid precursor protein; APP; secretase; BAP aggregation;
 KW abnormal proteolytic cleavage; ds.
 XX
 XX Homo sapiens.
 OS
 OS Key Location/Qualifiers
 FH 2393..3871
 FT /*tag= a
 FT CDS
 PN US5703209-A.
 XX
 XX 30-DEC-1997.
 PD
 XX
 XX 05-JUN-1995; 95US-00464248.
 XX
 XX 01-MAY-1992; 92US-00877675.
 PR 20-SEP-1993; 93US-00123659.
 XX
 XX (AMCY) AMERICAN CYANAMID CO.
 PA
 XX
 XX Jacobsen JS, Vitek MP;
 DR WPI; 1998-076482/07.
 DR P-PSDB; AAW42978.
 XX
 XX Amyloid precursor protein fusion polypeptides - comprising APP fragment
 PT and marker, useful for research and drug screening.
 PT
 XX
 XX Disclosure; Fig 7A-Q; 84pp; English.
 XX
 XX The present sequence encodes an amyloid precursor protein (APP), which
 CC has a deletion of 276 amino acids to within 15 amino acids of the beta-
 CC amyloid peptide (BAP) domain. The protein also contains the Met-
 CC enkephalin reporter epitope at the carboxy terminus. Abnormal
 CC accumulation of extracellular BAP in plaques and cerebrovascular deposits
 CC is characteristic in brains of individuals suffering from Alzheimer's
 CC disease and Downs syndrome. BAP is a poorly soluble, self-aggregating
 CC protein which is derived from a larger amyloid precursor protein (APP).
 CC APP is expressed as an integral membrane protein, and is cleaved by
 CC secretase, between BAP 16lys and 17leu. Cleavage at this site precludes
 CC amyloidogenesis and results in the release of the amino-terminal APP
 CC fragment. Three major isoforms of APP exist: APP-695, APP-751 and APP-
 CC 770. These isoforms are derived by alternative splicing. APP-RP 751 is
 CC constructed by ligating restriction fragments representing N- and C-
 CC terminal APP-751 cDNA and substrate P reporter epitope sequences. APP
 CC can be used as a substrate for studying abnormal proteolytic cleavage
 CC which results in the release of BAP, and also to screen for drugs that
 CC will inhibit such cleavage
 XX
 SQ Sequence 8591 BP; 2225 A; 2038 C; 2247 G; 2081 T; 0 U; 0 Other;

Query Match 100.0%; Score 63; DB 2; Length 8591;
 Best Local Similarity 100.0%; Pred. No. 3.9e-14; Indels 0; Gaps 0;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCCATTTGACCATTCACCATTTGGTGGCAC 60
 |||||
 Db 5177 TTTAAGTGGCTAGCTCGATACATAAAGCCCATTTGACCATTCACCATTTGGTGGCAC 5236

QY 61 CTC 63
 |||||

Db 5237 CTC 5239

RESULT 40
 AAV05850
 ID AAV05850 standard; cDNA; 8591 BP.
 XX
 AC AAV05850;
 XX
 XX 01-JUN-1998 (first entry)
 XX
 XX APP-RP 751 gene from pCLL621.
 XX
 XX Amyloid precursor protein; APP; APP 751 isoform; deletion; substrate P;
 KW epitope; Met-enkephalin; detection; secretase; beta-amyloid protein; BAP;
 KW Alzheimer's disease; cleavage; cyclic; circular; ds.
 XX
 XX Homo sapiens.
 OS
 OS Synthetic.
 FH Key Location/Qualifiers
 FT 2393..3856
 FT /*tag= a
 FT /product= "APP_REP_751"
 FT
 XX
 XX US5693478-A.
 XX
 XX 02-DEC-1997.
 XX
 XX 05-JUN-1995; 95US-00464247.
 XX
 XX 01-MAY-1992; 92US-00877675.
 PR 20-SEP-1993; 93US-00123659.
 XX
 XX (AMCY) AMERICAN CYANAMID CO.
 PA
 XX
 XX Jacobsen JS, Vitek MP;
 XX WPI; 1998-031744/03.
 DR P-PSDB; AAW44745.
 XX
 XX Amyloid precursor mutin reporter molecule assay containing antibody
 PT recognised marker - used to study pathways associated with Alzheimer's
 FT disease.
 XX
 XX Disclosure; Fig 8; 84pp; English.
 XX
 XX This is the nucleotide sequence encoding a novel amyloid precursor
 CC protein (APP) designated APP-RP 751, contained in construct pCLL621. The
 CC sequence encodes a mutant version of the APP 751 isoform of human APP
 CC which contains a deletion of 276 amino acids from the central region. The
 CC deleted region is replaced by a substrate P reporter epitope sequence
 CC (RPRPQQFFFGIM). In contrast to the APP-RP 751 encoded by the construct
 CC pCLL602 (AAV05849), this sequence does not contain a Met-enkephalin
 CC reporter epitope (YGGFM) fused at the C-terminus of the coding sequence.
 CC The shorter protein is generated for ease of detection based on size
 CC difference with the wild type APP protein and also by detection of the
 CC reporter epitopes. The mutant protein can be used in a method to study
 CC secretase and beta-amyloid protein (BAP)-generating pathways associated
 CC with Alzheimer's disease by studying proteolytic cleavage of the reporter
 CC polypeptides
 XX

SQ Sequence 8591 BP; 2225 A; 2038 C; 2248 G; 2080 T; 0 U; 0 Other;

Query Match 100.0%; Score 63; DB 2; Length 8591;
Best Local Similarity 100.0%; Pred. No. 3.9e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCCTAGCTCGATACAAATAAGCGCATTTGACCATTCACCATTCACCATTCGTTGTGCAC 60
DB 5177 TTTAAGTCCCTAGCTCGATACAAATAAGCGCATTTGACCATTCACCATTCACCATTCGTTGTGCAC 5236

QY 61 CTC 63
DB 5237 CTC 5239

RESULT 41
AAV05849 ID AAV05849 standard; cDNA; 8591 BP.
XX AC AAV05849;
XX DT 01-JUN-1998 (first entry)
XX DE APP-REP 751 gene from pCLL602.
XX KW Amyloid precursor protein; APP; APP 751 isoform; deletion; substrate P;
XX KW epitope; Met-enkephalin; detection; secretase; beta-amyloid protein; BAP;
XX KW Alzheimer's disease; cleavage; cyclic; circular; ds.
XX OS Homo sapiens.
XX OS Synthetic.
XX PH Key Location/Qualifiers
XX FT CDS 2393..3871
XX FT /*tag= a
XX FT /*product= "APP-REP_751"
XX PN US5693478-A.
XX PD 02-DEC-1997.
XX PF 05-JUN-1995; 95US-00464247.
XX PR 01-MAY-1992; 92US-00877675.
XX PR 20-SEP-1993; 93US-00123659.
XX PA (ANCY) AMERICAN CYANAMID CO.
XX PI Jacobsen JS, Vitex WP;
XX DR WPI; 1998-031744/03.
XX DR P-PSDB; AAW44744.
XX FT Amyloid precursor muten reporter molecule assay containing antibody
XX FT recognised marker - used to study pathways associated with Alzheimer's
XX FT disease.
XX PS Disclosure; Fig 7; 84pp; English.
XX CC This is the nucleotide sequence encoding a novel amyloid precursor
XX CC protein (APP) designated APP-REP 751, contained in construct pCLL602. The
XX CC sequence encodes a mutant version of the APP 751 isoform of human APP
XX CC which contains a deletion of 276 amino acids from the central region. The
XX CC deleted region is replaced by a substrate P reporter epitope sequence
XX CC (RPKQQQFGLM) and a Met-enkephalin reporter epitope (YGGFM) is fused at
XX CC the C-terminus. The shorter protein is generated for ease of detection
XX CC based on size difference with the wild type APP protein and also by
XX CC detection of the reporter epitopes. The mutant protein can be used in a
XX CC method to study secretase and beta-amyloid protein (BAP)-generating
XX CC pathways associated with Alzheimer's disease by studying proteolytic
XX CC cleavage of the reporter polypeptides
XX SQ Sequence 8591 BP; 2225 A; 2038 C; 2247 G; 2081 T; 0 U; 0 Other;

Query Match 100.0%; Score 63; DB 2; Length 8591;
Best Local Similarity 100.0%; Pred. No. 3.9e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCCTAGCTCGATACAAATAAGCGCATTTGACCATTCACCATTCACCATTCGTTGTGCAC 60
DB 5177 TTTAAGTCCCTAGCTCGATACAAATAAGCGCATTTGACCATTCACCATTCACCATTCGTTGTGCAC 5236

QY 61 CTC 63
DB 5237 CTC 5239

RESULT 42
ABL57333 ID ABL57333 standard; DNA; 8902 BP.
XX AC ABL57333;
XX DT 29-AUG-2003 (revised)
XX DT 09-AUG-2002 (first entry)
XX DE Vector plasmid pRIG-MP1.
XX KW Vector; pRIG-MP1; promoter; ds.
XX KW Cytomegalovirus.
XX OS Escherichia coli.
XX OS Rhesus macaque polyoma virus.
XX OS Rous sarcoma virus.
XX OS Chimeric.
XX PN US2002055172-A1.
XX PD 09-MAY-2002.
XX PF 05-DEC-2000; 2000US-00729416.
XX PR 07-OCT-1999; 99US-00414369.
XX PA (HARR/) HARRINGTON J J.
XX PI Harrington JJ;
XX DR WPI; 2002-425568/45.
XX FT Nucleic acid construct, for producing an expression product, comprises
XX FT two units each with a promoter sequence operably linked to an exon and
XX FT unpaired splice donor site.
XX PS Disclosure; Page 23-27; 43pp; English.
XX CC The present sequence is the nucleotide sequence of vector plasmid pRIG-
XX CC MP1. This plasmid includes 3 promoter/activation exon units, each
XX CC followed by a splice donor sequence, where the promoter is a
XX CC cytomegalovirus promoter and the activation exons do not encode a
XX CC translation start codon. A BamHI site is present downstream of the
XX CC promoter/exon units, and can be used to linearise the vector or to clone
XX CC a gene of interest into the vector. A neomycin-resistance selectable
XX CC marker gene under the control of a rous sarcoma virus is also present, as
XX CC well as a dihydrofolate reductase amplifiable marker under the control of
XX CC an SV40 promoter. A pUC plasmid origin of replication and a beta-
XX CC lactamase antibiotic resistance gene are also contained within pRIG-MP1.
XX CC The invention relates to improved methods for gene expression using
XX CC vectors with multiple promoters. A desired nucleic acid sequence is
XX CC introduced into the vector by conventional cloning or is expressed from
XX CC an endogenous sequence in the genome that is activated by the vector. The
XX CC vectors can be used to express cDNA clones, genomic DNA, chemically
XX CC synthesised nucleic acid molecules, antisense nucleic acids and
XX CC ribozymes, and also to activate endogenous genes in situ by homologous or
XX CC non-homologous recombination. The vectors may be transposon or retroviral
XX CC vectors. They can also be used to modify a gene of interest, and to

CC express a gene as a full-length or truncated protein. (Updated on 29-AUG-2003 to standardise OS field)

XX Sequence 8902 BP; 2182 A; 2185 C; 2172 G; 2363 T; 0 U; 0 Other;

Query Match 100.0%; Score 63; DB 6; Length 8902;

Best Local Similarity 100.0%; Pred. No. 3.9e-14;

Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCCTAGCTCGATACATTAAGCGCCATTGACCATTCACACATTGGTGTGCAC 60

DB 3826 TTTAAGTCCCTAGCTCGATACATTAAGCGCCATTGACCATTCACACATTGGTGTGCAC 3885

QY 61 CTC 63

DB 3886 CTC 3888

RESULT 43

AAA53873

ID AAA53873 standard; DNA; 9725 BP.

XX

AC AAA53873;

XX

DT 03-JAN-2001 (first entry)

XX

DE Expression vector pRIG19.

XX

KW Vector; endogenous gene; activation; over-expression; erythropoietin;

KW growth hormone; drug discovery; granulocyte colony stimulating factor;

KW ds.

XX

OS Synthetic.

XX

PN WO2000049162-A2.

XX

PD 24-AUG-2000.

XX

PF 22-FEB-2000; 2000WO-US004429.

XX

PR 19-FEB-1999; 99US-00253022.

PR 08-MAR-1999; 99US-00263814.

PR 26-MAR-1999; 99US-00276820.

XX

PA (ATHE-) ATHERSYS INC.

XX

PI Harrington JJ, Sherf B, Rundlett S;

XX

DR WPI; 2000-549276/50.

XX

PT Non-targeted activation of endogenous genes, e.g. for the production of erythropoietin, growth hormone or granulocyte-colony stimulating factor proteins and for drug discovery.

XX

PS Disclosure; Fig 30; 240pp; English.

XX

CC New methods, vectors and cells are described for non-targeted activation and over-expression of endogenous genes. The vector constructs comprise transcriptional regulatory sequences (TRS) and unpaired splice donor sequences (USDS), preferably the vectors comprise (in sequential order) a TRS, an USDS, a rare cutting restriction site (RCRS) and a linearization site (LS) with a second TRS linked to a selectable marker (SM) lacking a polyadenylation signal. The methods, vectors and cells comprising the vectors may be used for the non-targeted activation and over-expression of endogenous genes, e.g. for the production of proteins (including erythropoietin, growth hormone or granulocyte-colony stimulating factor) and drug discovery. The advantage of these methods are that endogenous genes including those associated with human disease and development, may be activated and isolated without prior knowledge of the sequence structure, function or expression profile of the genes being known

XX

SQ Sequence 9725 BP; 2425 A; 2507 C; 2448 G; 2343 T; 0 U; 2 Other;

Query Match 100.0%; Score 63; DB 3; Length 9725;

Best Local Similarity 100.0%; Pred. No. 4e-14;

Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCCTAGCTCGATACATTAAGCGCCATTGACCATTCACACATTGGTGTGCAC 60

DB 1610 TTTAAGTCCCTAGCTCGATACATTAAGCGCCATTGACCATTCACACATTGGTGTGCAC 1669

QY 61 CTC 63

DB 1670 CTC 1672

RESULT 44

AAA53879

ID AAA53879 standard; DNA; 9732 BP.

XX

AC AAA53879;

XX

DT 03-JAN-2001 (first entry)

XX

DE Expression vector pRIG-TP.

XX

KW Vector; endogenous gene; activation; over-expression; erythropoietin;

KW growth hormone; drug discovery; granulocyte colony stimulating factor;

KW ds.

XX

OS Synthetic.

XX

PN WO2000049162-A2.

XX

PD 24-AUG-2000.

XX

PF 22-FEB-2000; 2000WO-US004429.

XX

PR 19-FEB-1999; 99US-00253022.

PR 08-MAR-1999; 99US-00263814.

PR 26-MAR-1999; 99US-00276820.

XX

PA (ATHE-) ATHERSYS INC.

XX

PI Harrington JJ, Sherf B, Rundlett S;

XX

DR WPI; 2000-549276/50.

XX

PT Non-targeted activation of endogenous genes, e.g. for the production of erythropoietin, growth hormone or granulocyte-colony stimulating factor proteins and for drug discovery.

XX

PS Example 15; Fig 37; 240pp; English.

XX

CC New methods, vectors and cells are described for non-targeted activation and over-expression of endogenous genes. The vector constructs comprise transcriptional regulatory sequences (TRS) and unpaired splice donor sequences (USDS), preferably the vectors comprise (in sequential order) a TRS, an USDS, a rare cutting restriction site (RCRS) and a linearization site (LS) with a second TRS linked to a selectable marker (SM) lacking a polyadenylation signal. The methods, vectors and cells comprising the vectors may be used for the non-targeted activation and over-expression of endogenous genes, e.g. for the production of proteins (including erythropoietin, growth hormone or granulocyte-colony stimulating factor) and drug discovery. The advantage of these methods are that endogenous genes including those associated with human disease and development, may be activated and isolated without prior knowledge of the sequence structure, function or expression profile of the genes being known

XX

SQ Sequence 9732 BP; 2427 A; 2512 C; 2443 G; 2348 T; 0 U; 2 Other;

Query Match 100.0%; Score 63; DB 3; Length 9732;

Best Local Similarity 100.0%; Pred. No. 4e-14;

Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCCTAGCTCGATACATTAAGCGCCATTGACCATTCACACATTGGTGTGCAC 60

Db 1613 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACACATTGGTGTGCAC 1672
 QY 61 CTC 63
 Db 1673 CTC 1675

RESULT 45
 ID AAA53874 standard; DNA; 9738 BP.
 AC AAA53874;
 DT 03-JAN-2001 (first entry)
 DE Expression vector pRIG20.
 KW Vector; endogenous gene; activation; over-expression; erythropoietin;
 KW growth hormone; drug discovery; granulocyte colony stimulating factor;
 KW ds.
 OS Synthetic.
 PN WO2000049162-A2.
 PD 24-AUG-2000.
 PF 22-FEB-2000; 2000WO-US004429.
 PR 19-FEB-1999; 99US-00253022.
 PR 08-MAR-1999; 99US-00263814.
 PR 26-MAR-1999; 99US-00276820.
 XX (ATHE-) ATHERSYS INC.
 XX Harrington JJ, Sherf B, Rundlett S;
 WPI; 2000-549276/50.
 XX Non-targeted activation of endogenous genes, e.g. for the production of
 erythropoietin, growth hormone or granulocyte-colony stimulating factor
 proteins and for drug discovery.
 XX Disclosure; Fig 31; 240pp; English.
 XX New methods, vectors and cells are described for non-targeted activation
 and over-expression of endogenous genes. The vector constructs comprise
 transcriptional regulatory sequences (TRS) and unpaired splice donor
 sequences (USDS), preferably the vectors comprise (in sequential order) a
 TRS, an USDS, a rare cutting restriction site (RCRS) and a linearization
 site (LS) with a second TRS linked to a selectable marker (SM) lacking a
 polyadenylation signal. The methods, vectors and cells comprising the
 vectors may be used for the non-targeted activation and over-expression
 of endogenous genes, e.g. for the production of proteins (including
 erythropoietin, growth hormone or granulocyte-colony stimulating factor)
 and drug discovery. The advantage of these methods are that endogenous
 genes including those associated with human disease and development, may
 be activated and isolated without prior knowledge of the sequence
 structure, function or expression profile of the genes being known
 XX Sequence 9738 BP; 2428 A; 2514 C; 2447 G; 2347 T; 0 U; 2 Other;
 Query Match 100.0%; Score 63; DB 3; Length 9738;
 Best Local Similarity 100.0%; Pred. No. 4e-14;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACACATTGGTGTGCAC 60
 Db 1613 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACACATTGGTGTGCAC 1672
 QY 61 CTC 63

Db 1673 CTC 1675

RESULT 46
 ID AAA53875 standard; DNA; 9873 BP.
 AC AAA53875;
 DT 03-JAN-2001 (first entry)
 DE Expression vector pRIGadl.
 KW Vector; endogenous gene; activation; over-expression; erythropoietin;
 KW growth hormone; drug discovery; granulocyte colony stimulating factor;
 KW ds.
 OS Synthetic.
 PN WO2000049162-A2.
 PD 24-AUG-2000.
 PF 22-FEB-2000; 2000WO-US004429.
 PR 19-FEB-1999; 99US-00253022.
 PR 08-MAR-1999; 99US-00263814.
 PR 26-MAR-1999; 99US-00276820.
 XX (ATHE-) ATHERSYS INC.
 XX Harrington JJ, Sherf B, Rundlett S;
 WPI; 2000-549276/50.
 XX Non-targeted activation of endogenous genes, e.g. for the production of
 erythropoietin, growth hormone or granulocyte-colony stimulating factor
 proteins and for drug discovery.
 XX Disclosure; Fig 32; 240pp; English.
 XX New methods, vectors and cells are described for non-targeted activation
 and over-expression of endogenous genes. The vector constructs comprise
 transcriptional regulatory sequences (TRS) and unpaired splice donor
 sequences (USDS), preferably the vectors comprise (in sequential order) a
 TRS, an USDS, a rare cutting restriction site (RCRS) and a linearization
 site (LS) with a second TRS linked to a selectable marker (SM) lacking a
 polyadenylation signal. The methods, vectors and cells comprising the
 vectors may be used for the non-targeted activation and over-expression
 of endogenous genes, e.g. for the production of proteins (including
 erythropoietin, growth hormone or granulocyte-colony stimulating factor)
 and drug discovery. The advantage of these methods are that endogenous
 genes including those associated with human disease and development, may
 be activated and isolated without prior knowledge of the sequence
 structure, function or expression profile of the genes being known
 XX Sequence 9873 BP; 2450 A; 2557 C; 2501 G; 2363 T; 0 U; 2 Other;
 Query Match 100.0%; Score 63; DB 3; Length 9873;
 Best Local Similarity 100.0%; Pred. No. 4e-14;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACACATTGGTGTGCAC 60
 Db 1752 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACACATTGGTGTGCAC 1811
 QY 61 CTC 63
 Db 1812 CTC 1814

RESULT 47
 ID AAA53876

ID AA53876 standard; DNA; 10054 BP.
 AC AA53876;
 XX
 DT 03-JAN-2001 (first entry)
 XX
 DE Expression vector pRIGbdl.
 XX
 KW Vector; endogenous gene; activation; over-expression; erythropoietin;
 KW growth hormone; drug discovery; granulocyte colony stimulating factor;
 KW ds.
 KW
 OS Synthetic.
 XX
 XX WO200049162-A2.
 PN
 XX
 XX 24-AUG-2000.
 PD
 XX
 XX 22-FEB-2000; 2000WO-US004429.
 PF
 XX
 XX 19-FEB-1999; 99US-00253022.
 PR
 XX 08-MAR-1999; 99US-00263814.
 PR
 XX 26-MAR-1999; 99US-00276820.
 PR
 XX (ATHE-) ATHERSYS INC.
 PA
 XX Harrington JJ, Sherf B, Rundlett S;
 PI
 XX WPI; 2000-549276/50.
 DR
 XX
 XX Non-targeted activation of endogenous genes, e.g. for the production of
 PT erythropoietin, growth hormone or granulocyte-colony stimulating factor
 PT proteins and for drug discovery.
 PT
 XX
 XX Disclosure; Fig 33; 240pp; English.
 XX
 XX New methods, vectors and cells are described for non-targeted activation
 CC and over-expression of endogenous genes. The vector constructs comprise
 CC transcriptional regulatory sequences (TRS) and unpaired splice donor
 CC sequences (USDS), preferably the vectors comprise (in sequential order) a
 CC TRS, a USDS, a rare cutting restriction site (RCRS) and a linearization
 CC site (LS) with a second TRS linked to a selectable marker (SM) lacking a
 CC polyadenylation signal. The methods, vectors and cells comprising the
 CC vectors may be used for the non-targeted activation and over-expression
 CC of endogenous genes, e.g. for the production of proteins (including
 CC erythropoietin, growth hormone or granulocyte-colony stimulating factor)
 CC and drug discovery. The advantage of these methods are that endogenous
 CC genes including those associated with human disease and development, may
 CC be activated and isolated without prior knowledge of the sequence
 CC structure, function or expression profile of the genes being known.
 XX
 XX Sequence 10054 BP; 2548 A; 2562 C; 2515 G; 2427 T; 0 U; 2 Other;
 SQ
 Query Match 100.0%; Score 63; DB 3; Length 10054;
 Best Local Similarity 100.0%; Pred. No. 4e-14;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCACATTGGTGAC 60
 Db 1935 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCACATTGGTGAC 1994
 QY 61 CTC 63
 Db 1995 CTC 1997
 RESULT 48
 AAV59501
 ID AAV59501 standard; DNA; 11265 BP.
 XX
 AC AAV59501;
 XX
 DT 17-OCT-2003 (revised)

DT 02-FEB-1999 (first entry)
 XX
 DE Plasmid pREP7::CTLA4-hlg.
 XX
 KW pREP7::CTLA4-hlg; plasmid; CTLA4; immunoglobulin; vaccine;
 KW DNA immunisation; human; mouse; ds; circular; cyclic.
 XX
 OS Homo sapiens.
 OS Mus sp.
 OS Chimeric.
 XX
 XX WO9844129-A1.
 PN
 XX
 XX 08-OCT-1998.
 PD
 XX
 XX 26-MAR-1998; 98WO-AU000208.
 PF
 XX
 XX 27-MAR-1997; 97AU-00005891.
 PR
 XX 13-FEB-1998; 98AU-00001830.
 PR
 XX
 XX (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
 PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
 PA (UTWE) UNIV MELBOURNE.
 PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
 PA (CSLC-) CSL LTD.
 XX
 XX Boyle JS, Brady JL, Lew AM;
 FI
 XX WPI; 1998-557122/47.
 DR
 XX
 XX DNA molecule for raising an immune response to antigen - comprises
 PT sequence encoding dimerisation or multimerisation polypeptide.
 PT
 XX Disclosure; Page 32-37; 64pp; English.
 PS
 XX
 XX This is the DNA sequence of expression plasmid pREP7::CTLA4-hlg that
 CC encodes a secreted form of the Fc fragment of human IgG1 fused to murine
 CC CTLA4. The invention provides a new DNA molecule for use in raising an
 CC immune response to an antigen. The DNA molecule comprises: (i) a first
 CC sequence encoding a targeting molecule (e.g. CTLA4, which acts as a
 CC targeting molecule to antigen-presenting cells expressing B-7); (ii) a
 CC second sequence encoding the antigen or its epitope, and (iii) optionally
 CC a third sequence encoding a polypeptide (e.g. an immunoglobulin) which
 CC promotes dimerisation or multimerisation of the product encoded by the
 CC DNA molecule. Also claimed are a polypeptide encoded by the DNA molecule,
 CC and a vector including the DNA molecule. The inventors have shown that
 CC fusion proteins consisting of antigen and cell surface receptor ligands
 CC can deliver antigen to sites of immune induction which enhance the immune
 CC response and possibly the efficacy of genetic vaccines. The DNA molecule
 CC can be used in a claimed method for deviating an immune response to an
 CC antigen in an individual. (Updated on 17-OCT-2003 to standardise OS
 CC field)
 XX
 XX Sequence 11265 BP; 2717 A; 2979 C; 3002 G; 2567 T; 0 U; 0 Other;
 SQ
 Query Match 100.0%; Score 63; DB 2; Length 11265;
 Best Local Similarity 100.0%; Pred. No. 4.1e-14;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCACATTGGTGAC 60
 Db 571 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCACATTGGTGAC 630
 QY 61 CTC 63
 Db 631 CTC 633
 RESULT 49
 AAV59077
 ID AAV59077 standard; DNA; 11600 BP.
 XX
 AC AAV59077;

XX 07-NOV-2000 (first entry)
XX Nucleotide sequence of plasmid pMNeoE2a-3.1.
XX Adenovirus; tripartite leader; adenovirus vector particle; gene delivery;
KW ss.
XX Synthetic.
XX WO200042208-A1.
XX 20-JUL-2000.
XX 14-JAN-2000; 2000WO-EP000265.
XX 14-JAN-1999; 99US-0115920P.
XX (NOVS) NOVARTIS AG.
XX (SCRI) NOVARTIS-ERFINDUNGEN VERW GES MEH.
XX (SCRI) SCRIPPS RES INST.
XX Nemerow GR, Von Seggern DJ, Hallenbeck PL, Stevenson SC;
PI Skripchenko Y;
XX WPI; 2000-476068/41.
XX New nucleic acid comprising an adenovirus tripartite leader nucleotide
PT for producing high-capacity and targeted vectors for adenovirus-based
PT gene therapy.
XX Example 6; Page 192-195; 212pp; English.
XX The specification describes a nucleic acid molecule comprising an
CC adenovirus (AV) tripartite leader (TPL) nucleotide with a sequence
CC comprising two different TPL exons or three same or different TPL exons.
CC The nucleic acid is used to produce an adenovirus vector particle,
CC deliver an exogenous gene to a target cell, pseudotype recombinant viral
CC vectors, target an adenovirus vector to a cell, produce a modified
CC adenovirus, deliver a heterologous gene to an animal and produce a
CC plasmid adenoviral vector particle. The present sequence represents
CC plasmid pMNeoE2a-3.1, which is used in the course of the invention
XX
XX Sequence 11600 BP; 2929 A; 2747 C; 3012 G; 2912 T; 0 U; 0 Other;
Query Match 100.0%; Score 63; DB 3; Length 11600;
Best Local Similarity 100.0%; Pred. No. 4.2e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTAAGTGCTAGCTCGATACATATAACGCCATTGGACCATTCACCATTTGGTGTGCAC 60
DB 27 TTTAAGTGCTAGCTCGATACATATAACGCCATTGGACCATTCACCATTTGGTGTGCAC 86
QY 61 CTC 63
DB 87 CTC 89
RESULT 50
ABA94279
ID ABA94279 standard; DNA; 11600 BP.
XX ABA94279;
XX ABA94279;
XX 13-MAR-2002 (first entry)
XX Nucleotide sequence of plasmid MMTV-E2a-SV40-Neo.
XX Adenovirus; inverter terminal repeat sequence; ITRS; ocular disease;
KW fiber protein; photoreceptor; rhodopsin; stargardt disease gene; STDG1;
KW opthalmological; antiinflammatory; antidiabetic; cytostatic;
KW gene therapy; tripartite leader; TPL; ss.
XX

OS Synthetic.
XX WO200183729-A2.
XX 08-NOV-2001.
XX 30-APR-2001; 2001WO-EP004863.
XX 01-MAY-2000; 2000US-00562934.
XX (NOVS) NOVARTIS AG.
XX (SCRI) SCRIPPS RES INST.
XX (NEME/) NEMEROW G R.
XX (VSEG/) VON SEGGERN D J.
XX (FRIE/) FRIEDLANDER M.
XX Nemerow GR, Von Seggern DJ, Friedlander M;
XX WPI; 2002-082846/11.
XX Polynucleotide for making vectors, useful for treating ocular diseases,
PT e.g., retinitis pigmentosa, comprises adenovirus inverter terminal repeat
PT sequences, packaging signal and photoreceptor-specific promoter.
XX Example 5; Page 141-145; 149pp; English.
XX The invention provides an isolated polynucleotide comprising adenovirus
CC (AV) inverter terminal repeat sequences (ITRS), AV packaging signal
CC operatively linked to ITRS and a photoreceptor-specific promoter. A
CC recombinant AV vector (AAV) comprising the polynucleotide is useful for
CC targeted delivery of a gene product to the eye (especially to the
CC vitreous cavity), for treating an ocular disease, e.g., retinal
CC degenerative disease, retinitis pigmentosa, and retinoblastoma, of a mammal
CC preferably human. The AAV comprises a fiber protein that specifically or
CC selectively binds to receptors that are expressed on cells (preferably
CC photoreceptors in the eye). Preferably, the recombinant virus comprise a
CC fiber protein from an adenovirus type D subgroup or is a chimeric protein
CC containing a portion of the N-terminus of an adenovirus type 2 or type 5
CC penton, and the therapeutic product is a trophic factor, an anti-
CC apoptotic factor, a gene encoding a rhodopsin protein, a wild-type
CC stargardt disease gene (STDG1), an anti-cancer agent and a protein that
CC regulates expression of a photoreceptor specific gene product. The viral
CC nucleic acid of AAV comprises ITRS and packaging signal derived from AAV
CC subgroup B or C, especially an AV type 2 or type 5. AAV is also useful
CC for targeted gene therapy, where the vector comprises an AV type 37 fiber
CC protein or its portion, and selectively transduces photoreceptors and
CC delivers a gene product encoded by AAV. The present sequence represents
CC the nucleotide sequence of plasmid MMTV-E2a-SV40-Neo
XX Sequence 11600 BP; 2929 A; 2747 C; 3011 G; 2913 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 63; DB 6; Length 11600;
Best Local Similarity 100.0%; Pred. No. 4.2e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTAAGTGCTAGCTCGATACATATAACGCCATTGGACCATTCACCATTTGGTGTGCAC 60
DB 27 TTTAAGTGCTAGCTCGATACATATAACGCCATTGGACCATTCACCATTTGGTGTGCAC 86
QY 61 CTC 63
DB 87 CTC 89
RESULT 51
AAL56865
ID AAL56865 standard; DNA; 11600 BP.
XX AAL56865;
XX AAL56865;
XX 06-NOV-2003 (first entry)
XX

DE DNA sequence of the plasmid MMTV-E2a-SV40-Neo construct.

XX Fibre shaft modification; adenoviral vector; cell entry pathway; penton;

KW CAR; coxsackie adenovirus receptor; heparin sulphate proteoglycan; HSP;

KW gene therapy; fibre knob; ds.

XX Rhesus macaque polyoma virus.

OS Unidentified adenovirus.

OS Unidentified.

XX WO2003062400-A2.

PN 31-JUL-2003.

XX 24-JAN-2003; 2003WO-US002295.

XX 24-JAN-2002; 2002US-0350388P.

PR 26-JUN-2002; 2002US-0391967P.

XX (SCRI) SCRIPPS RES INST.

PA (NOVS) NOVARTIS AG.

XX Kaleko M, Nemerow GR, Smith T, Stevenson SC;

PI WPI; 2003-627459/59.

XX New modified adenovirus capsid protein, useful as a base vector for

PT producing redirected adenoviruses.

XX Disclosure; Page 143-146; 132pp; English.

XX This invention relates to novel fibre shaft modifications in adenoviral

CC vectors. Adenoviral vector-mediated gene therapy aims to transduce a

CC specific targeted tissue or organ, accordingly gene therapy requires the

CC ablation of normal virus tropism. If successful, systemic vector delivery

CC into a peripheral vein would be targeted to the desired location in the

CC body without any associated side effects, which would permit lower, less

CC toxic vector doses that are also potentially less immunogenic. The

CC present invention describes capsid modifications, specifically fibre

CC shaft mutations that when expressed on adenoviral particles ablates

CC binding to heparin sulphate proteoglycans (HSP) thus providing detargeted

CC vectors. Furthermore, when this is combined with modifications of other

CC adenoviral proteins involved in the cell entry pathway such as the fibre

CC knob, penton or CAR (coxsackie adenovirus receptor) proteins, the vectors

CC become fully detargeted. As such, these fully ablated particles can be

CC used in vivo as base vectors for producing redirected adenoviruses with

CC the desired cell specificity. This polynucleotide sequence is the plasmid

CC MMTV-E2a-SV40-Neo construct used to provide complementation of the

CC adenoviral E2a function of the invention

XX

SQ Sequence 11600 BP; 2929 A; 2747 C; 3011 G; 2913 T; 0 U; 0 Other;

Query Match 100.0%; Score 63; DB 8; Length 11600;

Best local Similarity 100.0%; Pred. No. 4.2e-14;

Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTAACTGCTAGCTCGACATTAATAGCCATTTGACCATTCACCATTTGGTGTGCAC 60

Db TTTTAACTGCTAGCTCGACATTAATAGCCATTTGACCATTCACCATTTGGTGTGCAC 86

QY 61 CTC 63

Db 87 CTC 89

RESULT 52

ADB75125

ID ADB75125 standard; DNA; 11600 BP.

AC ADB75125;

XX 04-DEC-2003 (first entry)

DT

XX

DE Chromosomal insertion pWNeO2a-3.1.

XX ophthalmological; antiinflammatory; antidiabetic; gene therapy;

KW adenovirus inverted terminal repeat sequence;

KW adenovirus packaging signal; photoreceptor-specific promoter;

KW adenovirus type 37; adenovirus type D serotype; adenovirus type 2;

KW rhodopsin; wild-type Stargardt disease gene; STGD1; anti-cancer agent;

KW retinal degenerative disease; retinitis pigmentosa; Stargardt's disease;

KW diabetic retinopathy; retinal vascularisation; chorioideraemia;

KW gyrate atrophy; macular dystrophy; retinoblastoma;

KW photoreceptor-restricted transgene expression;

KW recombinant adenovirus vector; adenovirus type 5; E2a;

KW chromosomal insertion; ds.

XX Homo sapiens.

OS US2002193327-A1.

PN 19-DEC-2002.

XX 01-MAY-2001; 2001US-00847101.

PF 01-MAY-2000; 2000US-00562934.

PR (SCRI) SCRIPPS RES INST.

XX Nemerow GR, Von Seggern DJ, Friedlander M;

PI WPI; 2003-657234/62.

XX Novel nucleic acids comprising adenovirus inverted terminal repeat

PT sequences, adenovirus packaging signals operatively linked to the

PT sequences and photoreceptor-specific promoters, useful for treating

PT retinitis pigmentosa.

XX Example 5; Page 93-98; 106pp; English.

PS The invention describes an isolated nucleic acid (I) comprising

CC adenovirus inverted terminal repeat sequence, an adenovirus packaging

CC signal operatively linked to the sequence, and a photoreceptor-specific

CC promoter. A Recombinant adenovirus vector (II) comprising (I) is useful

CC for targeted delivery of a gene product to the eye of a mammal which

CC involves administering (II) that comprises heterologous DNA encoding the

CC gene product or resulting in expression of the gene product, where the

CC recombinant virus comprises a fibre protein that specifically or

CC selectively binds to receptors that are expressed on cells which are

CC photoreceptors, in the eye. The recombinant virus comprises a fibre

CC protein which is an adenovirus type 37, from an adenovirus type D

CC serotype. The fibre is a chimeric protein containing a sufficient portion

CC of the N-terminus of an adenovirus type 2 or type 5 fibre protein for

CC interaction with an adenovirus type 2 or type 5 penton, and a sufficient

CC portion of an adenovirus serotype D knob portion of the fiber for

CC selective binding to photoreceptors in the eye of a mammal. The

CC encapsulated nucleic acid comprises a photoreceptor-specific promoter

CC operatively linked to a nucleic acid comprising the therapeutic product

CC which is chosen from tropic factor, anti-apoptotic factor, gene encoding

CC a rhodopsin protein, wild-type Stargardt disease gene (STGD1), an anti-

CC cancer agent and a protein that regulates expression of a photoreceptor-

CC specific gene product. The delivery is effected for treatment of an

CC ocular disease such as retinal degenerative disease e.g., retinitis

CC pigmentosa, Stargardt's disease, diabetic retinopathies, retinal

CC vascularisation, chorioideraemia, gyrate atrophy or macular dystrophy or

CC retinoblastoma inherited and acquired retinal and neovascular

CC degenerative diseases. The viral nucleic acid comprises an adenovirus

CC inverted terminal repeat (ITR) sequences, and an adenovirus packaging

CC signal operatively linked to the sequence. The ITRs and packaging signal

CC are derived from an adenovirus serotype B or C, or adenovirus type 2 or

CC 5. The viral nucleic acid further comprises a photoreceptor-specific

CC promoter. (II) includes photoreceptor promoters providing a means not

CC only for specific targeting of expression in these cells, but also for

CC photoreceptor-restricted transgene expression. This sequence represents a

CC chromosomal insertion found in adenoviral plasmids of the A549 lung

CC carcinoma cell line which provide a complement of adenoviral E2a gene
CC function.
XX Sequence 11600 BP; 2929 A; 2747 C; 3011 G; 2913 T; 0 U; 0 Other;
SQ Query Match 100.0%; Score 63; DB 9; Length 11600;
Best Local Similarity 100.0%; Pred. No. 4.2e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACATAAAGCCCATTTGACATTCACCATTTGGTGTGCAC 60
DB 27 TTTAAGTCCTAGCTCGATACATAAAGCCCATTTGACATTCACCATTTGGTGTGCAC 86

QY 61 CTC 63
DB 87 CTC 89

RESULT 53
AAL55269
ID AAL55269 standard; DNA; 16958 BP.
AC AAL55269;
XX 10-MAY-2003 (first entry)
XX DNA of expression vector RC77, SEQ ID No 3.
XX Vector; excisable; site-specific recombinase; enzyme; exogenous;
KW signalling molecule; transcription factor; cell metabolism;
KW differentiation state; kinase; phosphatase; ds.
XX Unidentified.
XX WO2003002735-A2.
XX 09-JAN-2003.
XX 28-JUN-2002; 2002WO-CA000997.
XX 28-JUN-2001; 2001US-0301149P.
XX (PHEN-) PHENOGENE THERAPEUTICS INC.
XX Lanctot C, Gingras R, Gaumont M;
XX WPI; 2003-210275/20.
XX New vector having a nucleic acid sequence excisable by site-specific
XX recombination, useful for identifying or selecting exogenous nucleic
XX acids with desired features, e.g. nucleic acids encoding transcription
XX factors or kinases.
XX Claim 24; Page 103-112; 122pp; English.
XX The invention relates to novel vectors comprising nucleic acid sequences
XX excisable by a site-specific recombinase. The vectors or cells are useful
XX for identifying or selecting an exogenous nucleic acid having a desired
XX feature, e.g. nucleic acids encoding signalling molecules, transcription
XX factors or other proteins involved in changes of cell metabolism or
XX differentiation state (e.g. kinase or phosphatase). This polynucleotide
XX sequence represents the DNA of the vector RC77 relating to the invention
XX Sequence 16958 BP; 4816 A; 4210 C; 4125 G; 3807 T; 0 U; 0 Other;
SQ Query Match 100.0%; Score 63; DB 7; Length 16958;
Best Local Similarity 100.0%; Pred. No. 4.5e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACATAAAGCCCATTTGACATTCACCATTTGGTGTGCAC 60
DB 14710 TTTAAGTCCTAGCTCGATACATAAAGCCCATTTGACATTCACCATTTGGTGTGCAC 14769

QY 61 CTC 63
DB 14770 CTC 14772

RESULT 54
AAL56867
ID AAL56867 standard; DNA; 33622 BP.
XX AAL56867;
AC AAL56867;
XX 06-NOV-2003 (first entry)
XX DNA sequence of the recombinant adenoviral Av3nBg vector.
XX Fibre shaft modification; adenoviral vector; cell entry pathway; penton;
XX CAR; coxsackie adenovirus receptor; heparin sulphate proteoglycan; HSP;
XX gene therapy; fibre knob; Av3nBg; ds.
XX Human adenovirus type 5.
XX Unidentified.
XX WO2003062400-A2.
XX 31-JUL-2003.
XX 24-JAN-2003; 2003WO-US002295.
XX 24-JAN-2002; 2002US-0350388P.
XX 26-JUN-2002; 2002US-0391967P.
XX (SCRI) SCRIPPS RES INST.
XX (NOVS) NOVARTIS AG.
XX Kaleko M, Nemerow GR, Smith T, Stevenson SC;
XX WPI; 2003-627459/59.
XX New modified adenovirus capsid protein, useful as a base vector for
XX producing redirected adenoviruses.
XX Example 1; Page 156-165; 132pp; English.
XX This invention relates to novel fibre shaft modifications in adenoviral
XX vectors. Adenoviral vector-mediated gene therapy aims to transduce a
XX specific targeted tissue or organ, accordingly gene therapy requires the
XX ablation of normal virus tropism. If successful, systemic vector delivery
XX into a peripheral vein would be targeted to the desired location in the
XX body without any associated side effects, which would permit lower, less
XX toxic vector doses that are also potentially less immunogenic. The
XX present invention describes capsid modifications, specifically fibre
XX shaft mutations that when expressed on adenoviral particles ablates
XX binding to heparin sulphate proteoglycans (HSP) thus providing detargeted
XX vectors. Furthermore, when this is combined with modifications of other
XX adenoviral proteins involved in the cell entry pathway such as the fibre
XX knob, penton or CAR (coxsackie adenovirus receptor) proteins, the vectors
XX become fully detargeted. As such, these fully ablated particles can be
XX used in vivo as base vectors for producing redirected adenoviruses with
XX the desired cell specificity. This polynucleotide sequence is the
XX recombinant E1, E2a and E3-deleted adenoviral vector (Av3nBg) that
XX encodes a nuclear localising beta-galactosidase, used in the
XX exemplification of the invention
XX Sequence 33622 BP; 7857 A; 9539 C; 9277 G; 6949 T; 0 U; 0 Other;
SQ Query Match 100.0%; Score 63; DB 8; Length 33622;
Best Local Similarity 100.0%; Pred. No. 5.3e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACATAAAGCCCATTTGACATTCACCATTTGGTGTGCAC 60
DB 734 TTTAAGTCCTAGCTCGATACATAAAGCCCATTTGACATTCACCATTTGGTGTGCAC 793

```

QY      61 CTC 63
Db      794 CTC 796

RESULT 55
AAZ94163
ID      AAZ94163 standard; DNA; 34302 BP.
XX
AC      AAZ94163;
XX
DT      15-SEP-2003 (revised)
DT      19-JUN-2000 (first entry)
XX
DE      Adenovirus vector Ad5RSVp16 used for prostate cancer gene therapy.
XX
KW      Ad5RSVp16; adenovirus; vector; RSV; promoter; human; p16;
KW      tumour suppressor gene; prostate cancer; gene therapy; ds.
XX
OS      Human adenovirus type 5.
OS      Rous sarcoma virus.
OS      Homo sapiens.
OS      Chimeric.
XX
FH      Key Location/Qualifiers
FT      promoter 410..805
FT      /*tag= a
FT      misc_feature 1055..2014
FT      /*tag= b
FT      /*note= "p16 sense cDNA"
XX
XX      WO200014211-A1.
XX
XX      16-MAR-2000.
XX
XX      02-SEP-1999; 99WO-US018833.
XX
XX      02-SEP-1998; 98US-00145729.
XX
XX      (GENO-) GENOTHERAPEUTICS INC.
XX
XX      Steiner WS, Lu Y;
XX
XX      WPI; 2000-256967/22.
XX
XX      Replication-deficient adenovirus type 5 expression vector, useful in gene
XX      therapy of prostate cancer, comprises a nucleic acid encoding p16 under
XX      the control of a Rous Sarcoma virus promoter.
XX
XX      Disclosure; Fig 13; 118pp; English.
XX
XX      The present sequence is that of replication-deficient adenovirus vector
XX      Ad5RSVp16, deposited as ATCC VR 2626. The vector is a type 5 adenovirus
XX      in which the E1 and E3 regions of the genome have been removed, and a p16
XX      tumour suppressor gene (see AAZ94162) has been inserted under control of
XX      a Rous sarcoma virus (RSV) promoter (see AAZ94161). Ad5RSVp16 can be used
XX      in the gene therapy of prostate cancer to replace a missing, mutated or
XX      inactivated p16 gene. In vitro, PC3 cells which were stably transfected
XX      with the vector showed a 70% reduction in cell number. The vector also
XX      inhibited growth of prostate cancer cells PPC-1, DU145 and PC3 in
XX      culture. PPC-1 tumours grown in nude mice treated by a single injection
XX      of Ad5RSVp16 had a marked reduction in tumour size when compared to
XX      untreated control. The mice also survived for longer. Transduction rates
XX      were over 90%, with transgene expression detectable in tumours for up to
XX      2 wk. (Updated on 15-SEP-2003 to standardise OS field)
XX
XX      Sequence 34302 BP; 7995 A; 9797 C; 9303 G; 7207 T; 0 U; 0 Other;

Query Match      100.0%; Score 63; DB 3; Length 34302;
Best Local Similarity 100.0%; Pred. No. 5.3e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTTAAGTGGCTAGCTCGATACATTAACGCCATTGACCATTTGCGTGCAC 60

Db      742 TTTAAGTGGCTAGCTCGATACATTAACGCCATTGACCATTTGCGTGCAC 801
QY      61 CTC 63
Db      802 CTC 804

RESULT 56
AAL56866
ID      AAL56866 standard; DNA; 35211 BP.
XX
AC      AAL56866;
XX
DT      06-NOV-2003 (first entry)
XX
DE      DNA sequence of the recombinant adenoviral AvinBg vector.
XX
KW      Fibre shaft modification; adenoviral vector; cell entry pathway; penton;
KW      CAR; coxsackie adenovirus receptor; heparin sulphate proteoglycan; HSP;
KW      gene therapy; fibre knob; AvinBg; ds.
XX
OS      Human adenovirus type 5.
OS      Unidentified.
XX
XX      WO2003062400-A2.
XX
XX      31-JUL-2003.
XX
XX      24-JAN-2003; 2003WO-US002295.
XX
XX      24-JAN-2002; 2002US-0350388P.
XX
XX      26-JUN-2002; 2002US-0391967P.
XX
XX      (SCRI ) SCRIPPS RES INST.
XX
XX      (NOVS ) NOVARTIS AG.
XX
XX      Kaleko M, Nemerow GR, Smith T, Stevenson SC;
XX
XX      WPI; 2003-627459/59.
XX
XX      New modified adenovirus capsid protein, useful as a base vector for
XX      producing redirected adenoviruses.
XX
XX      Example 1; Page 146-156; 132pp; English.
XX
XX      This invention relates to novel fibre shaft modifications in adenoviral
XX      vectors. Adenoviral vector-mediated gene therapy aims to transduce a
XX      specific targeted tissue or organ, accordingly gene therapy requires the
XX      ablation of normal virus tropism. If successful, systemic vector delivery
XX      into a peripheral vein would be targeted to the desired location in the
XX      body without any associated side effects, which would permit lower, less
XX      toxic vector doses that are also potentially less immunogenic. The
XX      present invention describes capsid modifications, specifically fibre
XX      shaft mutations that when expressed on adenoviral particles ablates
XX      binding to heparin sulphate proteoglycans (HSP) thus providing detargeted
XX      vectors. Furthermore, when this is combined with modifications of other
XX      adenoviral proteins involved in the cell entry pathway such as the fibre
XX      knob, penton or CAR (coxsackie adenovirus receptor) proteins, the vectors
XX      become fully detargeted. As such, these fully ablated particles can be
XX      used in vivo as base vectors for producing redirected adenoviruses with
XX      the desired cell specificity. This polynucleotide sequence is the
XX      recombinant E1 and E3-deleted adenoviral vector (AvinBg) that encodes a
XX      nuclear localising beta-galactosidase, used in the exemplification of the
XX      invention
XX
XX      Sequence 35211 BP; 8136 A; 10028 C; 9704 G; 7343 T; 0 U; 0 Other;

Query Match      100.0%; Score 63; DB 8; Length 35211;
Best Local Similarity 100.0%; Pred. No. 5.3e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTTAAGTGGCTAGCTCGATACATTAACGCCATTGACCATTTGCGTGCAC 60

```

Db 848 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 907
QY 61 CTC 63
Db 908 CTC 910

RESULT 57
AA02780
ID AAX02780 standard; DNA; 37808 BP.
XX AC AAX02780;
XX 14-MAY-1999 (first entry)
XX Vector pMVX-BG DNA.
XX Vector pMVX-BG; cloning; adenoviral minimal virus; AdMV; ITR; plasmid;
KW inverted terminal repeats; ITR; packaging signal; PSI; bacteriophage;
KW virus bank; genomic analysis; transgenic animal; ss.
XX Synthetic.
XX WO9902647-A2.
XX 21-JAN-1999.
XX 06-JUL-1998; 98WO-DE001940.
XX 10-JUL-1997; 97DE-01029571.
PR 10-OCT-1997; 97DE-01044768.
XX (HEPA-) HEPAVEC GENTHERAPIE AG.
XX Hillgenberg M, Loeser P, Schmieders F, Sandig V, Strauss M;
WPI; 1999-120851/10.
XX New cloning vector for producing adenoviral minimal viruses - useful for
PT gene therapy or for preparation of virus banks and transgenic animals.
XX Disclosure; Page 16-41; 57pp; German.
XX This invention describes a novel cloning vector (A) for production of
CC adenoviral minimal viruses (AdMV). The vector is composed of two
CC adenoviral inverted terminal repeats (ITR) and a bacterial plasmid
CC backbone that includes an origin of replication (ori) and bacterial
CC resistance gene, in which a packaging signal (PS1) for a bacteriophage is
CC cloned. ITR are flanked by two cleavage sites for a restriction
CC endonuclease (RE) and they frame an adenoviral packaging signal (PS2), a
CC multiple cloning site for insertion of a therapeutic DNA (in which
CC optionally additional, non-coding chromosomal mammalian DNA is cloned),
CC optionally a recognition site for a recombinase (between the ITR and PS2)
CC and optionally a reporter gene cassette (RGS). AdMV produced from this
CC vector are useful for all adenoviral gene transfer applications, for
CC production of virus banks (e.g. for genomic analysis) and for preparation
CC of transgenic animals. AdMV are safe, compatible with all helper systems,
CC and can accommodate large DNA inserts, (particularly complete genes with
CC the native chromosomal organisation, including the native promoter so
CC that problems of over-expression caused by viral promoters are avoided).
CC The use of PSI makes possible the use of very efficient and size
CC selecting cosmid cloning techniques. When used for transgenic animal
CC production, the AdMV can include long homologous regions to provide a
CC higher frequency of recombination
XX
SQ Sequence 37808 BP; 10910 A; 7906 C; 8561 G; 10423 T; 0 U; 8 Other;
Query Match 100.0%; Score 63; DB 2; Length 37808;
Best Local Similarity 100.0%; Pred. No. 5.4e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60

Db 848 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 907
QY 61 CTC 63
Db 908 CTC 910

RESULT 58
ABL59282
ID ABL59282 standard; DNA; 92 BP.
XX AC ABL59282;
XX 07-AUG-2003 (revised)
DT 07-OCT-2002 (first entry)
XX Nucleotide sequence of fragment 9190300 from LTR of ALSV.
XX Long terminal repeat; LTR; ALSV; lung cancer; ALSV-induced cancer; ss.
XX Avian leukosis virus.
XX US6391555-B1.
XX 21-MAY-2002.
XX 07-JAN-2000; 2000US-00479770.
PF 07-JAN-1999; 99US-0115087P.
FR (JOHN/) JOHNSON E S.
XX Johnson ES;
XX WPI; 2002-478534/51.
XX Detecting avian leukosis/sarcoma virus (ALSV) nucleic acids, particularly
PT long terminal repeats, in a DNA sample from a patient indicates that the
PT patient has, or is likely to develop ALSV-induced lung cancer.
XX Disclosure; Fig 8; 25pp; English.
XX ABL59276-86 represent PCR amplified fragments from a conserved region of
CC the long terminal repeat (LTR) of avian leukosis/sarcoma virus (ALSV).
CC ABL59283 represents a positive control from a chicken tumour induced by
CC ALSV. ABL59284 is also a positive control, and is derived from plasmid
CC containing ALSV sequences. ABL59285-86 represent subgroup A isolates to
CC which the amplified sequence showed closest homology. The primers used
CC for amplification were used to screen for an increased potential for
CC developing ALSV-induced lung cancer. The method comprises detecting ALSV
CC nucleic acid sequences in DNA from a sample from the patient. The method
CC is useful for the detection of ALSV-induced cancer. (Updated on 07-AUG-
XX 2003 to correct OS field.)
SQ Sequence 92 BP; 25 A; 21 C; 19 G; 27 T; 0 U; 0 Other;
Query Match 98.4%; Score 62; DB 6; Length 92;
Best Local Similarity 100.0%; Pred. No. 3.4e-14;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
Db 27 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 86
QY 61 CT 62
Db 87 CT 88

RESULT 59
ABL59283
ID ABL59283 standard; DNA; 178 BP.

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XX AC ABL59283;
XX DT 07-AUG-2003 (revised)
XX DT 07-OCT-2002 (first entry)
XX DE Nucleotide sequence of fragment 1L3B from LTR of ALSV.
XX KW Long terminal repeat; LTR; ALSV; lung cancer; ALSV-induced cancer; ss.
XX OS Avian leukosis virus.
XX PN US6391555-B1.
XX PD 21-MAY-2002.
XX PF 07-JAN-2000; 2000US-00479770.
XX PR 07-JAN-1999; 99US-0115087P.
XX PA (JOHN/) JOHNSON E S.
XX PI Johnson ES;
XX DR WPI; 2002-478534/51.
XX XX
XX PT Detecting avian leucosis/sarcoma virus (ALSV) nucleic acids, particularly
XX PT long terminal repeats, in a DNA sample from a patient indicates that the
XX PT patient has, or is likely to develop ALSV-induced lung cancer.
XX PS Disclosure; Fig 8; 25pp; English.
XX CC ABL59276-86 represent PCR amplified fragments from a conserved region of
XX CC the long terminal repeat (LTR) of avian leucosis/sarcoma virus (ALSV).
XX CC ABL59283 represents a positive control from a chicken tumour induced by
XX CC ALSV. ABL59284 is also a positive control, and is derived from plasmid
XX CC containing ALSV sequences. ABL59285-86 represent subgroup A isolates to
XX CC which the amplified sequence showed closest homology. The primers used
XX CC for amplification were used to screen for an increased potential for
XX CC developing ALSV-induced lung cancer. The method comprises detecting ALSV
XX CC nucleic acid sequences in DNA from a sample from the patient. The method
XX CC is useful for the detection of ALSV-induced cancer. (Updated on 07-AUG-
XX CC 2003 to correct OS field.)
XX SQ Sequence 178 BP; 45 A; 44 C; 44 G; 44 T; 0 U; 1 Other;

Query Match 98.4%; Score 62; DB 6; Length 178;
Best Local Similarity 100.0%; Pred. No. 4e-14;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTAAGTGCTAGCTCGATACATATAACGCCATTTCACCATTCACCATTCGGTGTGCAC 60
Db 55 TTTAAGTGCTAGCTCGATACATATAACGCCATTTCACCATTCACCATTCGGTGTGCAC 114

Qy 61 CT 62
Db 115 CT 116

RESULT 60
ABL59278
ID ABL59278 standard; DNA; 181 BP.
XX AC ABL59278;
XX DT 07-AUG-2003 (revised)
XX DT 07-OCT-2002 (first entry)
XX DE Nucleotide sequence of fragment 1832107 from LTR of ALSV.
XX KW Long terminal repeat; LTR; ALSV; lung cancer; ALSV-induced cancer; ss.
XX OS Avian leukosis virus.

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XX PN US6391555-B1.
XX PD 21-MAY-2002.
XX PF 07-JAN-2000; 2000US-00479770.
XX PR 07-JAN-1999; 99US-0115087P.
XX PA (JOHN/) JOHNSON E S.
XX PI Johnson ES;
XX DR WPI; 2002-478534/51.
XX XX
XX PT Detecting avian leucosis/sarcoma virus (ALSV) nucleic acids, particularly
XX PT long terminal repeats, in a DNA sample from a patient indicates that the
XX PT patient has, or is likely to develop ALSV-induced lung cancer.
XX PS Disclosure; Fig 8; 25pp; English.
XX CC ABL59276-86 represent PCR amplified fragments from a conserved region of
XX CC the long terminal repeat (LTR) of avian leucosis/sarcoma virus (ALSV).
XX CC ABL59283 represents a positive control from a chicken tumour induced by
XX CC ALSV. ABL59284 is also a positive control, and is derived from plasmid
XX CC containing ALSV sequences. ABL59285-86 represent subgroup A isolates to
XX CC which the amplified sequence showed closest homology. The primers used
XX CC for amplification were used to screen for an increased potential for
XX CC developing ALSV-induced lung cancer. The method comprises detecting ALSV
XX CC nucleic acid sequences in DNA from a sample from the patient. The method
XX CC is useful for the detection of ALSV-induced cancer. (Updated on 07-AUG-
XX CC 2003 to correct OS field.)
XX SQ Sequence 181 BP; 45 A; 44 C; 47 G; 44 T; 0 U; 1 Other;

Query Match 98.4%; Score 62; DB 6; Length 181;
Best Local Similarity 100.0%; Pred. No. 4e-14;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTAAGTGCTAGCTCGATACATATAACGCCATTTCACCATTCACCATTCGGTGTGCAC 60
Db 55 TTTAAGTGCTAGCTCGATACATATAACGCCATTTCACCATTCACCATTCGGTGTGCAC 114

Qy 61 CT 62
Db 115 CT 116

RESULT 61
ABL59280
ID ABL59280 standard; DNA; 210 BP.
XX AC ABL59280;
XX DT 07-AUG-2003 (revised)
XX DT 07-OCT-2002 (first entry)
XX DE Nucleotide sequence of fragment 1765805B from LTR of ALSV.
XX KW Long terminal repeat; LTR; ALSV; lung cancer; ALSV-induced cancer; ss.
XX OS Avian leukosis virus.
XX PN US6391555-B1.
XX PD 21-MAY-2002.
XX PF 07-JAN-2000; 2000US-00479770.
XX PR 07-JAN-1999; 99US-0115087P.
XX PA (JOHN/) JOHNSON E S.
XX XX

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PI Johnson ES;
 XX WPI; 2002-478534/51.
 XX
 XX Detecting avian leucosis/sarcoma virus (ALSV) nucleic acids, particularly
 PT long terminal repeats, in a DNA sample from a patient indicates that the
 PT patient has, or is likely to develop ALSV-induced lung cancer.
 XX
 XX Disclosure; Fig 8; 25pp; English.
 XX
 CC ABL59276-86 represent PCR amplified fragments from a conserved region of
 CC the long terminal repeat (LTR) of avian leucosis/sarcoma virus (ALSV).
 CC ABL59283 represents a positive control from a chicken tumour induced by
 CC ALSV. ABL59284 is also a positive control, and is derived from plasmid
 CC containing ALSV sequences. ABL59285-86 represent subgroup A isolates to
 CC which the amplified sequence showed closest homology. The primers used
 CC for amplification were used to screen for an increased potential for
 CC developing ALSV-induced lung cancer. The method comprises detecting ALSV
 CC nucleic acid sequences in DNA from a sample from the patient. The method
 CC is useful for the detection of ALSV-induced cancer. (Updated on 07-AUG-
 CC 2003 to correct OS field.)
 XX
 XX Sequence 210 BP; 54 A; 49 C; 53 G; 53 T; 0 U; 1 Other;
 SQ
 Query Match 98.4%; Score 62; DB 6; Length 210;
 Best Local Similarity 100.0%; Pred. No. 4.1e-14;
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTAAGTGGCTAGCTCGATCAATAAAGCCATTGACCATTCACCATTTGGTGGTGCAC 60
 DB 84 TTTAAGTGGCTAGCTCGATCAATAAAGCCATTGACCATTCACCATTTGGTGGTGCAC 143
 QY 61 CT 62
 DB 144 CT 145
 RESULT 62
 ABL59286
 ID ABL59286 standard; DNA; 211 BP.
 XX
 AC ABL59286;
 XX
 XX 07-AUG-2003 (revised)
 DT 07-OCT-2002 (first entry)
 XX
 DE Nucleotide sequence of fragment V01168 from LTR of ALSV.
 XX
 KW Long terminal repeat; LTR; ALSV; lung cancer; ALSV-induced cancer; ss.
 OS Avian leukosis virus.
 XX
 XX US6391555-B1.
 XX
 XX 21-MAY-2002.
 XX
 XX 07-JAN-2000; 2000US-00479770.
 XX
 XX 07-JAN-1999; 99US-0115087P.
 XX
 XX (JOHN/) JOHNSON E S.
 XX
 XX Johnson ES;
 XX
 XX WPI; 2002-478534/51.
 XX
 XX Detecting avian leucosis/sarcoma virus (ALSV) nucleic acids, particularly
 PT long terminal repeats, in a DNA sample from a patient indicates that the
 PT patient has, or is likely to develop ALSV-induced lung cancer.
 XX
 XX Disclosure; Fig 8; 25pp; English.
 XX
 CC ABL59276-86 represent PCR amplified fragments from a conserved region of

CC the long terminal repeat (LTR) of avian leucosis/sarcoma virus (ALSV).
 CC ABL59283 represents a positive control from a chicken tumour induced by
 CC ALSV. ABL59284 is also a positive control, and is derived from plasmid
 CC containing ALSV sequences. ABL59285-86 represent subgroup A isolates to
 CC which the amplified sequence showed closest homology. The primers used
 CC for amplification were used to screen for an increased potential for
 CC developing ALSV-induced lung cancer. The method comprises detecting ALSV
 CC nucleic acid sequences in DNA from a sample from the patient. The method
 CC is useful for the detection of ALSV-induced cancer. (Updated on 07-AUG-
 CC 2003 to correct OS field.)
 XX
 XX Sequence 211 BP; 56 A; 50 C; 52 G; 53 T; 0 U; 0 Other;
 SQ
 Query Match 98.4%; Score 62; DB 6; Length 211;
 Best Local Similarity 100.0%; Pred. No. 4.1e-14;
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTAAGTGGCTAGCTCGATCAATAAAGCCATTGACCATTCACCATTTGGTGGTGCAC 60
 DB 83 TTTAAGTGGCTAGCTCGATCAATAAAGCCATTGACCATTCACCATTTGGTGGTGCAC 142
 QY 61 CT 62
 DB 143 CT 144
 RESULT 63
 ABL59276
 ID ABL59276 standard; DNA; 213 BP.
 XX
 AC ABL59276;
 XX
 XX 07-AUG-2003 (revised)
 DT 07-OCT-2002 (first entry)
 XX
 DE Nucleotide sequence of fragment R-1366571 from LTR of ALSV.
 XX
 KW Long terminal repeat; LTR; ALSV; lung cancer; ALSV-induced cancer; ss.
 OS Avian leukosis virus.
 XX
 XX US6391555-B1.
 XX
 XX 21-MAY-2002.
 XX
 XX 07-JAN-2000; 2000US-00479770.
 XX
 XX 07-JAN-1999; 99US-0115087P.
 XX
 XX (JOHN/) JOHNSON E S.
 XX
 XX Johnson ES;
 XX
 XX WPI; 2002-478534/51.
 XX
 XX Detecting avian leucosis/sarcoma virus (ALSV) nucleic acids, particularly
 PT long terminal repeats, in a DNA sample from a patient indicates that the
 PT patient has, or is likely to develop ALSV-induced lung cancer.
 XX
 XX Disclosure; Fig 8; 25pp; English.
 XX
 CC ABL59276-86 represent PCR amplified fragments from a conserved region of
 CC the long terminal repeat (LTR) of avian leucosis/sarcoma virus (ALSV).
 CC ABL59283 represents a positive control from a chicken tumour induced by
 CC ALSV. ABL59284 is also a positive control, and is derived from plasmid
 CC containing ALSV sequences. ABL59285-86 represent subgroup A isolates to
 CC which the amplified sequence showed closest homology. The primers used
 CC for amplification were used to screen for an increased potential for
 CC developing ALSV-induced lung cancer. The method comprises detecting ALSV
 CC nucleic acid sequences in DNA from a sample from the patient. The method
 CC is useful for the detection of ALSV-induced cancer. (Updated on 07-AUG-
 CC 2003 to correct OS field.)
 XX

SQ Sequence 213 BP; 56 A; 50 C; 53 G; 53 T; 0 U; 1 Other;
 Query Match 98.4%; Score 62; DB 6; Length 213;
 Best Local Similarity 100.0%; Pred. No. 4.1e-14;
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTAAGTGCTAGCTCGATACATAAAGCCGCTTTGACCATTCACCATTTGGTGTGCAC 60
 |||||
 Db 83 TTTAAGTGCTAGCTCGATACATAAAGCCGCTTTGACCATTCACCATTTGGTGTGCAC 142
 |||||

Qy 61 CT 62
 ||
 Db 143 CT 144

RESULT 64
 ABL59285
 ID ABL59285 standard; DNA; 213 BP.
 AC ABL59285;
 XX
 DT 07-AUG-2003 (revised)
 DT 07-OCT-2002 (first entry)
 XX
 XX Nucleotide sequence of fragment L29198 from LTR of ALSV.
 XX
 XX Long terminal repeat; LTR; ALSV; lung cancer; ALSV-induced cancer; ss.
 XX
 OS Avian leukosis virus.
 XX
 XX US6391555-B1.
 XX
 XX 21-MAY-2002.
 XX
 PF 07-JAN-2000; 2000US-00479770.
 XX
 XX 07-JAN-1999; 99US-0115087P.
 XX
 XX (JOHN/) JOHNSON E S.
 XX
 XX Johnson ES;
 FI
 XX
 XX WPI; 2002-478534/51.
 XX
 XX Detecting avian leukosis/sarcoma virus (ALSV) nucleic acids, particularly
 PT long terminal repeats, in a DNA sample from a patient indicates that the
 PT patient has, or is likely to develop ALSV-induced lung cancer.
 XX
 PS Disclosure; Fig 8; 25pp; English.
 XX
 CC ABL59276-86 represent PCR amplified fragments from a conserved region of
 CC the long terminal repeat (LTR) of avian leukosis/sarcoma virus (ALSV).
 CC ABL59283 represents a positive control from a chicken tumour induced by
 CC ALSV. ABL59284 is also a positive control, and is derived from plasmid
 CC containing ALSV sequences. ABL59285-86 represent subgroup A isolates to
 CC which the amplified sequence showed closest homology. The primers used
 CC for amplification were used to screen for an increased potential for
 CC developing ALSV-induced lung cancer. The method comprises detecting ALSV
 CC nucleic acid sequences in DNA from a sample from the patient. The method
 CC is useful for the detection of ALSV-induced cancer. (Updated on 07-AUG-
 CC 2003 to correct OS field.)
 XX
 SQ Sequence 213 BP; 56 A; 50 C; 53 G; 54 T; 0 U; 0 Other;
 Query Match 98.4%; Score 62; DB 6; Length 213;
 Best Local Similarity 100.0%; Pred. No. 4.1e-14;
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTAAGTGCTAGCTCGATACATAAAGCCGCTTTGACCATTCACCATTTGGTGTGCAC 60
 |||||
 Db 83 TTTAAGTGCTAGCTCGATACATAAAGCCGCTTTGACCATTCACCATTTGGTGTGCAC 142
 |||||

Qy 61 CT 62

Db 143 CT 144

RESULT 65
AAT71261

ID AAT71261 standard; DNA; 565 BP.

XX AAT71261;
AC AAT71261;

XX 30-MAR-1998 (first entry)

XX Rous sarcoma virus v-src gene.
DE
XX
XX Cognate transgene; v-src gene; lymphoma; cellular immunogen; cancer;
KW self-determinant immunoreactivity; cancer vaccination; breast carcinoma;
KW colon carcinoma; immunotherapy; proto-oncogene; rous sarcoma virus; ss.
XX
OS Rous sarcoma virus.
XX
XX W09725860-A1.
PN
XX
XX 24-JUL-1997.
PD
XX
XX 13-JAN-1997; 97WO-US000582.
PF
XX
XX 19-JAN-1996; 96US-0010262P.
PR
XX
XX (UYAL-) UNIV ALLEGHENY HEALTH SCI.
PA
XX
XX Halpern MS, England JM;
PI
XX
XX WPI; 1997-384993/35.
DR
XX
PT Proto-oncogene immunogen - used in vaccine for the prevention and
PT treatment of cancer.
XX
XX Disclosure; Page 69; 81pp; English.
XX
XX This sequence represents the Rous sarcoma virus v-src cognate transgene
CC (CRG). Deletion of amino acids 430-433 of the encoded protein renders the
CC CTG non-transforming. This sequence can be used in the cellular immunogen
CC of the invention. The cellular immunogen of the invention is for
CC immunising against the product of a target proto-oncogene, over-
CC expression of which is associated with cancer, comprises host cells
CC transfected with a construct containing at least one transgene related to
CC the proto-oncogene and driven by a strong promoter. The product of the
CC transgene induces immunoreactivity to host self-determinants on the
CC product of proto-oncogene. The cellular immunogens are used for
CC protective vaccination against cancer (e.g. carcinoma of breast or colon,
CC or various lymphomas) and for immunotherapy of cancer. Use of the
CC immunogen eliminates the need to isolate immunogenic, HLA host-matched
CC peptides. The method is not based on immune recognition of a determinant
CC defined by a cancer-specific mutation and generates a systemic (anti-
CC metastatic) response
XX
SQ Sequence 565 BP; 148 A; 114 C; 162 G; 141 T; 0 U; 0 Other;

Query Match 98.4%; Score 62; DB 2; Length 565;

Best Local Similarity 100.0%; Pred. No. 5.1e-14;

Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTAAGTGCTAGCTCGATACATAAAGCCGCTTTGACCATTCACCATTTGGTGTGCAC 60
|||||Db 439 TTTAAGTGCTAGCTCGATACATAAAGCCGCTTTGACCATTCACCATTTGGTGTGCAC 498
|||||

Qy 61 CT 62

Db 499 CT 500

RESULT 66
AAZ60824

ID	AAZ60824 standard; DNA; 565 BP.
XX	
AC	AAZ60824;
XX	
DT	16-MAY-2000 (first entry)
XX	
DE	Nucleotide sequence of a cognate transgene of v-src.
XX	
XX	Cognate transgene; CTG; tumorigenic; cellular immunogen; immunisation;
KW	proto-oncogene; malignancy; allogenic cell; vaccine; cancer; ss.
XX	
OS	Rat sarcoma virus.
XX	
PN	W0200004927-AL.
PD	
XX	03-FEB-2000.
XX	
PF	08-JUL-1999; 99WO-US015594.
XX	
PR	24-JUL-1998; 98US-0093965P.
XX	
PA	(UVAL-) UNIV ALLEGHNEY HEALTH SCI.
PA	(HALP/) HALPERN M S.
PA	(ENGL/) ENGLAND J M.
PI	Halpern MS, England JM;
XX	
DR	WPI; 2000-182543/16.
XX	
PT	Cellular immunogens comprising allogenic donor cells transfected with a
PT	construct comprising a proto-oncogene cognate, useful as cancer vaccines.
XX	
PS	Disclosure; Page 75-76; 77pp; English.
XX	
CC	The present sequence represents a cognate transgene (CTG) which is
CC	rendered non-tumorigenic by deletion of amino acids 9-155. The CTG is
CC	used in the course of the invention. The specification describes a
CC	cellular immunogen for immunizing a host against the effects of the
CC	product of a target proto-oncogene which is associated with a
CC	malignancy. The cellular immunogen comprises allogenic cells transfected
CC	with transgene construct comprising a transgene cognate to target proto-
CC	oncogene and a strong promoter. The cellular immunogen is useful for
CC	vaccinating a host against cancer by inserting the transgene construct
CC	into the body of the host for the expression of the transgene. The method
CC	of the invention is designed to target mutation-driven non-self-
CC	determinants. The cellular immunogens induce reactivity for self-
CC	determinants in the over expressed product of tumour associated and over
CC	expressed proto-oncogenes
XX	
SQ	Sequence 565 BP; 148 A; 114 C; 162 G; 141 T; 0 U; 0 Other;
	Query Match 98.4%; Score 62; DB 3; Length 565;
	Best local Similarity 100.0%; Pred. No. 5.1e-14;
	Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY	1 TTTTAGTGCTAGCTCGATACAAATAAGCGCCATTTCACCATTCACCACTTGGTGTGCAC 60
Db	439 TTTTAGTGCTAGCTCGATACAAATAAGCGCCATTTCACCATTCACCACTTGGTGTGCAC 498
QY	61 CT 62
Db	499 CT 500
RESULT 67	
AAZ62602	
ID	AAZ62602 standard; DNA; 7223 BP.
AC	AAT62602;
XX	
XX	25-MAR-2003 (revised)
DT	12-MAY-1997 (first entry)
XX	

XX PD 12-DEC-2002.
 XX PD 03-JUN-2002; 2002WO-RP006054.
 XX PF 01-JUN-2001; 2001GB-00013318.
 XX PR (LONZ) LONZA BIOLOGICS PLC.
 XX PA Al-Rubeai M, Shuttleworth J;
 XX PI WPI; 2003-148669/14.
 XX DR
 XX PD Producing recombinant protein, particularly for maximizing or enhancing
 XX PT e.g. therapeutic protein production, by co-expressing protein with
 XX PT recombinant cell cycle inhibitor protein (p21) in producer cell line.
 XX PR Example 1; Page 15-16; 33pp; English.
 XX CC The present sequence represents a lac repressor operated p21-expression
 XX CC cassette comprising the Rous sarcoma virus (RSV)-LTR promoter. p21 is a
 XX CC cell cycle inhibitor protein. The present sequence is used to produce
 XX CC vectors for use in the method of the invention. The specification
 XX CC describes a method for producing a protein, preferably a recombinant
 XX CC protein, in a mammalian anchorage-independent producer cell line. The
 XX CC method comprises co-expressing with the protein in the producer cell line
 XX CC a recombinant cell cycle inhibitor protein (preferably p21). The method
 XX CC is useful for producing a recombinant protein in a producer cell line.
 XX CC This is particularly useful for maximizing or enhancing the production of
 XX CC e.g. therapeutic proteins at an industrial scale
 XX SQ Sequence 2245 BP; 532 A; 555 C; 625 G; 533 T; 0 U; 0 Other;
 Query Match 96.8%; Score 61; DB 7; Length 2245;
 Best Local Similarity 100.0%; Pred. No. 1.7e-13;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGGCAC 60
 DB 506 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGGCAC 565
 QY 61 C 61
 DB 566 C 566
 RESULT 70
 AAS15665
 ID AAS15665 standard; DNA; 262 BP.
 XX AC AAS15665;
 XX DT 29-JAN-2002 (first entry)
 XX DE Human respiratory syncytial virus promoter.
 XX KW Ecdysone receptor; EcR; ligand binding domain; ds; retinoid X receptor;
 XX KW RXRalpha; DNA-binding domain; RSV promoter; transactivation domain;
 XX KW nuclear receptor; ultraspiracle; gene therapy; protein production;
 XX KW antibody production; high throughput screening; HTS; transgenic plant;
 XX KW transgenic animal.
 XX OS Human respiratory syncytial virus.
 XX PN WO200170816-A2.
 XX PD 27-SEP-2001.
 XX PF 21-MAR-2001; 2001WO-US009050.
 XX PR 22-MAR-2000; 2000US-0191355P.
 XX PR 20-FEB-2001; 2001US-0269799P.
 XX PR

PA (ROHM) ROHM & HAAS CO.
 XX PI Palli SR, Kapitkaya MZ, Cress DE;
 XX XX WPI; 2001-656841/75.
 XX DR
 XX PT Bcdysone and retinoid X receptor based inducible gene expression systems
 XX PT for use in e.g. gene therapy, large scale production of proteins and cell
 XX PT -based high-throughput screening assays.
 XX XX Example 1; Page 141; 144pp; English.
 XX CC The invention relates to Ecdysone and retinoid X receptor based inducible
 XX CC gene expression systems useful for modulating gene expression in host
 XX CC cells. The gene expression system encodes a polypeptide with a DNA-
 XX CC binding domain recognizes a response element associated with a gene whose
 XX CC expression is to be modulated and/or a ligand binding domain (LBD)
 XX CC comprising a LBD from a nuclear receptor and a second gene expression
 XX CC cassette capable of being expressed in a host cell comprising a
 XX CC polynucleotide sequence encoding a second polypeptide comprising a trans-
 XX CC activation domain and/or a LBD comprising a LBD from a nuclear receptor
 XX CC other than ultraspiracle (USP) (the trans-activation domain is from a
 XX CC nuclear receptor other than an ecdysone receptor, a retinoid X receptor
 XX CC or a USP receptor and the LBDs from the first and second polypeptides are
 XX CC different and dimerize). The ecdysone and retinoid X receptor based
 XX CC inducible gene expression systems useful for modulating gene expression
 XX CC in host cells, for use in gene therapy, large scale production of
 XX CC proteins and antibodies, cell-based high-throughput screening assays
 XX CC (HTS), functional genomic and regulation of traits in transgenic plants
 XX CC and animals. The present sequence represents promoter from human
 XX CC respiratory syncytial virus (RSV) which is used in an inducible gene
 XX CC expression system of the invention
 XX SQ Sequence 262 BP; 79 A; 53 C; 64 G; 66 T; 0 U; 0 Other;
 Query Match 95.9%; Score 60.4; DB 4; Length 262;
 Best Local Similarity 98.4%; Pred. No. 1.8e-13;
 Matches 61; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGGCAC 60
 DB 201 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGGCAC 260
 QY 61 CT 62
 DB 261 CT 262
 RESULT 71
 ABL90071
 ID ABL90071 standard; cDNA; 766 BP.
 XX AC ABL90071;
 XX DT 24-MAY-2002 (first entry)
 XX DE Human polynucleotide SEQ ID NO 633.
 XX KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
 XX KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antitumor;
 XX KW vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;
 XX KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
 XX KW neurological disease; infection; human; secreted protein; gene; ss.
 XX OS Homo sapiens.
 XX PN WO200190304-A2.
 XX PD 29-NOV-2001.
 XX PF 18-MAY-2001; 2001WO-US016450.
 XX PR 19-MAY-2000; 2000US-0205515P.
 XX PR

XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PI Birse CE, Rosen CA;
 XX DR WPI; 2002-122018/16.
 XX DR P-PSDB; ABB89662.
 XX PT Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
 XX PT prevention of neural, immune system, muscular, reproductive,
 XX PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative
 XX PT disorders.
 XX PS Claim 4; SEQ ID NO 633; 2081pp + Sequence Listing, English.
 XX CC The invention relates to novel genes (ABL89449-ABL90853) and proteins
 XX CC (ABP89040-ABP90444) useful for preventing, treating or ameliorating
 XX CC medical conditions e.g. by protein or gene therapy. The genes are
 XX CC isolated from a range of human tissues disclosed in the specification.
 XX CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
 XX CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
 XX CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
 XX CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
 XX CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
 XX CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
 XX CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
 XX CC cardiovascular disorders such as myocardial ischaemia; (d) wound healing
 XX CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
 XX CC infectious diseases such as viral, bacterial, fungal and parasitic
 XX CC infections. Note: The sequence data for this patent did not form part of
 XX CC the printed specification, but was obtained in electronic format directly
 XX CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 766 BP; 172 A; 206 C; 191 G; 191 T; 0 U; 6 Other;
 Query Match 95.9%; Score 60.4; DB 6; Length 766;
 Best Local Similarity 98.4%; Pred. No. 2.3e-13;
 Matches 61; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TTAAAGTGGCTAGCTCGATACATAAAGCGCATTTGACCATTCACACATTGGTGTGCAC 60
 Db 169 TTTAAGTGGCTAGCTCGATACATAAAGCGCATTTGACCATTCACACATTGGTGTGCAC 228
 QY 61 CT 62
 Db 229 CT 230
 RESULT 72
 AAC92489
 ID AAC92489 standard; DNA; 858 BP.
 XX AAC92489;
 XX AC AAC92489;
 XX DT 26-MAR-2001 (first entry)
 XX DE Fragment of RSV DNA including tandem repeat LTR and non-coding region.
 XX KW Integrase; transgenic animal; transgenic bird; gene therapy; cancer; ds.
 XX KW Rous sarcoma virus.
 XX OS WO200075342-A1.
 XX PN 14-DEC-2000.
 XX PD 27-APR-2000; 2000WO-JP002785.
 XX PF 04-JUN-1999; 99JP-00158351.
 XX PR (NIPPON) NIPPON INST BIOLOGICAL SCIENCE.
 XX PA Katsumata A, Hoshi S, Ihara T, Ueda S;
 XX PI

XX WPI; 2001-061729/07.
 XX PT Plasmid vector for efficient insertion of foreign DNA into host cells to
 XX PT give transformants with stable quality, useful e.g. in producing DNA
 XX PT vaccines on large scale, and in gene therapy with ease and safely and
 XX PT without pathogenicity.
 XX PS Disclosure; Page 88-89; 94pp; Japanese.
 XX CC This invention relates to a vector which consists of an integrase gene, a
 XX CC regulatory region of DNA involved in the expression of the integrase
 XX CC gene, and a DNA fragment constituting a recognition region used in the
 XX CC catalysis of the integrase in the integrase reaction. The invention
 XX CC includes methods for the production of transgenic animals and birds using
 XX CC the vector of the invention. The plasmid vector can be for inserting
 XX CC foreign DNA into host cells to yield transformants. The transformants may
 XX CC be useful in producing DNA vaccines, and in gene therapy against cancer,
 XX CC congenital genetic diseases or infections. The present sequence
 XX CC represents a fragment of DNA from Rous sarcoma virus, including tandem
 XX CC repeat LTRs and adjacent non-coding region. The DNA fragment is used in
 XX CC the production of the vector of the invention
 XX SQ Sequence 858 BP; 215 A; 202 C; 246 G; 195 T; 0 U; 0 Other;
 Query Match 95.9%; Score 60.4; DB 5; Length 858;
 Best Local Similarity 98.4%; Pred. No. 2.3e-13;
 Matches 61; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TTAAAGTGGCTAGCTCGATACATAAAGCGCATTTGACCATTCACACATTGGTGTGCAC 60
 Db 86 TTTAAGTGGCTAGCTCGATACATAAAGCGCATTTGACCATTCACACATTGGTGTGCAC 145
 QY 61 CT 62
 Db 146 CT 147
 RESULT 73
 ABK10062
 ID ABK10062 standard; DNA; 5283 BP.
 XX ABK10062;
 XX AC ABK10062;
 XX DT 21-MAY-2002 (first entry)
 XX DE Expression vector construct pVGI.1 containing VEGF-2 insert.
 XX KW Human; vascular endothelial growth factor 2; VEGF-2; ds; pVGI.1;
 XX KW chronic limb ischaemia; myocardial ischaemia; autoimmune disorder; pHE4a;
 XX KW allergic reaction; organ rejection; inflammatory condition; arrhythmia;
 XX KW hyperproliferative disorder; viral infection; bacterial infection;
 XX KW fungal infection; parasitic infection; cardiovascular disorder; embolism;
 XX KW heart valve disease; aneurysm; arterial occlusive disorder; gene therapy.
 XX OS Synthetic.
 XX PN WO200211769-A1.
 XX PD 14-FEB-2002.
 XX PF 03-AUG-2001; 2001WO-US024658.
 XX PR 04-AUG-2000; 2000US-0223276P.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PI Coleman TA;
 XX DR WPI; 2002-217153/27.
 XX PT Isolated nucleic acid having expression vector construct with vascular
 XX PT endothelial growth factor-2 insert, useful for treating chronic limb

ischemia or myocardial ischemia, autoimmune disorders and allergic conditions.

Disclosure; Fig 31; 241pp; English.

The invention relates to an isolated nucleic acid comprising pVGI.1 expression vector construct containing the vascular endothelial growth factor 2 (VEGF-2) insert. The nucleic acid is useful for producing a host cell by transducing, transforming or transfecting a host cell with the DNA and for treating a patient having chronic limb ischaemia or myocardial ischaemia, or a disease or disorder selected from autoimmune disorders (e.g. rheumatoid arthritis, dermatitis), allergic reactions or conditions (e.g. asthma), organ rejection, inflammatory conditions (e.g. Crohn's disease), hyperproliferative disorders (e.g. Gaucher's disease), diseases due to viral, bacterial, fungal or parasitic infection, cardiovascular disorders (e.g. cardiomyopathy), arrhythmia, heart valve diseases, aneurysms, arterial occlusive disorders and embolism. This sequence represents the pVGI.1 expression vector containing the VEGF-2 insert

Sequence 5283 BP; 1244 A; 1422 C; 1417 G; 1200 T; 0 U; 0 Other;

Query Match 95.9%; Score 60.4; DB 6; Length 5283;
Best Local Similarity 98.4%; Pred. No. 3.5e-13;
Matches 61; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGGCAC 60
|||||
Db 424 TTTAAGTGGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGGCAC 483
|||||

QY 61 CT 62
|||
Db 484 CT 485

RESULT 74
AAZ09997
ID AAZ09997 standard; cDNA; 5177 BP.
XX
AC AAZ09997;
XX
DT 03-DEC-1999 (first entry)
XX
DE Bovine scavenger receptor class A (ScR)/avidin fusion protein cDNA.
XX
KW Scavenger receptor class A; ScR; avidin; fusion protein; bovine; ECD;
KW membrane-spanning domain; extracellular domain; biotin-binding activity;
KW endocytosis; ss.
XX
OS Synthetic.
OS Bos taurus.

Key Location/Qualifiers
CDS 1071..2269
FT /*tag= a
FT /product= "ScR/avidin fusion protein"
FT
FN WC09942577-A2.
XX
XX PD 26-AUG-1999.
XX
XX 23-FEB-1999; 99WO-GB000546.
XX
XX 23-FEB-1998; 98GB-00003757.
XX
XX 24-JUN-1998; 98GB-00013653.
XX
XX (EURO-) EUROGENE LTD.
XX
XX Yla-Herttua S, Kulomaa M, Lehtolainen P, Marjomaki V, Airenne K;
XX WPI; 1999-561345/47.
XX P-PSDB; AAY03098.
XX

New fusion proteins having an extracellular domain with biotin-binding activity, used to target biotinylated molecules to specific sites in tissues.

Disclosure; Page 15-21; 23pp; English.

This invention describes a novel protein (A) which comprises a membrane-spanning domain and an extracellular domain (ECD), where the ECD comprises biotin-binding activity. Using the proteins or encoding nucleic acid molecules it is possible to target biotinylated molecules to specific sites in tissues. Molecules targeted in this way may be taken up by the tissues or cells by endocytosis, allowing the molecules to exert their effects within or on the cell. This sequence encodes a bovine scavenger receptor class A/avidin fusion protein which is used in the description of the invention

Sequence 5177 BP; 1356 A; 1222 C; 1390 G; 1209 T; 0 U; 0 Other;

Query Match 94.9%; Score 59.8; DB 2; Length 5177;
Best Local Similarity 96.8%; Pred. No. 6e-13;
Matches 61; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGGCAC 60
|||||
Db 3307 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGGCAC 3366
|||||

QY 61 CTC 63
|||
Db 3367 CTC 3369

RESULT 75
AAQ75973
ID AAQ75973 standard; cDNA; 4965 BP.
XX
AC AAQ75973;
XX
DT 25-MAR-2003 (revised)
DT 23-AUG-1995 (first entry)
XX
DE pHIA-B7/beta-2 microglobulin expression vector.
XX
KW expression vector; pHIA-B7/beta-2 microglobulin; heavy human HLA-B7;
KW light beta-2 microglobulin; class I major histocompatibility complex;
KW MHC; bicistronic mRNA; human leukocyte antigen; HLA;
KW covalently closed circular DNA; ds.
XX
OS Synthetic.

Key Location/Qualifiers
LTR 1..529
FT /*tag= a
FT /note= "Rous sarcoma virus LTR promoter domain, derived for the Schmidt-Rupin strain nucleotides 8673-9146. This region also includes a 56 bp region of a synthetic oligonucleotide which modifies this regulatory sequence to effect a higher level of expression of downstream sequences. The oligonucleotide removes a polyadenylation signal sequence originally found in the RSV DNA sequence."
FT misc_signal 531..534
FT /*tag= b
FT /label= consensus_Kozak_signal_sequence 535..1620
FT CDS 535..1620
FT /*tag= c
FT /note= "HLA-B7 heavy chain open reading frame"
FT sig_peptide 535..606
FT /*tag= d
FT /note= "encodes putative signal peptide of the HLA-B7 heavy chain"
FT mat_peptide 607..1620
FT /*tag= e
FT /note= "encodes putative HLA-B7 heavy chain mature"

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OM nucleic - nucleic search, using sw model

Run on: March 11, 2004, 08:11:32 ; Search time 11.6365 Seconds
(without alignments)
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Title: US-09-733-368a-1_COPY_550_612
Perfect score: 63
Sequence: 1 tttaagtcctagctcgata.....accacattggtgcaacctc 63

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 682709 seqs, 277475446 residues
Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued patents NA:
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4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:
5: /cgn2_6/ptodata/2/ina/PTUS_COMB.seq:
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	63	100.0	4059	5	PCT-US94-06069-2
3	63	100.0	5653	1	US-08-073-836-3
4	63	100.0	5653	1	US-08-235-277-1
5	63	100.0	6836	4	US-09-479-122-18
6	63	100.0	6836	4	US-09-484-997-18
7	63	100.0	6836	4	US-09-481-355-18
8	63	100.0	6836	4	US-09-481-282-18
9	63	100.0	6836	4	US-09-455-659A-18
10	63	100.0	6836	4	US-09-484-996-18
11	63	100.0	6836	4	US-09-479-123-18
12	63	100.0	6926	1	US-08-470-299-2
13	63	100.0	7492	1	US-09-299-141-5
14	63	100.0	8591	1	US-08-462-859A-6
15	63	100.0	8591	1	US-08-462-859A-8
16	63	100.0	8591	1	US-08-123-559A-6
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18	63	100.0	8591	1	US-08-464-247A-6
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20	63	100.0	8591	1	US-08-464-248A-6
21	63	100.0	8591	1	US-08-464-248A-8
22	63	100.0	9737	4	US-09-479-122-22
23	63	100.0	9737	4	US-09-479-122-23
24	63	100.0	9737	4	US-09-479-122-28
25	63	100.0	9737	4	US-09-484-997-22
26	63	100.0	9737	4	US-09-484-997-23
27	63	100.0	9737	4	US-09-484-997-28

28	63	100.0	9737	4	US-09-481-355-22	Sequence 22, Appl
29	63	100.0	9737	4	US-09-481-355-23	Sequence 23, Appl
30	63	100.0	9737	4	US-09-481-355-28	Sequence 28, Appl
31	63	100.0	9737	4	US-09-481-282-22	Sequence 22, Appl
32	63	100.0	9737	4	US-09-481-282-23	Sequence 23, Appl
33	63	100.0	9737	4	US-09-481-282-28	Sequence 28, Appl
34	63	100.0	9737	4	US-09-455-659A-22	Sequence 22, Appl
35	63	100.0	9737	4	US-09-455-659A-23	Sequence 23, Appl
36	63	100.0	9737	4	US-09-455-659A-28	Sequence 28, Appl
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40	63	100.0	9737	4	US-09-479-123-22	Sequence 22, Appl
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43	63	100.0	9871	4	US-09-479-122-24	Sequence 24, Appl
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49	63	100.0	9871	4	US-09-479-123-24	Sequence 24, Appl
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57	62	98.4	565	4	US-09-167-322-13	Sequence 13, Appl
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59	58.2	92.4	4965	5	PCT-US94-06069-1	Sequence 1, Appl
60	58.2	92.4	4965	5	PCT-US94-06069-1	Sequence 1, Appl
61	42.8	57.9	3001	1	US-08-272-533-1	Sequence 1, Appl
62	33	52.4	47	3	US-08-379-452-9	Sequence 9, Appl
63	33	52.4	47	3	US-08-682-794-5	Sequence 5, Appl
64	33	52.4	47	3	US-09-409-670-9	Sequence 9, Appl
65	33	52.4	47	3	US-09-467-952-5	Sequence 5, Appl
66	29	46.0	74	2	US-08-989-394-10	Sequence 10, Appl
67	29	46.0	74	2	US-08-989-394-11	Sequence 11, Appl
68	29	46.0	74	3	US-09-271-365-10	Sequence 10, Appl
69	29	46.0	74	3	US-09-271-365-11	Sequence 11, Appl
70	29	46.0	74	4	US-09-604-013A-10	Sequence 10, Appl
71	29	46.0	74	4	US-09-604-013A-11	Sequence 11, Appl
72	28.4	45.1	1897	4	US-09-167-322-10	Sequence 10, Appl
73	25	39.7	25	2	US-08-404-531B-19	Sequence 19, Appl
74	25	39.7	25	3	US-08-476-900A-19	Sequence 19, Appl
75	25	39.7	25	3	US-08-488-546A-19	Sequence 19, Appl
76	23.8	37.8	1959	3	US-09-342-461-1	Sequence 1, Appl
77	23.8	37.8	2279	3	US-09-081-686-3	Sequence 3, Appl
78	23.4	37.1	25	4	US-09-479-770A-6	Sequence 6, Appl
79	23	36.5	23	5	PCT-US95-09588-2	Sequence 2, Appl
80	22.4	35.6	793	1	US-07-930-678-1	Sequence 1, Appl
81	22.4	35.6	1488	4	US-09-479-645A-1	Sequence 1, Appl
82	22.4	35.6	1488	4	US-09-479-645A-3	Sequence 3, Appl
83	22.4	35.6	2848	1	US-08-936-165A-197	Sequence 197, Appl
84	22.4	35.6	3637	1	US-08-161-286-1	Sequence 1, Appl
85	22.4	35.6	17310	4	US-08-956-171E-23	Sequence 23, Appl
86	22.2	35.2	498	4	US-09-540-236-1360	Sequence 1360, Ap
87	22.2	35.2	8697	4	US-08-961-527-123	Sequence 123, App
88	22.2	35.2	269223	4	US-09-596-002-41	Sequence 41, Appl
89	22	34.9	22	2	US-08-671-975A-11	Sequence 11, Appl
90	22	34.9	270	4	US-09-313-294A-124	Sequence 124, Appl
91	22	34.9	2028	3	US-09-003-574-33	Sequence 33, Appl
92	22	34.9	2028	3	US-09-003-570-33	Sequence 33, Appl
93	22	34.9	2028	4	US-09-864-541A-33	Sequence 33, Appl
94	22	34.9	2032	3	US-09-003-574-32	Sequence 32, Appl
95	22	34.9	2032	3	US-09-003-570-32	Sequence 32, Appl
96	22	34.9	2032	4	US-09-864-541A-32	Sequence 32, Appl
97	22	34.9	2076	3	US-09-003-574-30	Sequence 30, Appl
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99	22	34.9	2076	4	US-09-864-541A-30	Sequence 30, Appl
100	22	34.9	2126	1	US-08-463-262A-2	Sequence 2, Appl

NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States of America
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/073,836
FILING DATE: 07-JUN-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UM 9646
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5653 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-073-836-3

Query Match 100.0%; Score 63; DB 1; Length 5653;
Best Local Similarity 100.0%; Pred. No. 5.3e-15;
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DB 542 TTTAAGTGCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 601
QY 61 CTC 63
DB 602 CTC 604

RESULT 4
US-08-235-277-1
Sequence 1, Application US/08235277
Patent No. 5733543
GENERAL INFORMATION:
APPLICANT: NABEL, GARY J
APPLICANT: WOFFENDIN, CLIVE
APPLICANT: YANG, NIN-SUN
APPLICANT: SHERBY, MICHAEL J
TITLE OF INVENTION: INTRODUCTION OF HIV-PROTECTIVE GENES
TITLE OF INVENTION: INTO CELLS BY PARTICLE-MEDIATED GENE TRANSFER
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/235,277
FILING DATE: 29-APR-1994

CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5733543man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 6042-008-68
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5653 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: Other nucleic acid
US-08-235-277-1

Query Match 100.0%; Score 63; DB 1; Length 5653;
Best Local Similarity 100.0%; Pred. No. 5.3e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTAAGTGCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
DB 542 TTTAAGTGCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 601
QY 61 CTC 63
DB 602 CTC 604

RESULT 5
US-09-479-122-18
Sequence 18, Application US/09479122
Patent No. 6410266
GENERAL INFORMATION:
APPLICANT: HARRINGTON, JOHN J.
APPLICANT: SHERF, BRUCE
APPLICANT: RUNDLETT, STEPHEN
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
TITLE OF INVENTION: ENDOGENOUS GENES
FILE REFERENCE: 0221-0003C
CURRENT APPLICATION NUMBER: US/09/479,122
CURRENT FILING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: 09/276,820
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 09/159,643
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 08/941,223
PRIOR FILING DATE: 1997-09-26
PRIOR APPLICATION NUMBER: 09/263,814
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/253,022
PRIOR FILING DATE: 1999-02-19
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 18
LENGTH: 6836
TYPE: DNA
ORGANISM: Homo sapiens
US-09-479-122-18

Query Match 100.0%; Score 63; DB 4; Length 6836;
Best Local Similarity 100.0%; Pred. No. 5.6e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTAAGTGCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
DB 1760 TTTAAGTGCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 1819
QY 61 CTC 63
DB 1820 CTC 1822

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-481-355-18

Query Match      100.0%; Score 63; DB 4; Length 6836;
Best Local Similarity 100.0%; Pred. No. 5.6e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTTACTCGATACATAAAGCCCAATTGACCAATTGCACATTCACACATTTGGTGTGCAC 60
Db 1760 TTTAAGTGCTTAGTCGTACATAAAGCCCAATTGACCAATTGACCAATTCACACATTTGGTGTGCAC 1819
QY 61 CTC 63
Db 1820 CTC 1822

RESULT 8
US-09-481-282-18
; Sequence 18, Application US/09481282
; Patent No. 6541221
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHEPP, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; TITLE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003US
; CURRENT APPLICATION NUMBER: US/09/481,282
; CURRENT FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 6836
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-481-282-18

Query Match      100.0%; Score 63; DB 4; Length 6836;
Best Local Similarity 100.0%; Pred. No. 5.6e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTTACTCGATACATAAAGCCCAATTGACCAATTGCACATTCACACATTTGGTGTGCAC 60
Db 1760 TTTAAGTGCTTAGTCGTACATAAAGCCCAATTGACCAATTGACCAATTCACACATTTGGTGTGCAC 1819
QY 61 CTC 63
Db 1820 CTC 1822

RESULT 9
US-09-455-659A-18
; Sequence 18, Application US/09455659A
; Patent No. 6602686
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHEPP, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; TITLE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003A
; CURRENT APPLICATION NUMBER: US/09/455,659A
; CURRENT FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 09/276,820

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; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 18
; LENGTH: 6836
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-455-659A-18

Query Match 100.0%; Score 63; DB 4; Length 6836;
Best Local Similarity 100.0%; Pred. No. 5.6e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGGACCATTCACCAATTGGTGTGCAC 60
|||||
Db 1760 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGGACCATTCACCAATTGGTGTGCAC 1819
|||||

QY 61 CTC 63
|||
Db 1820 CTC 1822

RESULT 10
US-09-484-996-18
; Sequence 18, Application US/09484996
; Patent No. 6623958
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003H
; CURRENT APPLICATION NUMBER: US/09/484,996
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1998-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 18
; LENGTH: 6836
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-484-996-18

Query Match 100.0%; Score 63; DB 4; Length 6836;
Best Local Similarity 100.0%; Pred. No. 5.6e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGGACCATTCACCAATTGGTGTGCAC 60
|||||
Db 1760 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGGACCATTCACCAATTGGTGTGCAC 1819
|||||

QY 61 CTC 63
|||
Db 1820 CTC 1822

RESULT 11
US-09-479-123-18
; Sequence 18, Application US/09479123
; Patent No. 6670185
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003B
; CURRENT APPLICATION NUMBER: US/09/479,123
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 18
; LENGTH: 6836
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-479-123-18

Query Match 100.0%; Score 63; DB 4; Length 6836;
Best Local Similarity 100.0%; Pred. No. 5.6e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGGACCATTCACCAATTGGTGTGCAC 60
|||||
Db 1760 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGGACCATTCACCAATTGGTGTGCAC 1819
|||||

QY 61 CTC 63
|||
Db 1820 CTC 1822

RESULT 12
US-08-470-299-2
; Sequence 2, Application US/08470299
; Patent No. 5783181
; GENERAL INFORMATION:
; APPLICANT: Browne, Michael J.
; APPLICANT: Murphy, Kay E.
; APPLICANT: Chapman, Conrad G.
; APPLICANT: Clinkenbeard, Helen E.
; APPLICANT: Young, Peter R.
; APPLICANT: Shatzman, Allan R.
; TITLE OF INVENTION: No. 5783181el Compounds
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road, P.O. Box 1539
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,299
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

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; OTHER INFORMATION: Description of Artificial Sequence:p43C-AT-IN
US-09-299-141-S

Query Match      100.0%; Score 63; DB 4; Length 7492;
Best Local Similarity 100.0%; Pred. No. 5.7e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TTTTAAGTCGCTAGCTCGATACATTAACGCCATTGTGACATTCCACCATTTGTTGGCAC 60
      |||||
Db      27  TTTTAAGTCGCTAGCTCGATACATTAACGCCATTGTGACATTCCACCATTTGTTGGCAC 86

QY      61  CTC 63
      ||||
Db      87  CTC 89

RESULT 14
US-08-462-859A-6
; Sequence 6, Application US/08462859A
; Patent No. 5652092
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vittek, M. P.
; TITLE OF INVENTION: No. 5652092el Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; APPLICATION NUMBER: US/08/462,859A
;; FILING DATE: 05-JUN-1995
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Barnhard, Elizabeth M.
;; REGISTRATION NUMBER: 31,088
;; REFERENCE/DOCKET NUMBER: 31,844-04
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (201)831-3246
;; TELEFAX: (201)831-3305
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 8591 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: circular
;; MOLECULE TYPE: cDNA
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 2393..3853
US-08-462-859A-8

Query Match 100.0%; Score 63; DB 1; Length 8591;
Best Local Similarity 100.0%; Pred. No. 5.9e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAAAGTGCCTAGCTCGATCAATAAAGCCATTGTGACCAATTCACCAATTTGGTGTGCAC 60
Db 5177 TTTAAAGTGCCTAGCTCGATCAATAAAGCCATTGTGACCAATTTGGTGTGCAC 5236

QY 61 CTC 63
Db 5237 CTC 5239

RESULT 16
US-08-123-659A-6
; Sequence 6, Application US/08123659A
; Patent No. 5656477
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vittek, M. P.
; TITLE OF INVENTION: No. 5656477el Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Anne Rosenblum
; STREET: 163 Delaware Avenue, Suite 212
; CITY: Delmar
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 12054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/123,659A
; FILING DATE: 20-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rosenblum, Anne M.
; REGISTRATION NUMBER: 30,419
; REFERENCE/DOCKET NUMBER: 31,844-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (518)475-0611
; TELEFAX: (518)475-0619
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8591 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2393..3853
US-08-123-659A-8

;; LENGTH: 8591 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: circular
;; MOLECULE TYPE: cDNA
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 2393..3868
US-08-123-659A-6

Query Match 100.0%; Score 63; DB 1; Length 8591;
Best Local Similarity 100.0%; Pred. No. 5.9e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAAAGTGCCTAGCTCGATCAATAAAGCCATTGTGACCAATTCACCAATTTGGTGTGCAC 60
Db 5177 TTTAAAGTGCCTAGCTCGATCAATAAAGCCATTGTGACCAATTTGGTGTGCAC 5236

QY 61 CTC 63
Db 5237 CTC 5239

RESULT 17
US-08-123-659A-8
; Sequence 8, Application US/08123659A
; Patent No. 5656477
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vittek, M. P.
; TITLE OF INVENTION: No. 5656477el Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Anne Rosenblum
; STREET: 163 Delaware Avenue, Suite 212
; CITY: Delmar
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 12054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/123,659A
; FILING DATE: 20-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rosenblum, Anne M.
; REGISTRATION NUMBER: 30,419
; REFERENCE/DOCKET NUMBER: 31,844-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (518)475-0611
; TELEFAX: (518)475-0619
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8591 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2393..3853
US-08-123-659A-8

Query Match 100.0%; Score 63; DB 1; Length 8591;
Best Local Similarity 100.0%; Pred. No. 5.9e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCGCAATTTGACCATTCACCATTTGGTGTGCAC 60
Db 5177 TTTAAGTGGCTAGCTCGATACATAAAGCCGCAATTTGACCATTCACCATTTGGTGTGCAC 5236
QY 61 CTC 63
Db 5237 CTC 5239

RESULT 18
US-08-464-247A-6
; Sequence 6, Application US/08464247A
; Patent No. 5693478
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vitek, M. P.
; TITLE OF INVENTION: No. 5693478el Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Campus Drive
; CITY: Parsippany
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 07054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,247A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 31,844-03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-683-2158
; TELEFAX: 201-683-4117
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8591 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2393..3868
; US-08-464-247A-6

Query Match 100.0%; Score 63; DB 1; Length 8591;
Best Local Similarity 100.0%; Pred. No. 5.9e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCGCAATTTGACCATTCACCATTTGGTGTGCAC 60
Db 5177 TTTAAGTGGCTAGCTCGATACATAAAGCCGCAATTTGACCATTCACCATTTGGTGTGCAC 5236
QY 61 CTC 63
Db 5237 CTC 5239

RESULT 19
US-08-464-247A-8
; Sequence 8, Application US/08464247A
; Patent No. 5693478
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vitek, M. P.
; TITLE OF INVENTION: No. 5703209el Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Campus Drive
; CITY: Parsippany
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 07054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,247A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 31,844-03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-683-2158
; TELEFAX: 201-683-4117
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8591 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2393..3868
; US-08-464-247A-6

Query Match 100.0%; Score 63; DB 1; Length 8591;
Best Local Similarity 100.0%; Pred. No. 5.9e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCGCAATTTGACCATTCACCATTTGGTGTGCAC 60
Db 5177 TTTAAGTGGCTAGCTCGATACATAAAGCCGCAATTTGACCATTCACCATTTGGTGTGCAC 5236
QY 61 CTC 63
Db 5237 CTC 5239

RESULT 20
US-08-464-248A-6
; Sequence 6, Application US/08464248A
; Patent No. 5703209
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vitek, M. P.
; TITLE OF INVENTION: No. 5703209el Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Campus Drive
; CITY: Parsippany
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 07054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,247A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 31,844-03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-683-2158
; TELEFAX: 201-683-4117
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8591 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2393..3853
; US-08-464-247A-8

Query Match 100.0%; Score 63; DB 1; Length 8591;
Best Local Similarity 100.0%; Pred. No. 5.9e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCGCAATTTGACCATTCACCATTTGGTGTGCAC 60
Db 5177 TTTAAGTGGCTAGCTCGATACATAAAGCCGCAATTTGACCATTCACCATTTGGTGTGCAC 5236
QY 61 CTC 63
Db 5237 CTC 5239
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/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/464,248A
/ FILING DATE: 05-JUN-1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Barnhard, Elizabeth M.
/ REGISTRATION NUMBER: 31,088
/ REFERENCE/DOCKET NUMBER: 31,844-02
/ TELEPHONE: (201)831-3246
/ TELEFAX: (201)831-3305
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 8591 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: circular
/ MOLECULE TYPE: cDNA
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 2393..3868
/ US-08-464-248A-6

Query Match          100.0%; Score 63; DB 1; Length 8591;
Best Local Similarity 100.0%; Pred. No. 5.9e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGGCTAGCTCGATACAAATAAAGCCATTGACCAATTCACCAATTTGGTGGCAC 60
Db 5177 TTTAAGTGGCTAGCTCGATACAAATAAAGCCATTGACCAATTCACCAATTTGGTGGCAC 5236

QY 61 CTC 63
Db 5237 CTC 5239

RESULT 21
US-08-464-248A-8
/ Sequence 8, Application US/08464248A
/ Patent No. 5703209
/ GENERAL INFORMATION:
/ APPLICANT: Jacobsen, J. S.
/ APPLICANT: Virek, M. P.
/ TITLE OF INVENTION: No. 5703209el Amyloid Precursor and Method of
/ TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
/ TITLE OF INVENTION: of B-Amyloid Peptide
/ NUMBER OF SEQUENCES: 19
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: American Cyanamid Company
/ STREET: One Cyanamid Plaza
/ CITY: Wayne
/ STATE: New Jersey
/ COUNTRY: United States
/ ZIP: 07470-8426
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/464,248A
/ FILING DATE: 05-JUN-1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Barnhard, Elizabeth M.
/ REGISTRATION NUMBER: 31,088
/ REFERENCE/DOCKET NUMBER: 31,844-02
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (201)831-3246
```

```
/ TELEFAX: (201)831-3305
/ INFORMATION FOR SEQ ID NO: 8:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 8591 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: circular
/ MOLECULE TYPE: cDNA
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 2393..3853
/ US-08-464-248A-8

Query Match          100.0%; Score 63; DB 1; Length 8591;
Best Local Similarity 100.0%; Pred. No. 5.9e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGGCTAGCTCGATACAAATAAAGCCATTGACCAATTCACCAATTTGGTGGCAC 60
Db 5177 TTTAAGTGGCTAGCTCGATACAAATAAAGCCATTGACCAATTCACCAATTTGGTGGCAC 5236

QY 61 CTC 63
Db 5237 CTC 5239

RESULT 22
US-09-479-122-22
/ Sequence 22, Application US/09479122
/ Patent No. 6410266
/ GENERAL INFORMATION:
/ APPLICANT: HARRINGTON, JOHN J.
/ APPLICANT: SHERF, BRUCE
/ APPLICANT: RUNDLETT, STEPHEN
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
/ TITLE OF INVENTION: ENDOGENOUS GENES
/ FILE REFERENCE: 0221-0003C
/ CURRENT APPLICATION NUMBER: US/09/479,122
/ CURRENT FILING DATE: 2000-01-07
/ PRIOR APPLICATION NUMBER: 09/276,820
/ PRIOR FILING DATE: 1999-03-26
/ PRIOR APPLICATION NUMBER: 09/159,643
/ PRIOR FILING DATE: 1998-09-24
/ PRIOR APPLICATION NUMBER: 08/941,223
/ PRIOR FILING DATE: 1997-09-26
/ PRIOR APPLICATION NUMBER: 09/263,814
/ PRIOR FILING DATE: 1999-03-08
/ PRIOR APPLICATION NUMBER: 09/253,022
/ PRIOR FILING DATE: 1999-02-19
/ NUMBER OF SEQ ID NOS: 33
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 22
/ LENGTH: 9737
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: modified_base
/ LOCATION: (8347)
/ OTHER INFORMATION: a, c, t, g, other or unknown
/ NAME/KEY: modified_base
/ LOCATION: (8499)
/ OTHER INFORMATION: a, c, t, g, other or unknown
/ US-09-479-122-22

Query Match          100.0%; Score 63; DB 4; Length 9737;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGGCTAGCTCGATACAAATAAAGCCATTGACCAATTCACCAATTTGGTGGCAC 60
Db 1613 TTTAAGTGGCTAGCTCGATACAAATAAAGCCATTGACCAATTCACCAATTTGGTGGCAC 1672

QY 61 CTC 63
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Db 1673 CTC 1675

|||

PRIOR FILING DATE: 1997-09-26
 PRIOR APPLICATION NUMBER: 09/263,814
 PRIOR FILING DATE: 1999-03-08
 PRIOR APPLICATION NUMBER: 09/253,022
 PRIOR FILING DATE: 1999-02-19
 NUMBER OF SEQ ID NOS: 33
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 28
 LENGTH: 9737
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: modified_base
 LOCATION: (8347)
 OTHER INFORMATION: a, c, t, g, other or unknown
 NAME/KEY: modified_base
 LOCATION: (8499)
 OTHER INFORMATION: a, c, t, g, other or unknown
 US-09-479-122-28

Query Match 100.0%; Score 63; DB 4; Length 9737;
 Best Local Similarity 100.0%; Pred. No. 6.1e-15; Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTAAGTGCCTAGCTGCATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
 |||||
 Db 1613 TTTAAGTGCCTAGCTGCATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 1672

Qy 61 CTC 63
 |||

Db 1673 CTC 1675

RESULT 25

US-09-484-997-22
 Sequence 22, Application US/09484997
 Patent No. 6524818
 GENERAL INFORMATION:
 APPLICANT: HARRINGTON, JOHN J.
 APPLICANT: SHERF, BRUCE
 APPLICANT: RUNDLETT, STEPHEN
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
 FILE REFERENCE: 0221-0003J
 CURRENT APPLICATION NUMBER: US/09/484,997
 CURRENT FILING DATE: 2000-01-18
 PRIOR APPLICATION NUMBER: 09/276,820
 PRIOR FILING DATE: 1999-03-26
 PRIOR APPLICATION NUMBER: 09/159,643
 PRIOR FILING DATE: 1998-09-24
 PRIOR APPLICATION NUMBER: 08/941,223
 PRIOR FILING DATE: 1997-09-26
 PRIOR APPLICATION NUMBER: 09/263,814
 PRIOR FILING DATE: 1999-03-08
 PRIOR APPLICATION NUMBER: 09/253,022
 PRIOR FILING DATE: 1999-02-19
 NUMBER OF SEQ ID NOS: 33
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 22
 LENGTH: 9737
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: modified_base
 LOCATION: (8347)
 OTHER INFORMATION: a, c, t, g, other or unknown
 NAME/KEY: modified_base
 LOCATION: (8499)
 OTHER INFORMATION: a, c, t, g, other or unknown
 US-09-484-997-22

Query Match 100.0%; Score 63; DB 4; Length 9737;
 Best Local Similarity 100.0%; Pred. No. 6.1e-15; Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTAAGTGCCTAGCTGCATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
 |||||
 Db 1613 TTTAAGTGCCTAGCTGCATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 1672

Qy 61 CTC 63
 |||

Db 1673 CTC 1675

RESULT 24

US-09-479-122-28
 Sequence 28, Application US/09479122
 Patent No. 6410266
 GENERAL INFORMATION:
 APPLICANT: HARRINGTON, JOHN J.
 APPLICANT: SHERF, BRUCE
 APPLICANT: RUNDLETT, STEPHEN
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
 FILE REFERENCE: 0221-0003C
 CURRENT APPLICATION NUMBER: US/09/479,122
 CURRENT FILING DATE: 2000-01-07
 PRIOR APPLICATION NUMBER: 09/276,820
 PRIOR FILING DATE: 1999-03-26
 PRIOR APPLICATION NUMBER: 09/159,643
 PRIOR FILING DATE: 1998-09-24
 PRIOR APPLICATION NUMBER: 08/941,223
 PRIOR FILING DATE: 1997-09-26
 PRIOR APPLICATION NUMBER: 09/263,814
 PRIOR FILING DATE: 1999-03-08
 PRIOR APPLICATION NUMBER: 09/253,022
 PRIOR FILING DATE: 1999-02-19
 NUMBER OF SEQ ID NOS: 33
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 23
 LENGTH: 9737
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: modified_base
 LOCATION: (8347)
 OTHER INFORMATION: a, c, t, g, other or unknown
 NAME/KEY: modified_base
 LOCATION: (8499)
 OTHER INFORMATION: a, c, t, g, other or unknown
 US-09-479-122-23

Query Match 100.0%; Score 63; DB 4; Length 9737;
 Best Local Similarity 100.0%; Pred. No. 6.1e-15; Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTAAGTGCCTAGCTGCATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
 |||||
 Db 1613 TTTAAGTGCCTAGCTGCATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 1672

Qy 61 CTC 63
 |||

Db 1673 CTC 1675

RESULT 24

US-09-479-122-28
 Sequence 28, Application US/09479122
 Patent No. 6410266
 GENERAL INFORMATION:
 APPLICANT: HARRINGTON, JOHN J.
 APPLICANT: SHERF, BRUCE
 APPLICANT: RUNDLETT, STEPHEN
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
 FILE REFERENCE: 0221-0003C
 CURRENT APPLICATION NUMBER: US/09/479,122
 CURRENT FILING DATE: 2000-01-07
 PRIOR APPLICATION NUMBER: 09/276,820
 PRIOR FILING DATE: 1999-03-26
 PRIOR APPLICATION NUMBER: 09/159,643
 PRIOR FILING DATE: 1998-09-24
 PRIOR APPLICATION NUMBER: 08/941,223
 PRIOR FILING DATE: 1997-09-26
 PRIOR APPLICATION NUMBER: 09/263,814
 PRIOR FILING DATE: 1999-03-08
 PRIOR APPLICATION NUMBER: 09/253,022
 PRIOR FILING DATE: 1999-02-19
 NUMBER OF SEQ ID NOS: 33
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 23
 LENGTH: 9737
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: modified_base
 LOCATION: (8347)
 OTHER INFORMATION: a, c, t, g, other or unknown
 NAME/KEY: modified_base
 LOCATION: (8499)
 OTHER INFORMATION: a, c, t, g, other or unknown
 US-09-479-122-23

Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACAAATAAAGCGCAATTTGACCAATTCACACATTTGGTGTGCAC 60
|||||
Db 1613 TTTAAGTCCTAGCTCGATACAAATAAAGCGCAATTTGACCAATTCACACATTTGGTGTGCAC 1672
QY 61 CTC 63
|||
Db 1673 CTC 1675

RESULT 26

US-09-484-997-23
; Sequence 23, Application US/09484997
; Patent No. 6524818
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; TITLE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003J
; CURRENT APPLICATION NUMBER: US/09/484,997
; CURRENT FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-484-997-23

Query Match 100.0%; Score 63; DB 4; Length 9737;

Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACAAATAAAGCGCAATTTGACCAATTCACACATTTGGTGTGCAC 60
|||||
Db 1613 TTTAAGTCCTAGCTCGATACAAATAAAGCGCAATTTGACCAATTCACACATTTGGTGTGCAC 1672
QY 61 CTC 63
|||
Db 1673 CTC 1675

RESULT 27

US-09-484-997-28
; Sequence 28, Application US/09484997
; Patent No. 6524818
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; TITLE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003J

; CURRENT APPLICATION NUMBER: US/09/484,997
; CURRENT FILING DATE: 2000-01-18

; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-484-997-28

Query Match 100.0%; Score 63; DB 4; Length 9737;

Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACAAATAAAGCGCAATTTGACCAATTCACACATTTGGTGTGCAC 60
|||||
Db 1613 TTTAAGTCCTAGCTCGATACAAATAAAGCGCAATTTGACCAATTCACACATTTGGTGTGCAC 1672
QY 61 CTC 63
|||
Db 1673 CTC 1675

RESULT 28

US-09-481-355-22
; Sequence 22, Application US/09481355
; Patent No. 6524824
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; TITLE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003F
; CURRENT APPLICATION NUMBER: US/09/481,355
; CURRENT FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown

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; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-481-355-22

Query Match      100.0%; Score 63; DB 4; Length 9737;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TTTAAGTCCTAGCTCGATACATAAAGCCCAATTGACCAATTCACCACTGGTGTGCAC 60
      |||||
Db      1613 TTTAAGTCCTAGCTCGATACATAAAGCCCAATTGACCAATTCACCACTGGTGTGCAC 1672

QY      61 CTC 63
      |||
Db      1673 CTC 1675

RESULT 29
US-09-481-355-23
; Sequence 23, Application US/09481355
; Patent No. 6524824
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERP, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003F
; CURRENT APPLICATION NUMBER: US/09/481,355
; CURRENT FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-481-355-23

Query Match      100.0%; Score 63; DB 4; Length 9737;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TTTAAGTCCTAGCTCGATACATAAAGCCCAATTGACCAATTCACCACTGGTGTGCAC 60
      |||||
Db      1613 TTTAAGTCCTAGCTCGATACATAAAGCCCAATTGACCAATTCACCACTGGTGTGCAC 1672

QY      61 CTC 63
      |||
Db      1673 CTC 1675

RESULT 30
US-09-481-355-28
; Sequence 28, Application US/09481355
; Patent No. 6524824
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; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERP, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003F
; CURRENT APPLICATION NUMBER: US/09/481,355
; CURRENT FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-481-355-28

Query Match      100.0%; Score 63; DB 4; Length 9737;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TTTAAGTCCTAGCTCGATACATAAAGCCCAATTGACCAATTCACCACTGGTGTGCAC 60
      |||||
Db      1613 TTTAAGTCCTAGCTCGATACATAAAGCCCAATTGACCAATTCACCACTGGTGTGCAC 1672

QY      61 CTC 63
      |||
Db      1673 CTC 1675

RESULT 31
US-09-481-282-22
; Sequence 22, Application US/09481282
; Patent No. 6541221
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERP, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003US
; CURRENT APPLICATION NUMBER: US/09/481,282
; CURRENT FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 9737
; TYPE: DNA
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-481-282-22

Query Match 100.0%; Score 63; DB 4; Length 9737;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTAAGTGCTAGCTCGATCAATAAAGCCATTGGACCATTCACCATTTGGTGTGCAC 60
Db 1613 TTTAAGTGCTAGCTCGATCAATAAAGCCATTGGACCATTCACCATTTGGTGTGCAC 1672

Qy 61 CTC 63
Db 1673 CTC 1675

RESULT 32
US-09-481-282-23
; Sequence 23, Application US/09481282
; Patent No. 6541221
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; TITLE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003US
; CURRENT APPLICATION NUMBER: US/09/481,282
; CURRENT FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-481-282-23

Query Match 100.0%; Score 63; DB 4; Length 9737;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTAAGTGCTAGCTCGATCAATAAAGCCATTGGACCATTCACCATTTGGTGTGCAC 60
Db 1613 TTTAAGTGCTAGCTCGATCAATAAAGCCATTGGACCATTCACCATTTGGTGTGCAC 1672

Qy 61 CTC 63
Db 1673 CTC 1675

RESULT 33
US-09-481-282-28
; Sequence 28, Application US/09481282
; Patent No. 6541221
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; TITLE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003US
; CURRENT APPLICATION NUMBER: US/09/481,282
; CURRENT FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-481-282-28

Query Match 100.0%; Score 63; DB 4; Length 9737;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTAAGTGCTAGCTCGATCAATAAAGCCATTGGACCATTCACCATTTGGTGTGCAC 60
Db 1613 TTTAAGTGCTAGCTCGATCAATAAAGCCATTGGACCATTCACCATTTGGTGTGCAC 1672

Qy 61 CTC 63
Db 1673 CTC 1675

RESULT 34
US-09-455-659A-22
; Sequence 22, Application US/09455659A
; Patent No. 6602686
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; TITLE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003A
; CURRENT APPLICATION NUMBER: US/09/455,659A
; CURRENT FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223

Query Match 100.0%; Score 63; DB 4; Length 9737;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGGCAC 60
Db 1613 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGGCAC 1672
QY 61 CTC 63
Db 1673 CTC 1675
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: modified_base
LOCATION: (8347)
OTHER INFORMATION: a, c, t, g, other or unknown
FEATURE:
NAME/KEY: modified_base
LOCATION: (8499)
OTHER INFORMATION: a, c, t, g, other or unknown
US-09-455-659A-22

Query Match 100.0%; Score 63; DB 4; Length 9737;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGGCAC 60
Db 1613 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGGCAC 1672
QY 61 CTC 63
Db 1673 CTC 1675
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: modified_base
LOCATION: (8347)
OTHER INFORMATION: a, c, t, g, other or unknown
FEATURE:
NAME/KEY: modified_base
LOCATION: (8499)
OTHER INFORMATION: a, c, t, g, other or unknown
US-09-455-659A-22

RESULT 35
US-09-455-659A-23
; Sequence 23, Application US/09455659A
; Patent No. 6602686
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003A
; CURRENT APPLICATION NUMBER: US/09/455,659A
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-455-659A-23

Query Match 100.0%; Score 63; DB 4; Length 9737;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGGCAC 60
Db 1613 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGGCAC 1672
QY 61 CTC 63
Db 1673 CTC 1675
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: modified_base
LOCATION: (8347)
OTHER INFORMATION: a, c, t, g, other or unknown
FEATURE:
NAME/KEY: modified_base
LOCATION: (8499)
OTHER INFORMATION: a, c, t, g, other or unknown
US-09-455-659A-22

RESULT 36
US-09-455-659A-28
; Sequence 28, Application US/09455659A
; Patent No. 6602686
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003A
; CURRENT APPLICATION NUMBER: US/09/455,659A
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-455-659A-28

Query Match 100.0%; Score 63; DB 4; Length 9737;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGGCAC 60
Db 1613 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGGCAC 1672
QY 61 CTC 63
Db 1673 CTC 1675
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: modified_base
LOCATION: (8347)
OTHER INFORMATION: a, c, t, g, other or unknown
FEATURE:
NAME/KEY: modified_base
LOCATION: (8499)
OTHER INFORMATION: a, c, t, g, other or unknown
US-09-455-659A-28

RESULT 37
US-09-484-996-22
; Sequence 22, Application US/09484996
; Patent No. 6623958
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003H
; CURRENT APPLICATION NUMBER: US/09/484,996

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; CURRENT FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1998-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-484-996-22

Query Match      100.0%; Score 63; DB 4; Length 9737;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCTAGCTCGATACAAATAAAGCCATTGACCATTCACCAATTGGTGTGCAC 60
    |||||
Db 1613 TTTAAGTGCTAGCTCGATACAAATAAAGCCATTGACCATTCACCAATTGGTGTGCAC 1672

QY 61 CTC 63
Db 1673 CTC 1675

RESULT 38
US-09-484-996-23
; Sequence 23, Application US/09484996
; Patent No. 6623958
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003H
; CURRENT APPLICATION NUMBER: US/09/484,996
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-484-996-22

Query Match      100.0%; Score 63; DB 4; Length 9737;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCTAGCTCGATACAAATAAAGCCATTGACCATTCACCAATTGGTGTGCAC 60
    |||||
Db 1613 TTTAAGTGCTAGCTCGATACAAATAAAGCCATTGACCATTCACCAATTGGTGTGCAC 1672

QY 61 CTC 63
Db 1673 CTC 1675

RESULT 39
US-09-484-996-28
; Sequence 28, Application US/09484996
; Patent No. 6623958
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003H
; CURRENT APPLICATION NUMBER: US/09/484,996
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1998-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-484-996-28

Query Match      100.0%; Score 63; DB 4; Length 9737;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCTAGCTCGATACAAATAAAGCCATTGACCATTCACCAATTGGTGTGCAC 60
    |||||
Db 1613 TTTAAGTGCTAGCTCGATACAAATAAAGCCATTGACCATTCACCAATTGGTGTGCAC 1672

QY 61 CTC 63
Db 1673 CTC 1675

RESULT 40
US-09-479-123-22
; Sequence 22, Application US/09479123
; Patent No. 6670185
; GENERAL INFORMATION:
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; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-484-996-23

Query Match      100.0%; Score 63; DB 4; Length 9737;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCTAGCTCGATACAAATAAAGCCATTGACCATTCACCAATTGGTGTGCAC 60
    |||||
Db 1613 TTTAAGTGCTAGCTCGATACAAATAAAGCCATTGACCATTCACCAATTGGTGTGCAC 1672

QY 61 CTC 63
Db 1673 CTC 1675

RESULT 39
US-09-484-996-28
; Sequence 28, Application US/09484996
; Patent No. 6623958
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003H
; CURRENT APPLICATION NUMBER: US/09/484,996
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1998-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-484-996-28

Query Match      100.0%; Score 63; DB 4; Length 9737;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCTAGCTCGATACAAATAAAGCCATTGACCATTCACCAATTGGTGTGCAC 60
    |||||
Db 1613 TTTAAGTGCTAGCTCGATACAAATAAAGCCATTGACCATTCACCAATTGGTGTGCAC 1672

QY 61 CTC 63
Db 1673 CTC 1675

RESULT 40
US-09-479-123-22
; Sequence 22, Application US/09479123
; Patent No. 6670185
; GENERAL INFORMATION:
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; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003B
; CURRENT APPLICATION NUMBER: US/09/479,123
; CURRENT FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-479-123-22

Query Match      100.0%; Score 63; DB 4; Length 9737;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1      TTTAAGTGGCTAGCTCGATACATAAAAGCCATTGGACCATTCACACATTGGTGTGCAC 60
Db      1613    TTTAAGTGGCTAGCTCGATACATAAAAGCCATTGGACCATTCACACATTGGTGTGCAC 1672

QY      61      CTC 63
Db      1673    CTC 1675

RESULT 41
US-09-479-123-23
; Sequence 23, Application US/09479123
; Patent No. 6670185
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003B
; CURRENT APPLICATION NUMBER: US/09/479,123
; CURRENT FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
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; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-479-123-23

Query Match      100.0%; Score 63; DB 4; Length 9737;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1      TTTAAGTGGCTAGCTCGATACATAAAAGCCATTGGACCATTCACACATTGGTGTGCAC 60
Db      1613    TTTAAGTGGCTAGCTCGATACATAAAAGCCATTGGACCATTCACACATTGGTGTGCAC 1672

QY      61      CTC 63
Db      1673    CTC 1675

RESULT 42
US-09-479-123-28
; Sequence 28, Application US/09479123
; Patent No. 6670185
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003B
; CURRENT APPLICATION NUMBER: US/09/479,123
; CURRENT FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-479-123-28

Query Match      100.0%; Score 63; DB 4; Length 9737;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1      TTTAAGTGGCTAGCTCGATACATAAAAGCCATTGGACCATTCACACATTGGTGTGCAC 60
Db      1613    TTTAAGTGGCTAGCTCGATACATAAAAGCCATTGGACCATTCACACATTGGTGTGCAC 1672

QY      61      CTC 63
Db      1673    CTC 1675

RESULT 43
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; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 9871
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8481)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8633)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-484-997-24

Query Match      100.0%; Score 63; DB 4; Length 9871;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TTTAAGTGGCTAGCTGCATACATAAAGCGCATTTGACCATTCACCATTTGGTGTGCAC 60
          |||||
Db      1747 TTTAAGTGGCTAGCTGCATACATAAAGCGCATTTGACCATTCACCATTTGGTGTGCAC 1806

QY      61  CTC 63
          |||
Db      1807 CTC 1809

RESULT 45
US-09-481-355-24
; Sequence 24; Application US/09481355
; Patent No. 6524824
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHEFF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003F
; CURRENT APPLICATION NUMBER: US/09/481,355
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 9871
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8481)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8633)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-481-355-24

Query Match      100.0%; Score 63; DB 4; Length 9871;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TTTAAGTGGCTAGCTGCATACATAAAGCGCATTTGACCATTCACCATTTGGTGTGCAC 60
          |||||
Db      1747 TTTAAGTGGCTAGCTGCATACATAAAGCGCATTTGACCATTCACCATTTGGTGTGCAC 1806

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QY 61 CTC 63
|||
Db 1807 CTC 1809

RESULT 46

US-09-481-282-24
; Sequence 24, Application US/09481282
; Patent No. 6541221
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; TITLE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003US
; CURRENT APPLICATION NUMBER: US/09/481,282
; CURRENT FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 9871
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8481)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8633)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-481-282-24

Query Match 100.0%; Score 63; DB 4; Length 9871;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTAAGTGCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
Db 1747 TTTAAGTGCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 1806

QY 61 CTC 63
|||
Db 1807 CTC 1809

RESULT 47

US-09-455-659A-24
; Sequence 24, Application US/09455659A
; Patent No. 6602686
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; TITLE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003A
; CURRENT APPLICATION NUMBER: US/09/455,659A
; CURRENT FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08

; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 9871
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8481)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8633)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-455-659A-24

Query Match 100.0%; Score 63; DB 4; Length 9871;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
Db 1747 TTTAAGTGCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 1806

QY 61 CTC 63
|||
Db 1807 CTC 1809

RESULT 48

US-09-484-996-24
; Sequence 24, Application US/09484996
; Patent No. 6623958
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; TITLE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003H
; CURRENT APPLICATION NUMBER: US/09/484,996
; CURRENT FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1998-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 9871
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8481)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8633)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-484-996-24

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Query Match      100.0%; Score 63; DB 4; Length 9871;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCTAGCTCGATACATAAAGCCCAATTGACCAATTCACCAATTGGTGTGCAC 60
    |||||
Db 1747 TTTAAGTGCTAGCTCGATACATAAAGCCCAATTGACCAATTCACCAATTGGTGTGCAC 1806

QY 61 CTC 63
    |||
Db 1807 CTC 1809

RESULT 49
US-09-479-123-24
; Sequence 24, Application US/09479123
; Patent No. 6670185
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERP, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003B
; CURRENT APPLICATION NUMBER: US/09/479,123
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 9871
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8481)
; OTHER INFORMATION: a, c, t, g, other or unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8633)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-479-123-24

Query Match      100.0%; Score 63; DB 4; Length 9871;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCTAGCTCGATACATAAAGCCCAATTGACCAATTCACCAATTGGTGTGCAC 60
    |||||
Db 1747 TTTAAGTGCTAGCTCGATACATAAAGCCCAATTGACCAATTCACCAATTGGTGTGCAC 1806

QY 61 CTC 63
    |||
Db 1807 CTC 1809

RESULT 50
US-09-479-122-25
; Sequence 25, Application US/09479122
; Patent No. 6410266
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERP, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003J
; CURRENT APPLICATION NUMBER: US/09/484,997
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 10060
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8670)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-479-122-25

Query Match      100.0%; Score 63; DB 4; Length 10060;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCTAGCTCGATACATAAAGCCCAATTGACCAATTCACCAATTGGTGTGCAC 60
    |||||
Db 1936 TTTAAGTGCTAGCTCGATACATAAAGCCCAATTGACCAATTCACCAATTGGTGTGCAC 1995

QY 61 CTC 63
    |||
Db 1996 CTC 1998

RESULT 51
US-09-484-997-25
; Sequence 25, Application US/09484997
; Patent No. 6524818
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERP, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003J
; CURRENT APPLICATION NUMBER: US/09/484,997
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 10060
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8670)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-479-122-25
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; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8822)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-484-997-25

Query Match 100.0%; Score 63; DB 4; Length 10060;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTATAGTCCTAGCTCGATACATAAAGCGCCATTGACCAATTCACCAATGGTGTGCAC 60
DB 1936 TTATAGTCCTAGCTCGATACATAAAGCGCCATTGACCAATTCACCAATGGTGTGCAC 1995

QY 61 CTC 63
DB 1996 CTC 1998

RESULT 52

US-09-481-355-25
; Sequence 25, Application US/09481355
; Patent No. 6524824

; GENERAL INFORMATION:

; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003F

; CURRENT APPLICATION NUMBER: US/09/481,355
; CURRENT FILING DATE: 2000-01-12

; PRIOR APPLICATION NUMBER: 09/276,820

; PRIOR FILING DATE: 1999-03-26

; PRIOR APPLICATION NUMBER: 09/159,643

; PRIOR FILING DATE: 1998-09-24

; PRIOR APPLICATION NUMBER: 08/941,223

; PRIOR FILING DATE: 1997-09-26

; PRIOR APPLICATION NUMBER: 09/263,814

; PRIOR FILING DATE: 1999-03-08

; PRIOR APPLICATION NUMBER: 09/253,022

; PRIOR FILING DATE: 1999-02-19

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 25

; LENGTH: 10060

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURES:

; NAME/KEY: modified_base

; LOCATION: (8670)

; OTHER INFORMATION: a, c, t, g, other or unknown

; NAME/KEY: modified_base

; LOCATION: (8822)

; OTHER INFORMATION: a, c, t, g, other or unknown

US-09-481-355-25

Query Match 100.0%; Score 63; DB 4; Length 10060;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTATAGTCCTAGCTCGATACATAAAGCGCCATTGACCAATTCACCAATGGTGTGCAC 60
DB 1936 TTATAGTCCTAGCTCGATACATAAAGCGCCATTGACCAATTCACCAATGGTGTGCAC 1995

QY 61 CTC 63
DB 1996 CTC 1998

RESULT 53

US-09-481-282-25
; Sequence 25, Application US/09481282

; Patent No. 6541221
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003US
; CURRENT APPLICATION NUMBER: US/09/481,282
; CURRENT FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 10060
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: modified_base
; LOCATION: (8670)
; OTHER INFORMATION: a, c, t, g, other or unknown
; FEATURE: modified_base
; NAME/KEY: (8822)
; LOCATION: (8822)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-481-282-25

Query Match 100.0%; Score 63; DB 4; Length 10060;

Best Local Similarity 100.0%; Pred. No. 6.1e-15;

Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTATAGTCCTAGCTCGATACATAAAGCGCCATTGACCAATTCACCAATGGTGTGCAC 60

DB 1936 TTATAGTCCTAGCTCGATACATAAAGCGCCATTGACCAATTCACCAATGGTGTGCAC 1995

QY 61 CTC 63

DB 1996 CTC 1998

RESULT 54

US-09-455-659A-25

; Sequence 25, Application US/09455659A

; Patent No. 6602686

; GENERAL INFORMATION:

; APPLICANT: HARRINGTON, JOHN J.

; APPLICANT: SHERF, BRUCE

; APPLICANT: RUNDLETT, STEPHEN

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF

; FILE REFERENCE: 0221-0003A

; CURRENT APPLICATION NUMBER: US/09/455,659A

; CURRENT FILING DATE: 1999-12-07

; PRIOR APPLICATION NUMBER: 09/276,820

; PRIOR FILING DATE: 1999-03-26

; PRIOR APPLICATION NUMBER: 09/263,814

; PRIOR FILING DATE: 1999-03-08

; PRIOR APPLICATION NUMBER: 09/253,022

; PRIOR FILING DATE: 1999-02-19

; PRIOR APPLICATION NUMBER: 09/159,643

; PRIOR FILING DATE: 1998-09-24

; PRIOR APPLICATION NUMBER: 08/941,223

; PRIOR FILING DATE: 1997-09-26

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 25

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; LENGTH: 10060
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8670)
; OTHER INFORMATION: a, c, t, g, other or unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8822)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-455-659A-25

Query Match      100.0%; Score 63; DB 4; Length 10060;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCCAATTGACCAATTCACCAATTTGGTGTGCAC 60
Db 1936 TTTAAGTGGCTAGCTCGATACATAAAGCCCAATTGACCAATTCACCAATTTGGTGTGCAC 1995

QY 61 CTC 63
Db 1996 CTC 1998

RESULT 55
US-09-484-996-25
; Sequence 25, Application US/09484996
; Patent No. 6623958
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; TITLE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003H
; CURRENT APPLICATION NUMBER: US/09/484,996
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1998-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 10060
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8670)
; OTHER INFORMATION: a, c, t, g, other or unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8822)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-484-996-25

Query Match      100.0%; Score 63; DB 4; Length 10060;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCCAATTGACCAATTCACCAATTTGGTGTGCAC 60
Db 1936 TTTAAGTGGCTAGCTCGATACATAAAGCCCAATTGACCAATTCACCAATTTGGTGTGCAC 1995

QY 61 CTC 63
Db 1996 CTC 1998
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Db 1996 CTC 1998

RESULT 56
US-09-479-123-25
; Sequence 25, Application US/09479123
; Patent No. 6670185
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; TITLE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003B
; CURRENT APPLICATION NUMBER: US/09/479,123
; CURRENT FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 10060
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8670)
; OTHER INFORMATION: a, c, t, g, other or unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8822)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-479-123-25

Query Match      100.0%; Score 63; DB 4; Length 10060;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCCAATTGACCAATTCACCAATTTGGTGTGCAC 60
Db 1936 TTTAAGTGGCTAGCTCGATACATAAAGCCCAATTGACCAATTCACCAATTTGGTGTGCAC 1995

QY 61 CTC 63
Db 1996 CTC 1998

RESULT 57
US-09-167-322-13
; Sequence 13, Application US/09167322
; Patent No. 6365151
; GENERAL INFORMATION:
; APPLICANT: Allegheny University of the Health
; Sciences, Halpern, Michael S.
; England, James M.
; TITLE OF INVENTION: CANCER VACCINE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seidel, Gonda, Lavoragna & Monaco, P.C.
; STREET: Suite 1800, Two Penn Center Plaza
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/167,322
; APPLICATION NUMBER: US/09/167,322
; FILING DATE: 07-Oct-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/00582
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 7933-33 PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 565 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-167-322-13

Query Match          98.4%; Score 62; DB 4; Length 565;
Best Local Similarity 100.0%; Pred. No. 7.5e-15;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTGATACATAAAGCGCATTTGACCAATTCACCAATGTTGTGCAC 60
Db 439 TTAAAGTCCTAGCTGATACATAAAGCGCATTTGACCAATTCACCAATGTTGTGCAC 498

QY 61 CT 62
Db 499 CT 500

RESULT 58
US-09-470-881-1
; Sequence 1, Application US/09470881
; Patent No. 6685938
; GENERAL INFORMATION:
; APPLICANT: ELICHEIRI, Brian
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR MODULATION OF
; TITLE OF INVENTION: ANGIOGENESIS AND VASCULAR PERMEABILITY USING SRC OR
; TITLE OF INVENTION: YES TYROSINE KINASES
; FILE REFERENCE: T891 651.2
; CURRENT APPLICATION NUMBER: US/09/470,881
; CURRENT FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: PCT/US99/11780
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,220
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 11627
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: RCASBP(A) based
; OTHER INFORMATION: on avian sarcoma virus
; NAME/KEY: misc feature
; LOCATION: (7649)..(11258)
; OTHER INFORMATION: pBR322 sequences
; NAME/KEY: LTR
; LOCATION: (7166)..(7494)
; OTHER INFORMATION: upstream
; NAME/KEY: LTR
; LOCATION: (1)..(101)
; OTHER INFORMATION: upstream (numbering begins at the upstream R)
; NAME/KEY: misc feature
; LOCATION: (11394)..(11623)
; OTHER INFORMATION: U3
; NAME/KEY: misc feature
; LOCATION: (1)..(21)
; OTHER INFORMATION: R
; NAME/KEY: misc feature
; LOCATION: (22)..(101)
; OTHER INFORMATION: U5
; NAME/KEY: misc feature
; LOCATION: (102)..(119)
; NAME/KEY: LTR
; LOCATION: (7166)..(7494)
; OTHER INFORMATION: downstream
; NAME/KEY: misc feature
; LOCATION: (7166)..(7393)
; OTHER INFORMATION: U3
; NAME/KEY: misc feature
; LOCATION: (7394)..(7414)
; OTHER INFORMATION: R
; NAME/KEY: misc feature
; LOCATION: (7415)..(7494)
; OTHER INFORMATION: U5
; NAME/KEY: misc feature
; LOCATION: (7154)..(7165)
; OTHER INFORMATION: PPT
; NAME/KEY: misc feature
; LOCATION: (388)..(391)
; OTHER INFORMATION: splice donor (AGGT)
; NAME/KEY: misc feature
; LOCATION: (5074)..(5077)
; OTHER INFORMATION: env splice acceptor (AGGC)
; NAME/KEY: misc feature
; LOCATION: (6982)..(6985)
; OTHER INFORMATION: ClaI splice acceptor (AGGA)
; NAME/KEY: gene
; LOCATION: (372)..(902)
; OTHER INFORMATION: gag p19
; NAME/KEY: gene
; LOCATION: (909)..(1094)
; OTHER INFORMATION: gag p10
; NAME/KEY: gene
; LOCATION: (1095)..(1814)
; OTHER INFORMATION: gag p27
; NAME/KEY: gene
; LOCATION: (1843)..(2108)
; OTHER INFORMATION: gag p12
; NAME/KEY: gene
; LOCATION: (2109)..(2480)
; OTHER INFORMATION: gag p15
; NAME/KEY: misc signal
; LOCATION: (2481)..(2483)
; OTHER INFORMATION: gag stop
; NAME/KEY: gene
; LOCATION: (2501)..(4216)
; OTHER INFORMATION: pol Rt
; NAME/KEY: gene
; LOCATION: (4217)..(5185)
; OTHER INFORMATION: pol IN
; NAME/KEY: misc signal
; LOCATION: (5186)..(5188)
; OTHER INFORMATION: pol stop
; NAME/KEY: gene
; LOCATION: (5244)..(6263)
; OTHER INFORMATION: env gp85
; NAME/KEY: gene
; LOCATION: (6264)..(6878)
; OTHER INFORMATION: env gp37
; NAME/KEY: misc signal
; LOCATION: (6879)..(6881)
; OTHER INFORMATION: env stop
; NAME/KEY: misc feature
```

```
; LOCATION: (7027)
; OTHER INFORMATION: ClaI site/ the ClaI site in gag is methylated in
; OTHER INFORMATION: Dam+ strains and does not cut
US-09-470-881-1

Query Match          98.4%; Score 62; DB 4; Length 11627;
Best Local Similarity 100.0%; Pred. No. 1.5e-14; Indels 0; Gaps 0;
Matches 62; Conservative 0; Mismatches 0;

QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCGCAATTGGACCAATTCACCAATGGTGTGCAC 60
Db 7367 TTTAAGTGGCTAGCTCGATACATAAAGCCGCAATTGGACCAATTCACCAATGGTGTGCAC 60

QY 61 CT 62
Db 7427 CT 7428

RESULT 59
US-08-564-313-1
; Sequence 1, Application US/08564313
; Patent No. 5910488
; GENERAL INFORMATION:
; APPLICANT: Nabel, Elizabeth
; APPLICANT: Nabel, Gary
; APPLICANT: Lew, Denise
; APPLICANT: Marquet, Magda
; TITLE OF INVENTION: PLASMIDS SUITABLE FOR GENE THERAPY
; CORRESPONDENCE ADDRESS:
; NUMBER OF SEQUENCES: 2
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/564,313
; FILING DATE: 01-DEC-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/074,344
; FILING DATE: 07-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Israel, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: VICAL.033CPI
; TELEPHONE: 619-235-8550
; TELEFAX: 619-235-0176
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4965 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; IMMEDIATE SOURCE:
; CLONE: HLA-B7 and Beta-2
US-08-564-313-1

Query Match          92.4%; Score 58.2; DB 2; Length 4965;
Best Local Similarity 95.2%; Pred. No. 3.7e-13;
Matches 60; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCGCAATTGGACCAATTCACCAATGGTGTGCAC 60
Db 461 TTTAAGTGGCTAGCTCGATACATAAAGCCGCAATTGGACCAATTCACCAATGGTGTGCAC 520

QY 61 CTC 63
Db 521 CTC 523

RESULT 60
PCT-US94-06069-1
; Sequence 1, Application PC/TUS9406069
; GENERAL INFORMATION:
; APPLICANT: Vical Incorporated
; APPLICANT: Regents of the University of Michigan
; APPLICANT: Nabel, Elizabeth
; APPLICANT: Nabel, Gary
; APPLICANT: Lew, Denise
; APPLICANT: Marquet, Magda
; TITLE OF INVENTION: PLASMIDS SUITABLE FOR GENE THERAPY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06069
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/074,344
; FILING DATE: 07-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Israel, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: VICAL.033VPC
; TELEPHONE: 619-235-8550
; TELEFAX: 619-235-0176
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4965 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; STRAIN: HLA-B7 and Beta-2
PCT-US94-06069-1

Query Match          92.4%; Score 58.2; DB 5; Length 4965;
Best Local Similarity 95.2%; Pred. No. 3.7e-13;
Matches 60; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCGCAATTGGACCAATTCACCAATGGTGTGCAC 60
Db 461 TTTAAGTGGCTAGCTCGATACATAAAGCCGCAATTGGACCAATTCACCAATGGTGTGCAC 520

QY 61 CTC 63
Db 521 CTC 523
```

Db 521 CTC 523

RESULT 61

US-08-272-513-1
 ; Sequence 1, Application US/08272513
 ; Patent No. 5558867
 ; GENERAL INFORMATION:
 ; APPLICANT: Sakaguchi, Masaaki
 ; APPLICANT: Yamamoto, Michitaka
 ; TITLE OF INVENTION: RECOMBINANT MAREK'S DISEASE VIRUS,
 ; TITLE OF INVENTION: PROCESS FOR PREPARING THE SAME AND VACCINE CONTAINING THE
 ; TITLE OF INVENTION: SAME
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Wegner, Cantor, Mueller & Player
 ; STREET: 1233 20th Street, N.W.
 ; CITY: Washington
 ; STATE: D.C.
 ; ZIP: 20036-8218
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/272,513
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/910,554
 ; FILING DATE: 08-JUL-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Player, William E
 ; REGISTRATION NUMBER: 31,409
 ; REFERENCE/DOCKET NUMBER: P-500-23477
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-887-0400
 ; TELEFAX: 202-835-0605
 ; TELEX: 440706
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3001 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; ORIGINAL SOURCE:
 ; ORGANISM: Marek's disease gammaherpesvirus
 ; STRAIN: 61-554 and BC-1
 ; US-08-272-513-1

Query Match 67.9%; Score 42.8; DB 1; Length 3001;
 Best Local Similarity 80.6%; Pred. No. 3e-07;
 Matches 50; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
 QY 1 TTTAAGTCCTAGTCGATACATATAAGCCATTTCACCATTCACCATTCACCATTCGTCGAC 60
 Db 2110 TATAAGCTGTGGCCACCATCAATAAAGCCATTTTACCATTCACCATTCGTCGAC 2169
 QY 61 CT 62
 Db 2170 CT 2171

RESULT 62

US-08-379-452-9/C
 ; Sequence 9, Application US/08379452
 ; Patent No. 6040174
 ; GENERAL INFORMATION:
 ; APPLICANT: IMELER, Jean-Luc
 ; APPLICANT: MEHTALI, Majid
 ; APPLICANT: PAVIRANI, Andrea

; TITLE OF INVENTION: DEFECTIVE ADENOVIRUSES AND CORRESPONDING
 ; TITLE OF INVENTION: COMPLEMENTATION LINES
 ; NUMBER OF SEQUENCES: 43
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
 ; STREET: 1737 King Street, Suite 500
 ; CITY: Alexandria
 ; STATE: Virginia
 ; COUNTRY: United States
 ; ZIP: 22314-2756
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/379,452
 ; FILING DATE: 26-JAN-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: WO PCT/FR94/00624
 ; FILING DATE: 27-MAY-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: FR 93 06482
 ; FILING DATE: 28-MAY-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Dadio, Susan M.
 ; REGISTRATION NUMBER: 40,373
 ; REFERENCE/DOCKET NUMBER: 029395-002
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 47 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: YES
 ; ORIGINAL SOURCE:
 ; ORGANISM: Synthetic oligonucleotide (OTG5893)
 ; US-08-379-452-9

Query Match 52.4%; Score 33; DB 3; Length 47;
 Best Local Similarity 100.0%; Pred. No. 0.00068;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 30 CCATTTCACCATTCACCATTCGTCGACCT 62
 Db 47 CCATTTCACCATTCACCATTCGTCGACCT 15

RESULT 63

US-08-682-794-5/C
 ; Sequence 5, Application US/08682794
 ; Patent No. 6110735
 ; GENERAL INFORMATION:
 ; APPLICANT: Ccile CHARTIER et al.
 ; TITLE OF INVENTION: METHOD OF PREPARING A VIRAL VECTOR BY INTERMOLECULAR
 ; TITLE OF INVENTION: HOMOLOGOUS RECOMBINATION
 ; FILE REFERENCE: 032751-002
 ; CURRENT APPLICATION NUMBER: US/08/682,794
 ; CURRENT FILING DATE: 1996-08-01
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: Patent in Ver. 2.1
 ; SEQ ID NO 5
 ; LENGTH: 47
 ; TYPE: DNA
 ; ORGANISM: rous sarcoma virus
 ; US-08-682-794-5

Query Match 52.4%; Score 33; DB 3; Length 47;
 Best Local Similarity 100.0%; Pred. No. 0.00068;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 30 CCATTGACCAATTCACCACTGGTGTGCACCT 62
Db 47 CCAATTGACCAATTCACCACTGGTGTGCACCT 15

RESULT 64
US-09-409-670-9/c
; Sequence 9, Application US/09409670
; Patent No. 6133028
; GENERAL INFORMATION:
; APPLICANT: IMLER, Jean-Luc
; APPLICANT: MEHTALI, Majid
; APPLICANT: PAVIRANI, Andrea
; TITLE OF INVENTION: DEFECTIVE ADENOVIRUSES AND CORRESPONDING
; COMPLEMENTATION LINES
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: 1737 King Street, Suite 500
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22314-2756
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/409,670
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/379,452
; FILING DATE: 26-JAN-1995
; APPLICATION NUMBER: WO PCT/FR94/00624
; FILING DATE: 27-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93 06482
; FILING DATE: 28-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Dadlo, Susan M.
; REGISTRATION NUMBER: 40,373
; REFERENCE/DOCKET NUMBER: 029395-002
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 47 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; ORIGINAL SOURCE:
; ORGANISM: Synthetic oligonucleotide (OTG5893)
US-09-409-670-9

Query Match 52.4%; Score 33; DB 3; Length 47;
Best Local Similarity 100.0%; Pred. No. 0.00068;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CCATTGACCAATTCACCACTGGTGTGCACCT 62
Db 47 CCAATTGACCAATTCACCACTGGTGTGCACCT 15

RESULT 65
US-09-467-952-5/c
; Sequence 9, Application US/09409670
; Patent No. 6133028
; GENERAL INFORMATION:
; APPLICANT: IMLER, Jean-Luc
; APPLICANT: MEHTALI, Majid
; APPLICANT: PAVIRANI, Andrea
; TITLE OF INVENTION: DEFECTIVE ADENOVIRUSES AND CORRESPONDING
; COMPLEMENTATION LINES
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: 1737 King Street, Suite 500
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22314-2756
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/409,670
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/379,452
; FILING DATE: 26-JAN-1995
; APPLICATION NUMBER: WO PCT/FR94/00624
; FILING DATE: 27-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93 06482
; FILING DATE: 28-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Dadlo, Susan M.
; REGISTRATION NUMBER: 40,373
; REFERENCE/DOCKET NUMBER: 029395-002
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 47 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; ORIGINAL SOURCE:
; ORGANISM: Synthetic oligonucleotide (OTG5893)
US-09-409-670-9

Query Match 52.4%; Score 33; DB 3; Length 47;
Best Local Similarity 100.0%; Pred. No. 0.00068;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CCATTGACCAATTCACCACTGGTGTGCACCT 62
Db 47 CCAATTGACCAATTCACCACTGGTGTGCACCT 15

RESULT 66
US-08-989-394-10
; Sequence 10, Application US/08989394
; Patent No. 5994136
; GENERAL INFORMATION:
; APPLICANT: Naldini, Luigi
; APPLICANT: Dull, Thomas
; APPLICANT: Farson, Deborah A.
; APPLICANT: Witt, Rochelle
; TITLE OF INVENTION: METHOD AND MEANS FOR PRODUCING HIGH
; TITRE OF INVENTION: TITER, SAFE, RECOMBINANT LENTIVIRUS VECTORS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/989,394
; FILING DATE: 12-DEC-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Dean H.
; REGISTRATION NUMBER: 33,981
; REFERENCE/DOCKET NUMBER: A7086
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 74 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-989-394-10

Query Match 46.0%; Score 29; DB 2; Length 74;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCCTAGCTCGATACATAAAG 29
```


Db 27 TTTAAGTCCTAGCTCGATACATAAAGC 55
|||||

RESULT 67

US-08-989-394-11/c
; Sequence 11, Application US/08989394
; Patent No. 5994136
; GENERAL INFORMATION:
; APPLICANT: Naldini, Luigi
; APPLICANT: Dull, Thomas
; APPLICANT: Farson, Deborah A.
; APPLICANT: Witt, Rochelle
; TITLE OF INVENTION: METHOD AND MEANS FOR PRODUCING HIGH
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,394
FILING DATE: 12-DEC-1997
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Nakamura, Dean H.
REGISTRATION NUMBER: 33,981
REFERENCE/DOCKET NUMBER: A7086
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA

US-08-989-394-11
Query Match 46.0%; Score 29; DB 2; Length 74;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTTAAGTCCTAGCTCGATACATAAAGC 29
Db 52 TTTAAGTCCTAGCTCGATACATAAAGC 24
|||||

RESULT 68

US-09-271-365-10
; Sequence 10, Application US/09271365
; Patent No. 6165782
; GENERAL INFORMATION:
; APPLICANT: Naldini, Luigi
; APPLICANT: Dull, Thomas
; APPLICANT: Farson, Deborah A.
; APPLICANT: Witt, Rochelle
; TITLE OF INVENTION: METHOD AND MEANS FOR PRODUCING HIGH
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington

STATE: D.C.
COUNTRY: USA
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/271,365
FILING DATE: 18-Mar-1999
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/989,394
FILING DATE: 12-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Nakamura, Dean H.
REGISTRATION NUMBER: 33,981
REFERENCE/DOCKET NUMBER: A7086
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860

INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-271-365-10

Query Match 46.0%; Score 29; DB 3; Length 74;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTTAAGTCCTAGCTCGATACATAAAGC 29
Db 27 TTTAAGTCCTAGCTCGATACATAAAGC 55
|||||

RESULT 69

US-09-271-365-11/c
; Sequence 11, Application US/09271365
; Patent No. 6165782
; GENERAL INFORMATION:
; APPLICANT: Naldini, Luigi
; APPLICANT: Dull, Thomas
; APPLICANT: Farson, Deborah A.
; APPLICANT: Witt, Rochelle
; TITLE OF INVENTION: METHOD AND MEANS FOR PRODUCING HIGH
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/271,365
FILING DATE: 18-Mar-1999
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/989,394
FILING DATE: 12-DEC-1997
ATTORNEY/AGENT INFORMATION:

```

US-09-604-013A-10
Query Match          46.0%; Score 29; DB 4; Length 74;
Best Local Similarity 100.0%; Pred.No.0.027;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTTAAGTCCTAGCTCGATACATAAACG 29
        |||||
Db       27 TTTAAGTCCTAGCTCGATACATAAACG 55

RESULT 71
US-09-604-013A-11/c
; Sequence 11, Application US/09604013A
; Patent No. 6428953
; GENERAL INFORMATION:
; APPLICANT: Naldini, Luigi
;           Dull, Thomas
;           Farson, Deborah A.
;           Witt, Rochelle
; TITLE OF INVENTION: METHOD AND MEANS FOR PRODUCING HIGH
;                   TITER, SAFE, RECOMBINANT LENTIVIRUS VECTORS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSES: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/604.013A
; FILING DATE: 26-Jun-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/271,365
; FILING DATE: 18-Mar-1999
; APPLICATION NUMBER: 08/989,394
; FILING DATE: 12-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Dean H.
; REGISTRATION NUMBER: 33,981
; REFERENCE/DOCKET NUMBER: A7086
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 74 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:

US-09-604-013A-11
Query Match          46.0%; Score 29; DB 4; Length 74;
Best Local Similarity 100.0%; Pred.No.0.027;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTTAAGTCCTAGCTCGATACATAAACG 29
        |||||
Db       52 TTTAAGTCCTAGCTCGATACATAAACG 24

RESULT 72
US-09-167-322-10
; Sequence 10, Application US/09167322

```

```
; Patent No. 6365151
; GENERAL INFORMATION:
; APPLICANT: Allegheny University of the Health
; Sciences, Halpern, Michael S.
; England, James M.
; TITLE OF INVENTION: CANCER VACCINE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seidel, Gonda, Lavorigna & Monaco, P.C.
; STREET: Suite 1800, Two Penn Center Plaza
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 07-Oct-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/00582
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 7933-33 PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-5549
; TELEFAX: (215) 568-5549
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
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; RESULT 73
US-08-404-531B-19
; Sequence 19, Application US/08404531B
; Patent No. 5863724
; GENERAL INFORMATION:
; APPLICANT: Joseph Bryan, Lydia Aguilar Bryan, Daniel Nelson, Pamela
; APPLICANT: Thomas, Gilbert Cote, and Robert Gagel
; TITLE OF INVENTION: Sequence Encoding Mammalian Sulfonyleurea Receptor
; Patent No. 5863724
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: No. 5863724ris
; STREET: One Liberty Place 46th. Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Beardell, Lori Y.
; REGISTRATION NUMBER: 34,293
; REFERENCE/DOCKET NUMBER: BYLR-0027
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: NO
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-404-531B-19
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Best Local Similarity 100.0%; Pred. No. 0.73;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; RESULT 74
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; Sequence 19, Application US/08476900A
; Patent No. 6031150
; GENERAL INFORMATION:
; APPLICANT: Joseph Bryan, Lydia Aguilar Bryan, Daniel Nelson
; TITLE OF INVENTION: Sequence Encoding Mammalian Sulfonyleurea Receptor
; Patent No. 6031150
; TITLE OF INVENTION: and Method of Detecting Persistent Hyperinsulinemic Hypoglycemia
; TITLE OF INVENTION: Infancy
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: No. 6031150ris
; STREET: One Liberty Place 46th. Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Beardell, Lori Y.
; REGISTRATION NUMBER: 34,293
; REFERENCE/DOCKET NUMBER: BYLR-0027
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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; MOLECULE TYPE: nucleic acid
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-476-900A-19

Query Match 39.7%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.73;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 75

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; Sequence 19, Application US/08488546A
; Patent No. 6054313
; GENERAL INFORMATION:
; APPLICANT: Joseph Bryan, Lydia Aguilar Bryan, Daniel Nelson, Pamela
; APPLICANT: Thomas, Gilbert Cote, and Robert Gagel
; TITLE OF INVENTION: Sequence Encoding Mammalian Sulfonyleurea Receptor
; Patent No. 6054313
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: No. 6054313rls
; STREET: One Liberty Place 46th. Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,546A
; FILING DATE: 07-JUNE-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/404,531
; FILING DATE: 15-MARCH-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Beardsell, Lori Y.
; REGISTRATION NUMBER: 34,293
; REFERENCE/DOCKET NUMBER: BYLR-0026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: nucleic acid
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-488-546A-19

Query Match 39.7%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.73;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Search completed: March 11, 2004, 11:10:02

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	63	100.0	7492	14	US-10-340-112-5
4	63	100.0	8238	10	US-09-482-682-50
5	63	100.0	8902	9	US-09-729-416A-1
6	63	100.0	9737	14	US-10-331-329-22
7	63	100.0	9737	14	US-10-331-329-23
8	63	100.0	9737	14	US-10-331-329-28
9	63	100.0	9871	14	US-10-331-329-24
10	63	100.0	10060	14	US-10-331-329-25
11	63	100.0	11265	14	US-10-185-318-1
12	63	100.0	11265	14	US-10-185-799-1
13	63	100.0	11600	9	US-09-847-101B-35
14	63	100.0	11600	10	US-09-482-682-49
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22	60.4	95.9	262	12	US-10-239-134-61	Sequence 61, Appl
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51	23.2	36.8	834	15	US-10-027-632-165753	Sequence 165753, A
52	23	36.5	644	9	US-09-764-869-459	Sequence 459, App
53	23	36.5	644	14	US-10-031-504-459	Sequence 459, App
54	23	36.5	644	15	US-10-027-577-459	Sequence 459, App
55	23	36.5	798	15	US-10-027-632-115884	Sequence 115884, A
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76	22.4	35.6	611	15	US-10-027-632-35525	Sequence 35525, A
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79	22.4	35.6	926	15	US-10-027-632-325340	Sequence 325340, A
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81	22.4	35.6	1488	14	US-10-305-765-1	Sequence 1, Appl
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83	22.4	35.6	1488	14	US-10-305-633-1	Sequence 1, Appl
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85	22.4	35.6	2848	9	US-09-938-980-197	Sequence 197, App
86	22.4	35.6	7945	14	US-10-138-098-49	Sequence 49, Appl
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88	22.4	35.6	17310	8	US-08-781-986A-23	Sequence 23, Appl

89 22.4 35.6 17310 12 US-10-329-624-23 Sequence 23, Appl
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 c 92 22.2 35.2 305 12 US-10-424-599-28157 Sequence 28157, A
 c 93 22.2 35.2 822 15 US-10-369-493-23964 Sequence 23964, A
 c 94 22.2 35.2 5139 9 US-09-764-869-1894 Sequence 1894, Ap
 c 95 22.2 35.2 5139 14 US-10-091-504-1894 Sequence 1894, Ap
 c 96 22.2 35.2 5139 15 US-10-227-577-1894 Sequence 1894, Ap
 c 97 22.2 35.2 8697 12 US-10-158-844-123 Sequence 123, App
 c 98 22.2 35.2 78056 13 US-10-409-551-1 Sequence 1, Appli
 c 99 22 34.9 39 10 US-09-996-073-28 Sequence 28, Appl
 c 100 22 34.9 411 9 US-09-864-761-17008 Sequence 17008, A

ALIGNMENTS

RESULT 1
 US-10-331-329-18
 ; Sequence 18, Application US/10331329
 ; Publication No. US20030180267A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HARRINGTON, JOHN J.
 ; APPLICANT: SHERP, BRUCE
 ; APPLICANT: RUNDLETT, STEPHEN
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
 ; TITLE OF INVENTION: ENDOGENOUS GENES
 ; FILE REFERENCE: 0221-0003CON
 ; CURRENT APPLICATION NUMBER: US/10/331,329
 ; CURRENT FILING DATE: 2002-12-30
 ; PRIOR APPLICATION NUMBER: 09/276,820
 ; PRIOR FILING DATE: 1999-03-26
 ; PRIOR APPLICATION NUMBER: 09/263,814
 ; PRIOR FILING DATE: 1999-03-08
 ; PRIOR APPLICATION NUMBER: 09/253,022
 ; PRIOR FILING DATE: 1999-02-19
 ; PRIOR APPLICATION NUMBER: 09/159,643
 ; PRIOR FILING DATE: 1998-09-24
 ; PRIOR APPLICATION NUMBER: 08/941,223
 ; PRIOR FILING DATE: 1997-09-26
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 18
 ; LENGTH: 6836
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-331-329-18

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 Best Local Similarity 100.0%; Pred. No. 5.5e-14;
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 QY 61 CTC 63
 Db 1820 CTC 1822

RESULT 2
 US-10-267-117-5
 ; Sequence 5, Application US/10267117
 ; Publication No. US20030082162A1
 ; GENERAL INFORMATION:
 ; APPLICANT: FLOTTE, TERENCE R.
 ; APPLICANT: SONG, SIHONG
 ; APPLICANT: BYRNE, BARRY J.
 ; APPLICANT: MORGAN, MICHAEL
 ; TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
 ; FILE REFERENCE: 4300.011800
 ; CURRENT APPLICATION NUMBER: US/10/267,117

; CURRENT FILING DATE: 2002-10-08
 ; PRIOR APPLICATION NUMBER: US/09/299,141
 ; PRIOR FILING DATE: 1999-04-23
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/083,025
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-24
 ; NUMBER OF SEQ ID NOS: 13
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 ; OTHER INFORMATION: Description of Artificial Sequence:p43C-AT-IN
 US-10-267-117-5

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 Db 87 CTC 89

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 ; GENERAL INFORMATION:
 ; APPLICANT: FLOTTE, TERENCE R.
 ; APPLICANT: SONG, SIHONG
 ; APPLICANT: BYRNE, BARRY J.
 ; APPLICANT: MORGAN, MICHAEL
 ; TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
 ; FILE REFERENCE: 4300.011800
 ; CURRENT APPLICATION NUMBER: US/10/340,112
 ; CURRENT FILING DATE: 2003-01-10
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 Best Local Similarity 100.0%; Pred. No. 5.7e-14;
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RESULT 4
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 ; Sequence 50, Application US/09482682
 ; Publication No. US20030157688A1
 ; GENERAL INFORMATION:

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; APPLICANT: VON SEGGERN, DANIEL
; APPLICANT: NEMEROW, GLEN R.
; APPLICANT: HALLENBECK, PAUL
; APPLICANT: STEVENSON, SUSAN
; APPLICANT: SKIPCHENKO, YELENA
; TITLE OF INVENTION: ADENOVIRUS VECTORS, PACKAGING CELL LINES, COMPOSITIONS,
; TITLE OF INVENTION: AND METHODS FOR PREPARATION AND USE
; FILE REFERENCE: 1294.0010001
; CURRENT APPLICATION NUMBER: US/09/482,682
; CURRENT FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.1
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; LENGTH: 8238
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-09-482-682-50

Query Match          100.0%; Score 63; DB 10; Length 8238;
Best Local Similarity 100.0%; Pred. No. 5.8e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 802 CTC 804

RESULT 5
US-09-729-416A-1
; Sequence 1, Application US/03729416A
; Patent No. US20020055172A1
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; TITLE OF INVENTION: MULTIPLE PROMOTER EXPRESSION CONSTRUCTS AND METHODS OF
; TITLE OF INVENTION: USE
; FILE REFERENCE: 0221-0004C
; CURRENT APPLICATION NUMBER: US/09/729,416A
; CURRENT FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 8902
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
; OTHER INFORMATION: (PRIG-NEL)
US-09-729-416A-1

Query Match          100.0%; Score 63; DB 9; Length 8902;
Best Local Similarity 100.0%; Pred. No. 6e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
    |||||
Db 3826 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 3885
    |||||

Qy 61 CTC 63
    |||
Db 3886 CTC 3888

RESULT 6
US-10-331-329-22
; Sequence 22, Application US/10331329
; Publication No. US20030180267A1
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; TITLE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003CON
; CURRENT APPLICATION NUMBER: US/10/331,329
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
```

```
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; TITLE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003CON
; CURRENT APPLICATION NUMBER: US/10/331,329
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-10-331-329-22

Query Match          100.0%; Score 63; DB 14; Length 9737;
Best Local Similarity 100.0%; Pred. No. 6.2e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
    |||||
Db 1613 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 1672
    |||||

Qy 61 CTC 63
    |||
Db 1673 CTC 1675

RESULT 7
US-10-331-329-23
; Sequence 23, Application US/10331329
; Publication No. US20030180267A1
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; TITLE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003CON
; CURRENT APPLICATION NUMBER: US/10/331,329
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
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; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-10-331-329-23

Query Match      100.0%; Score 63; DB 14; Length 9737;
Best Local Similarity 100.0%; Pred. No. 6.2e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTTAAGTCCTAGCTCGATACATAAAGCCATTGACCAATTCACCAATGGTGTGCAC 60
Db      1613 TTTAAGTCCTAGCTCGATACATAAAGCCATTGACCAATTCACCAATGGTGTGCAC 1672

QY      61 CTC 63
Db      1673 CTC 1675

RESULT 8
US-10-331-329-28
; Sequence 28, Application US/10331329
; Publication No. US20030180267A1
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003CON
; CURRENT APPLICATION NUMBER: US/10/331,329
; PRIOR FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8633)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-10-331-329-24

Query Match      100.0%; Score 63; DB 14; Length 9737;
Best Local Similarity 100.0%; Pred. No. 6.2e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTTAAGTCCTAGCTCGATACATAAAGCCATTGACCAATTCACCAATGGTGTGCAC 60
Db      1613 TTTAAGTCCTAGCTCGATACATAAAGCCATTGACCAATTCACCAATGGTGTGCAC 1672

QY      61 CTC 63
Db      1673 CTC 1675

RESULT 9
US-10-331-329-24
; Sequence 24, Application US/10331329
; Publication No. US20030180267A1
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003CON
; CURRENT APPLICATION NUMBER: US/10/331,329
; PRIOR FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 9871
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8481)
; OTHER INFORMATION: a, c, t, g, other or unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8633)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-10-331-329-24

Query Match      100.0%; Score 63; DB 14; Length 9871;
Best Local Similarity 100.0%; Pred. No. 6.2e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTTAAGTCCTAGCTCGATACATAAAGCCATTGACCAATTCACCAATGGTGTGCAC 60
Db      1747 TTTAAGTCCTAGCTCGATACATAAAGCCATTGACCAATTCACCAATGGTGTGCAC 1806

QY      61 CTC 63
Db      1807 CTC 1809

RESULT 10
US-10-331-329-25
; Sequence 25, Application US/10331329
; Publication No. US20030180267A1
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003CON
; CURRENT APPLICATION NUMBER: US/10/331,329
; PRIOR FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/263,814
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; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 10060
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8670)
; OTHER INFORMATION: a, c, t, g, other or unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8922)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-10-331-329-25

Query Match 100.0%; Score 63; DB 14; Length 10060;
Best Local Similarity 100.0%; Pred. No. 6.2e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
|||||
Db 1936 TTTAAGTCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 1995

QY 61 CTC 63
|||
Db 1996 CTC 1998

RESULT 11
US-10-185-318-1
; Sequence 1, Application US/10185318
; Publication No. US20030035793A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, JEFFREY S.
; APPLICANT: BRADY, JAMIE L.
; APPLICANT: LEW, ANDREW M.
; TITLE OF INVENTION: NOVEL IMMUNE RESPONSE TARGETING MOLECULES
; FILE REFERENCE: FBRC:009USC2
; CURRENT APPLICATION NUMBER: US/10/185,318
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 09/402,020
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: PCT/AU98/00208
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: AU PP5891
; PRIOR FILING DATE: 1997-03-27
; PRIOR APPLICATION NUMBER: AU PP1830
; PRIOR FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 11265
; TYPE: DNA
; ORGANISM: Murine
US-10-185-318-1

Query Match 100.0%; Score 63; DB 14; Length 11265;
Best Local Similarity 100.0%; Pred. No. 6.5e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
|||||
Db 571 TTTAAGTCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 630

QY 61 CTC 63

Db 631 CTC 633
|||

RESULT 12
US-10-185-799-1
; Sequence 1, Application US/10185799
; Publication No. US20030072742A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, JEFFREY S.
; APPLICANT: BRADY, JAMIE L.
; APPLICANT: LEW, ANDREW M.
; TITLE OF INVENTION: ENHANCEMENT OF IMMUNE RESPONSE USING TARGETING
; TITLE OF INVENTION: MOLECULES
; FILE REFERENCE: FBRC:009USC1
; CURRENT APPLICATION NUMBER: US/10/185,799
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 09/402,020
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: PCT/AU98/00208
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: AU PP5891
; PRIOR FILING DATE: 1997-03-27
; PRIOR APPLICATION NUMBER: AU PP1830
; PRIOR FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 11265
; TYPE: DNA
; ORGANISM: Murine
US-10-185-799-1

Query Match 100.0%; Score 63; DB 14; Length 11265;
Best Local Similarity 100.0%; Pred. No. 6.5e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
|||||
Db 571 TTTAAGTCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 630

QY 61 CTC 63
|||
Db 631 CTC 633

RESULT 13
US-09-847-101B-35
; Sequence 35, Application US/09847101B
; Publication No. US20020193327A1
; GENERAL INFORMATION:
; APPLICANT: VON SEGGERN, DANIEL
; APPLICANT: NEMEROW, GLEN R.
; APPLICANT: FRIEDLANDER, MARTIN
; TITLE OF INVENTION: VECTORS FOR OCULAR TRANSDUCTION AND USE THEREFOR FOR GENETIC THERAPY
; FILE REFERENCE: 22908-1226B
; CURRENT APPLICATION NUMBER: US/09/847,101B
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/562,934
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 11600
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid MMTV-E2a-SV40-Neo
US-09-847-101B-35

Query Match 100.0%; Score 63; DB 9; Length 11600;
Best Local Similarity 100.0%; Pred. No. 6.5e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACATAAAGCGCATTTGACCAATTCACCAATTTGGTGTGCAC 60
|||||
Db 27 TTTAAGTCCTAGCTCGATACATAAAGCGCATTTGACCAATTCACCAATTTGGTGTGCAC 86
QY 61 CTC 63
|||
Db 87 CTC 89

RESULT 14
US-09-482-682-49
; Sequence 49, Application US/09482682
; Publication No. US20030157688A1
; GENERAL INFORMATION:
; APPLICANT: VON SEGGERN, DANIEL
; APPLICANT: NEMEROW, GLEN R.
; APPLICANT: HALLENBECK, PAUL
; APPLICANT: STEVENSON, SUSAN
; APPLICANT: SKRIPCHENKO, YELENA
; TITLE OF INVENTION: ADENOVIRUS VECTORS, PACKAGING CELL LINES, COMPOSITIONS,
; AND METHODS FOR PREPARATION AND USE
; FILE REFERENCE: 1294.0010001
; CURRENT APPLICATION NUMBER: US/09/482,682
; CURRENT FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 11600
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-09-482-682-49

Query Match 100.0%; Score 63; DB 10; Length 11600;
Best Local Similarity 100.0%; Pred. No. 6.5e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACATAAAGCGCATTTGACCAATTCACCAATTTGGTGTGCAC 60
|||||
Db 27 TTTAAGTCCTAGCTCGATACATAAAGCGCATTTGACCAATTCACCAATTTGGTGTGCAC 86
QY 61 CTC 63
|||
Db 87 CTC 89

RESULT 15
US-10-403-337-42
; Sequence 42, Application US/10403337
; Publication No. US20030215948A1
; GENERAL INFORMATION:
; APPLICANT: Kaleko, Michael
; APPLICANT: Nemerow, Glen R.
; APPLICANT: Smith, Theodore
; APPLICANT: Stevenson, Susan C.
; TITLE OF INVENTION: Fiber Shaft Modifications for Efficient Targeting
; FILE REFERENCE: 22908-1236B
; CURRENT APPLICATION NUMBER: US/10/403,337
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: 10/351,890
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 60/350,388
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/391,967
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 42
; LENGTH: 11600
; TYPE: DNA
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Plasmid MMTV-E2a-SV40-Nco
US-10-403-337-42

Query Match 100.0%; Score 63; DB 15; Length 11600;
Best Local Similarity 100.0%; Pred. No. 6.5e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACATAAAGCGCATTTGACCAATTCACCAATTTGGTGTGCAC 60
|||||
Db 27 TTTAAGTCCTAGCTCGATACATAAAGCGCATTTGACCAATTCACCAATTTGGTGTGCAC 86
QY 61 CTC 63
|||
Db 87 CTC 89

RESULT 16
US-10-351-890-42
; Sequence 42, Application US/10351890
; Publication No. US20040002060A1
; GENERAL INFORMATION:
; APPLICANT: Stevenson, Susan C.
; APPLICANT: Kaleko, Michael
; APPLICANT: Smith, Theodore
; APPLICANT: Nemerow, Glen R.
; TITLE OF INVENTION: Fiber Shaft Modifications for Efficient Targeting
; FILE REFERENCE: 22908-1236
; CURRENT APPLICATION NUMBER: US/10/351,890
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: 60/350,388
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/391,967
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 42
; LENGTH: 11600
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid MMTV-E2a-SV40-Nco
US-10-351-890-42

Query Match 100.0%; Score 63; DB 15; Length 11600;
Best Local Similarity 100.0%; Pred. No. 6.5e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACATAAAGCGCATTTGACCAATTCACCAATTTGGTGTGCAC 60
|||||
Db 27 TTTAAGTCCTAGCTCGATACATAAAGCGCATTTGACCAATTCACCAATTTGGTGTGCAC 86
QY 61 CTC 63
|||
Db 87 CTC 89

RESULT 17
US-10-403-337-44
; Sequence 44, Application US/10403337
; Publication No. US20030215948A1
; GENERAL INFORMATION:
; APPLICANT: Kaleko, Michael
; APPLICANT: Nemerow, Glen R.
; APPLICANT: Smith, Theodore
; APPLICANT: Stevenson, Susan C.
; TITLE OF INVENTION: Fiber Shaft Modifications for Efficient Targeting
; FILE REFERENCE: 22908-1236B
; CURRENT APPLICATION NUMBER: US/10/403,337
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: 10/351,890
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 60/350,388

```
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/391,967
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 44
; LENGTH: 33622
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid Av3nBg
US-10-403-337-44

Query Match          100.0%; Score 63; DB 15; Length 33622;
Best Local Similarity 100.0%; Pred. No. 9.2e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
    |||||
Db 734 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 793

QY 61 CTC 63
    |||
Db 794 CTC 796

RESULT 18
US-10-351-890-44
; Sequence 44, Application US/10351890
; Publication No. US20040002060A1
; GENERAL INFORMATION:
; APPLICANT: Stevenson, Susan C.
; APPLICANT: Kaleko, Michael
; APPLICANT: Smith, Theodore
; APPLICANT: Nemerow, Glen R.
; TITLE OF INVENTION: Fiber Shaft Modifications for Efficient Targeting
; FILE REFERENCE: 22908-1236
; CURRENT APPLICATION NUMBER: US/10/351,890
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: 60/350,388
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/391,967
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 44
; LENGTH: 33622
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid Av3nBg
US-10-351-890-44

Query Match          100.0%; Score 63; DB 15; Length 33622;
Best Local Similarity 100.0%; Pred. No. 9.2e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
    |||||
Db 734 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 793

QY 61 CTC 63
    |||
Db 794 CTC 796

RESULT 19
US-10-403-337-43
; Sequence 43, Application US/10403337
; Publication No. US20030215948A1
; GENERAL INFORMATION:
; APPLICANT: Kaleko, Michael
; APPLICANT: Nemerow, Glen R.
```

```
; APPLICANT: Smith, Theodore
; APPLICANT: Stevenson, Susan C.
; TITLE OF INVENTION: Fiber Shaft Modifications for Efficient Targeting
; FILE REFERENCE: 22908-1236B
; CURRENT APPLICATION NUMBER: US/10/403,337
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: 10/351,890
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 60/350,388
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/391,967
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 43
; LENGTH: 35211
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid Av3nBg
US-10-403-337-43

Query Match          100.0%; Score 63; DB 15; Length 35211;
Best Local Similarity 100.0%; Pred. No. 9.3e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
    |||||
Db 848 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 907

QY 61 CTC 63
    |||
Db 908 CTC 910

RESULT 20
US-10-351-890-43
; Sequence 43, Application US/10351890
; Publication No. US20040002060A1
; GENERAL INFORMATION:
; APPLICANT: Stevenson, Susan C.
; APPLICANT: Kaleko, Michael
; APPLICANT: Smith, Theodore
; APPLICANT: Nemerow, Glen R.
; TITLE OF INVENTION: Fiber Shaft Modifications for Efficient Targeting
; FILE REFERENCE: 22908-1236
; CURRENT APPLICATION NUMBER: US/10/351,890
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: 60/350,388
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/391,967
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 43
; LENGTH: 35211
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid Av3nBg
US-10-351-890-43

Query Match          100.0%; Score 63; DB 15; Length 35211;
Best Local Similarity 100.0%; Pred. No. 9.3e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
    |||||
Db 848 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 907

QY 61 CTC 63
    |||
Db 908 CTC 910
```

RESULT 21

US-09-965-703-69
; Sequence 69, Application US/09965703
; Patent No. US20020119521A1
; GENERAL INFORMATION:
; APPLICANT: Rohm and Haas Company
; APPLICANT: Palli, Subba Reddy
; APPLICANT: Kapitskaya, Marianna Zinovjevna
; APPLICANT: Cress, Dean Ervin
; TITLE OF INVENTION: No. US20020119521A1el Ecdysone Receptor-Based Inducible Gene Expression
; FILE REFERENCE: A01020B
; CURRENT APPLICATION NUMBER: US/09/965,703
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/191,355
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/269,799
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: PCT/US01/09050
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
; LENGTH: 262
; TYPE: DNA
; ORGANISM: Rous sarcoma virus
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: No. US20020119521A1el Sequence
US-09-965-703-69

Query Match 95.9%; Score 60.4; DB 9; Length 262;

Best Local Similarity 98.4%; Pred. No. 2e-13;
Matches 61; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTAAGTGCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTCACCATTCGATGTCAC 60
|||||
Db 201 TTTAAGTGCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTCACCATTCGATGTCAC 260
61 CT 62
261 CT 262

RESULT 22

US-10-239-134-61
; Sequence 61, Application US/10239134
; Publication No. US20040033600A1
; GENERAL INFORMATION:
; APPLICANT: Rohm and Haas Company
; APPLICANT: Palli, Subba Reddy
; APPLICANT: Kapitskaya, Marianna Zinovjevna
; APPLICANT: Cress, Dean Ervin
; TITLE OF INVENTION: No. US20040033600A1el Ecdysone Receptor-Based Inducible Gene Expression
; FILE REFERENCE: RH0020
; CURRENT APPLICATION NUMBER: US/10/239,134
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: 60/191,355
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/269,799
; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 61
; LENGTH: 262
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: No. US20040033600A1el Sequence
US-10-239-134-61

Query Match 95.9%; Score 60.4; DB 12; Length 262;
Best Local Similarity 98.4%; Pred. No. 2e-13;
Matches 61; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTAAGTGCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTCACCATTCGATGTCAC 60
|||||
Db 201 TTTAAGTGCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTCACCATTCGATGTCAC 260
61 CT 62
261 CT 262

RESULT 23

US-10-264-237-633
; Sequence 633, Application US/10264237
; Publication No. US20040009491A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 633
; LENGTH: 766
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (56)..(56)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (91)..(91)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (141)..(141)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (652)..(652)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (753)..(753)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (763)..(763)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-264-237-633

Query Match 95.9%; Score 60.4; DB 15; Length 766;

Best Local Similarity 98.4%; Pred. No. 2.8e-13;
Matches 61; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTAAGTGCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTCACCATTCGATGTCAC 60
|||||
Db 169 TTTAAGTGCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTCACCATTCGATGTCAC 228
61 CT 62
229 CT 230

RESULT 24

US-09-921-143-36
; Sequence 36, Application US/09921143
; Publication No. US2003021591A1
; GENERAL INFORMATION:
; APPLICANT: Coleman, Timothy
; TITLE OF INVENTION: Vascular Endothelial Growth Factor-2
; FILE REFERENCE: PF112P6
; CURRENT APPLICATION NUMBER: US/09/921,143
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/223,276
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 5283
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-921-143-36
Query Match 95.4%; Score 60.4; DB 11; Length 5283;
Best Local Similarity 99.4%; Pred. No. 5.2e-13;
Matches 61; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TTTAAGTCCCTAGCTCGATACATAAAGCGCATTTGACCATTCACCATTTGGTGTGCAC 60
Db 424 TTTAAGTCCCTAGCTCGATACATAAAGCGCATTTGACCATTCACCATTTGGTGTGCAC 483
QY 61 CT 62
Db 484 CT 485

RESULT 25
US-09-897-006-9
; Sequence 9, Application US/09897006
; Patent No. US20020106729A1
; GENERAL INFORMATION:
; APPLICANT: Bleck, Gregory
; TITLE OF INVENTION: Expression Vectors
; FILE REFERENCE: GALA-06415
; CURRENT APPLICATION NUMBER: US/09/897,006
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/215,851
; PRIOR FILING DATE: 2000-07-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 5130
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-897-006-9
Query Match 74.3%; Score 46.8; DB 9; Length 5130;
Best Local Similarity 93.8%; Pred. No. 9.7e-08;
Matches 60; Conservative 0; Mismatches 2; Indels 2; Gaps 1;
QY 1 TTTAAGTCCCTAGCTCGATACATAAAGCGCA--TTTGACCATTCACCATTTGGTGTGC 58
Db 2527 TTTAAGTCCCTAGCTCGATACATAAAGCGCA--TTTGACCATTCACCATTTGGTGTGC 2586
QY 59 ACCT 62
Db 2587 ACCT 2590

RESULT 26
US-09-897-511a-9
; Sequence 9, Application US/09897511a
; Publication No. US2003009282A1
; GENERAL INFORMATION:
; APPLICANT: Bremel, Robert

; APPLICANT: Miller, Linda
; APPLICANT: Bleck, Gregory
; TITLE OF INVENTION: Host Cells Containing Multiple Integrating Vectors
; FILE REFERENCE: GALA-06416
; CURRENT APPLICATION NUMBER: US/09/897,511a
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/215,925
; PRIOR FILING DATE: 2000-07-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 5130
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-897-511a-9
Query Match 74.3%; Score 46.8; DB 10; Length 5130;
Best Local Similarity 93.8%; Pred. No. 9.7e-08;
Matches 60; Conservative 0; Mismatches 2; Indels 2; Gaps 1;
QY 1 TTTAAGTCCCTAGCTCGATACATAAAGCGCA--TTTGACCATTCACCATTTGGTGTGC 58
Db 2527 TTTAAGTCCCTAGCTCGATACATAAAGCGCA--TTTGACCATTCACCATTTGGTGTGC 2586
QY 59 ACCT 62
Db 2587 ACCT 2590
RESULT 27
US-09-725-720-9/c
; Sequence 9, Application US/09725720
; Patent No. US20010049136A1
; GENERAL INFORMATION:
; APPLICANT: IMLER, Jean-Luc
; APPLICANT: MEHTALI, Majid
; APPLICANT: PAVIRANI, Andrea
; TITLE OF INVENTION: DEFECTIVE ADENOVIRUSES AND CORRESPONDING
; TITLE OF INVENTION: COMPLEMENTATION LINES
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: 1737 King Street, Suite 500
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22314-2756
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/725,720
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/379,452
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93 06482
; FILING DATE: 28-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Dadio, Susan M.
; REGISTRATION NUMBER: 40,373
; REFERENCE/DOCKET NUMBER: 029395-002
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 47 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

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; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/379,452
; FILING DATE: <Unknown>
; APPLICATION NUMBER: FR 93 06482
; FILING DATE: 28-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Dadio, Susan M.
; REGISTRATION NUMBER: 40,373
; REFERENCE/DOCKET NUMBER: 029395-002
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 47 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Synthetic oligonucleotide (OTG5893)
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-739-007-9

Query Match      52.4%; Score 33; DB 10; Length 47;
Best Local Similarity 100.0%; Pred. No. 0.0048;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 30 CCATTGACCATTCACCATTTGGTGACCT 62
    ||||||||||||||||||||||||||||
Db 47 CCATTGACCATTCACCATTTGGTGACCT 15

RESULT 30
US-10-192-085-10
; Sequence 10, Application US/10192085
; Publication No. US20020173030A1
; GENERAL INFORMATION:
; APPLICANT: Naldini, Luigi
; Farson, Deborah A.
; Witt, Rochelle
; TITLE OF INVENTION: METHOD AND MEANS FOR PRODUCING HIGH
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/192,085
; FILING DATE: 10-Jul-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/271,365
; FILING DATE: 18-Mar-1999
; APPLICATION NUMBER: 08/989,394
; FILING DATE: 12-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Dean H.
; REGISTRATION NUMBER: 33,981
; REFERENCE/DOCKET NUMBER: A7086
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860

; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/379,452
; FILING DATE: <Unknown>
; APPLICATION NUMBER: FR 93 06482
; FILING DATE: 28-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Dadio, Susan M.
; REGISTRATION NUMBER: 40,373
; REFERENCE/DOCKET NUMBER: 029395-002
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 47 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Synthetic oligonucleotide (OTG5893)
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-739-007-9

Query Match      52.4%; Score 33; DB 9; Length 47;
Best Local Similarity 100.0%; Pred. No. 0.0048;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 30 CCATTGACCATTCACCATTTGGTGACCT 62
    ||||||||||||||||||||||||||||
Db 47 CCATTGACCATTCACCATTTGGTGACCT 15

RESULT 28
US-09-938-491-5/c
; Sequence 5, Application US/09938491
; Patent No. US2002090715A1
; GENERAL INFORMATION:
; APPLICANT: Cicle CHARTIER et al.
; TITLE OF INVENTION: METHOD OF PREPARING A VIRAL VECTOR BY INTERMOLECULAR
; TITLE OF INVENTION: HOMOLOGOUS RECOMBINATION
; FILE REFERENCE: 032751-002
; CURRENT APPLICATION NUMBER: US/09/938,491
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: 08/682,794
; PRIOR FILING DATE: 1996-08-01
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 47
; TYPE: DNA
; ORGANISM: rous sarcoma virus
US-09-938-491-5

Query Match      52.4%; Score 33; DB 9; Length 47;
Best Local Similarity 100.0%; Pred. No. 0.0048;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 30 CCATTGACCATTCACCATTTGGTGACCT 62
    ||||||||||||||||||||||||||||
Db 47 CCATTGACCATTCACCATTTGGTGACCT 15

RESULT 29
US-09-739-007-9/c
; Sequence 9, Application US/09739007
; Publication No. US20030170895A1
; GENERAL INFORMATION:
; APPLICANT: IMLER, Jean-Luc
; MEHTALI, Majid
; BAVIRANI, Andrea
; TITLE OF INVENTION: DEFECTIVE ADENOVIRUSES AND CORRESPONDING
; COMPLEMENTATION LINES
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: 1737 King Street, Suite 500
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22314-2756
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/739,007
; FILING DATE: 19-Dec-2000

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; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 74 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-192-085-10

Query Match 46.0%; Score 29; DB 13; Length 74;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCTAGCTCGATCAATAAAG 29
Db 27 TTTAAGTGCTAGCTCGATCAATAAAG 55

RESULT 31
US-10-192-085-11/c
; Sequence 11, Application US/10192085
; Publication No. US20020173030A1
; GENERAL INFORMATION:
; APPLICANT: Naldini, Luigi
; Dull, Thomas
; Farson, Deborah A.
; Witt, Rochelle
; TITLE OF INVENTION: METHOD AND MEANS FOR PRODUCING HIGH
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSER: SUCHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/192,085
; FILING DATE: 10-Jul-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/271,365
; FILING DATE: 18-Mar-1999
; APPLICATION NUMBER: 08/989,394
; FILING DATE: 12-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Dean H.
; REGISTRATION NUMBER: 33,981
; REFERENCE/DOCKET NUMBER: A7086
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 74 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-192-085-11

Query Match 46.0%; Score 29; DB 13; Length 74;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCTAGCTCGATCAATAAAG 29
Db 27 TTTAAGTGCTAGCTCGATCAATAAAG 55

RESULT 32
US-10-155-736A-1
; Sequence 1, Application US/10155736A
; Publication No. US20030095948A1
; GENERAL INFORMATION:
; APPLICANT: Universit. di Torino
; TITLE OF INVENTION: Vector and methods of use for selective expression of genes in s
; FILE REFERENCE: 36019/MMM
; CURRENT APPLICATION NUMBER: US/10/155,736A
; CURRENT FILING DATE: 2002-05-28
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: -
; SEQ ID NO 1
; LENGTH: 10469
; TYPE: DNA
; ORGANISM: HIV-1
US-10-155-736A-1

Query Match 46.0%; Score 29; DB 14; Length 10469;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCTAGCTCGATCAATAAAG 29
Db 2420 TTTAAGTGCTAGCTCGATCAATAAAG 2448

RESULT 33
US-10-369-493-37332
; Sequence 37332, Application US/10369493
; Publication No. US2003023675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 37332
; LENGTH: 765
; TYPE: DNA
; ORGANISM: Pseudomonas fluorescens
US-10-369-493-37332

Query Match 39.4%; Score 24.8; DB 15; Length 765;
Best Local Similarity 67.3%; Pred. No. 18;
Matches 35; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 4 AAGTGCTAGCTCGATCAATAAAGCCATTGACCATTCACACATTGGTG 55
Db 115 AAGTCTGGTGGTCGTAAACAATGCGCGTATTCACACTGTCACATTGGTG 166

RESULT 34
US-10-424-599-110305/c
; Sequence 110305, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:

```



```
/ APPLICANT: La Rosa Thomas J
/ APPLICANT: Kovalic David K
/ APPLICANT: Zhou Yihua
/ APPLICANT: Cao Yongwei
/ TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(53223)B
/ CURRENT APPLICATION NUMBER: US/10/424,599
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 285684
/ SEQ ID NO 110305
/ LENGTH: 741
/ TYPE: DNA
/ ORGANISM: Glycine max
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT3847_70617C.1
US-10-424-599-110305

Query Match      38.1%; Score 24; DB 12; Length 741;
Best Local Similarity 64.3%; Pred. No. 37;
Matches 36; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACATAAAGCGCATTTGACCATTCACCATTTGGTGT 56
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 695 TTGATGGCTTAAATCAATTCAGTGAAGTCTTTCATCATTCATTCATGT 640

RESULT 35
US-10-424-599-43374
/ Sequence 43374, Application US/10424599
/ Publication No. US20040031072A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa Thomas J
/ APPLICANT: Kovalic David K
/ APPLICANT: Zhou Yihua
/ APPLICANT: Cao Yongwei
/ TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(53223)B
/ CURRENT APPLICATION NUMBER: US/10/424,599
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 285684
/ SEQ ID NO 43374
/ LENGTH: 328
/ TYPE: DNA
/ ORGANISM: Glycine max
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT3847_139166C.1
US-10-424-599-43374

Query Match      37.8%; Score 23.8; DB 12; Length 328;
Best Local Similarity 72.1%; Pred. No. 34;
Matches 31; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 18 ATACATTAAGCGCATTTGACCATTCACCATTCACCATTTGGTGTGCAC 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 99 AGACATCGAAGCAATTTGATCATTTAATCCCATTTGATGTGCAC 141

RESULT 36
US-10-424-599-63137/c
/ Sequence 63137, Application US/10424599
/ Publication No. US20040031072A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa Thomas J
/ APPLICANT: Kovalic David K
/ APPLICANT: Zhou Yihua
/ APPLICANT: Cao Yongwei
/ TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(53223)B
/ CURRENT APPLICATION NUMBER: US/10/424,599
/ CURRENT FILING DATE: 2003-04-28
```

```
/ NUMBER OF SEQ ID NOS: 285684
/ SEQ ID NO 63137
/ LENGTH: 414
/ TYPE: DNA
/ ORGANISM: Glycine max
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT3847_28026C.1
US-10-424-599-63137

Query Match      37.8%; Score 23.8; DB 12; Length 414;
Best Local Similarity 66.7%; Pred. No. 36;
Matches 34; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACATAAAGCGCATTTGACCATTCACCATTT 51
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 390 TTGTGTGCATCTCTCTTAAAAAAGCGCGTTTGTCCATCATTAATAAT 340

RESULT 37
US-10-027-632-245976
/ Sequence 245976, Application US/10027632
/ Publication No. US20030204075A9
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
/ TITLE OF INVENTION: Polymorphisms in the Human Genome
/ FILE REFERENCE: 108827.129
/ CURRENT APPLICATION NUMBER: US/10/027,632
/ CURRENT FILING DATE: 2002-04-30
/ PRIOR APPLICATION NUMBER: US 60/218,006
/ PRIOR FILING DATE: 2000-07-12
/ PRIOR APPLICATION NUMBER: US 60/198,676
/ PRIOR FILING DATE: 2000-04-20
/ PRIOR APPLICATION NUMBER: US 60/193,483
/ PRIOR FILING DATE: 2000-03-29
/ PRIOR APPLICATION NUMBER: US 60/185,218
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/167,363
/ PRIOR FILING DATE: 1999-11-23
/ PRIOR APPLICATION NUMBER: US 60/156,358
/ PRIOR FILING DATE: 1999-09-28
/ PRIOR APPLICATION NUMBER: US 60/146,002
/ PRIOR FILING DATE: 1999-08-09
/ NUMBER OF SEQ ID NOS: 325720
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 245976
/ LENGTH: 629
/ TYPE: DNA
/ ORGANISM: Human
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT3847_139166C.1
US-10-027-632-245976

Query Match      37.8%; Score 23.8; DB 15; Length 629;
Best Local Similarity 72.1%; Pred. No. 42;
Matches 31; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 2 TTAAGTCCTAGCTCGATACATAAAGCGCATTTGACCATTTCA 44
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 454 TGAAGATCCAAGCTAATTCATCAAGCTATTGTGATTCATCA 496

RESULT 38
US-10-027-632-245977
/ Sequence 245977, Application US/10027632
/ Publication No. US20030204075A9
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
/ TITLE OF INVENTION: Polymorphisms in the Human Genome
/ FILE REFERENCE: 108827.129
/ CURRENT APPLICATION NUMBER: US/10/027,632
/ CURRENT FILING DATE: 2002-04-30
/ PRIOR APPLICATION NUMBER: US 60/218,006
/ PRIOR FILING DATE: 2000-07-12
```

;; PRIOR APPLICATION NUMBER: US 60/198,676
;; PRIOR FILING DATE: 2000-04-20
;; PRIOR APPLICATION NUMBER: US 60/193,483
;; PRIOR FILING DATE: 2000-03-29
;; PRIOR APPLICATION NUMBER: US 60/185,218
;; PRIOR FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: US 60/167,363
;; PRIOR FILING DATE: 1999-11-23
;; PRIOR APPLICATION NUMBER: US 60/156,358
;; PRIOR FILING DATE: 1999-09-28
;; PRIOR APPLICATION NUMBER: US 60/146,002
;; PRIOR FILING DATE: 1999-08-09
;; NUMBER OF SEQ ID NOS: 325720
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 245977
;; LENGTH: 629
;; TYPE: DNA
;; ORGANISM: Human
US-10-027-632-245977

Query Match 37.8%; Score 23.8; DB 15; Length 629;
Best Local Similarity 72.1%; Pred. No. 42;
Matches 31; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 2 TTAAGTCCTAGCTGATACAAATAAGCGCATTTGACCATTCACATCA 44
Db 454 TGAAGATCAAGCTAATTTCAATCAAGCTATTGATCATCA 496

RESULT 39

US-10-012-697-1087
;; Sequence 1087, Application US/10012697
;; Publication No. US20030215803A1
;; GENERAL INFORMATION:
;; APPLICANT: Escobedo, Jaime
;; APPLICANT: Garcia, Pablo Dominguez
;; APPLICANT: Kassam, Altaf
;; APPLICANT: Lamson, George
;; APPLICANT: Scott, Beth
;; APPLICANT: Drmanac, Radoje
;; APPLICANT: Crkvenjakov, Radomir
;; APPLICANT: Dickson, Mark
;; APPLICANT: Drmanac, Snezana
;; APPLICANT: Labat, Ivan
;; APPLICANT: Leshkowitz, Dena
;; APPLICANT: Kita, David
;; APPLICANT: Garcia, Veronica
;; APPLICANT: Jones, Lee William
;; APPLICANT: Stache-Crain, Birgit
;; TITLE OF INVENTION: HUMAN GENES AND GENE EXPRESSION PRODUCTS
;; TITLE OF INVENTION: ISOLATED FROM HUMAN PROSTATE
;; FILE REFERENCE: 2300-16252
;; CURRENT APPLICATION NUMBER: US/012,697
;; CURRENT FILING DATE: 2003-01-21
;; PRIOR APPLICATION NUMBER: 60/254,648
;; PRIOR FILING DATE: 2000-12-07
;; PRIOR APPLICATION NUMBER: 60/275,668
;; PRIOR FILING DATE: 2001-03-13
;; NUMBER OF SEQ ID NOS: 1568
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 1087
;; LENGTH: 735
;; TYPE: DNA
;; ORGANISM: Homo sapiens

;; NAME/KEY: misc feature
;; LOCATION: 546_568, 624, 631, 649, 725, 731, 734
;; OTHER INFORMATION: n = A,T,C or G
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: 546_568, 624, 631, 649, 725, 731, 734
;; OTHER INFORMATION: n = A,T,C or G
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: 546_568, 624, 631, 649, 725, 731, 734
;; OTHER INFORMATION: n = A,T,C or G
;; FEATURE:

;; NAME/KEY: misc feature
;; LOCATION: 546_568, 624, 631, 649, 725, 731, 734
;; OTHER INFORMATION: n = A,T,C or G
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: 546_568, 624, 631, 649, 725, 731, 734
;; OTHER INFORMATION: n = A,T,C or G
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: 546_568, 624, 631, 649, 725, 731, 734
;; OTHER INFORMATION: n = A,T,C or G
US-10-012-697-1087

Query Match 37.8%; Score 23.8; DB 15; Length 735;
Best Local Similarity 66.7%; Pred. No. 44;
Matches 34; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 1 TTAAAGTCCTAGCTGATACAAATAAGCGCATTTGACCATTCACCATTT 51
Db 357 TTATCTCCCTTTCTCCATAGATGCGCAATTTGACCTTATGCTACCT 407

RESULT 40

US-10-369-493-37698/c
;; Sequence 37698, Application US/10369493
;; Publication No. US20030233675A1
;; GENERAL INFORMATION:
;; APPLICANT: Cao, Yongwei
;; APPLICANT: Hinkle, Gregory J.
;; APPLICANT: Slater, Steven C.
;; APPLICANT: Goldman, Barry S.
;; APPLICANT: Chen, Xianfeng
;; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
;; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
;; FILE REFERENCE: 38-10(52052)B
;; CURRENT APPLICATION NUMBER: US/10/369,493
;; CURRENT FILING DATE: 2003-02-28
;; PRIOR APPLICATION NUMBER: US 60/360,039
;; PRIOR FILING DATE: 2002-02-21
;; NUMBER OF SEQ ID NOS: 47374
;; SEQ ID NO 37698
;; LENGTH: 738
;; TYPE: DNA
;; ORGANISM: Pseudomonas fluorescens
US-10-369-493-37698

Query Match 37.8%; Score 23.8; DB 15; Length 738;
Best Local Similarity 66.7%; Pred. No. 44;
Matches 34; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 13 GCTGATACAAATAAGCGCATTTGACCATTCACCATTCACCATTCGTTGCACTC 63
Db 624 GATCGCAGATAGACGCGCATTTGATCGAACAGCCCGGTGTTCGCG 574

RESULT 41

US-10-012-697-1335
;; Sequence 1335, Application US/10012697
;; Publication No. US20030215803A1
;; GENERAL INFORMATION:
;; APPLICANT: Escobedo, Jaime
;; APPLICANT: Garcia, Pablo Dominguez
;; APPLICANT: Kassam, Altaf
;; APPLICANT: Lamson, George
;; APPLICANT: Scott, Beth
;; APPLICANT: Drmanac, Radoje
;; APPLICANT: Crkvenjakov, Radomir
;; APPLICANT: Dickson, Mark
;; APPLICANT: Drmanac, Snezana
;; APPLICANT: Labat, Ivan
;; APPLICANT: Leshkowitz, Dena
;; APPLICANT: Kita, David
;; APPLICANT: Garcia, Veronica

[illegible][illegible]

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; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 3677
; LENGTH: 1174
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-3677

Query Match      37.5%; Score 23.6; DB 11; Length 1174;
Best Local Similarity 61.3%; Pred. No. 61;
Matches 38; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCGCAATTGACCAATTGACCAATTGCGTGTGCAC 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 467 TTATGTTGTAAGTACGAACAATAAACAATCATGAAACACTCGAAATATTGTAGTAAC 526
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 CT 62
Db 527 TT 528

RESULT 45
US-10-027-632-56424/c
; Sequence 56424, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56424
; LENGTH: 469
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-56424

Query Match      37.1%; Score 23.4; DB 15; Length 469;
Best Local Similarity 64.7%; Pred. No. 54;
Matches 33; Conservative 1; Mismatches 17; Indels 0; Gaps 0;

QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCGCAATTGACCAATTGACCAATTGCGTGTGCAC 51
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 213 TTACTCCCTTCYCCATAGATGACGCAATTGACCTTATGTACTACT 163
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 46
US-10-027-632-293958/c
; Sequence 293958, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56424
; LENGTH: 469
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-293958/c

Query Match      37.1%; Score 23.4; DB 15; Length 469;
Best Local Similarity 64.7%; Pred. No. 54;
Matches 33; Conservative 1; Mismatches 17; Indels 0; Gaps 0;

QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCGCAATTGACCAATTGACCAATTGCGTGTGCAC 51
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 213 TTACTCCCTTCYCCATAGATGACGCAATTGACCTTATGTACTACT 163
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 46
US-10-027-632-293958/c
; Sequence 293958, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 226287
; LENGTH: 640
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-226287

Query Match      37.1%; Score 23.4; DB 15; Length 640;
Best Local Similarity 64.7%; Pred. No. 54;
Matches 33; Conservative 1; Mismatches 17; Indels 0; Gaps 0;

```

```

; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 293958
; LENGTH: 469
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-293958

Query Match      37.1%; Score 23.4; DB 15; Length 469;
Best Local Similarity 64.7%; Pred. No. 54;
Matches 33; Conservative 1; Mismatches 17; Indels 0; Gaps 0;

QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCGCAATTGACCAATTGACCAATTGCGTGTGCAC 51
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 213 TTACTCCCTTCYCCATAGATGACGCAATTGACCTTATGTACTACT 163
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 47
US-10-027-632-226287
; Sequence 226287, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 226287
; LENGTH: 640
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-226287

Query Match      37.1%; Score 23.4; DB 15; Length 640;
Best Local Similarity 64.7%; Pred. No. 54;
Matches 33; Conservative 1; Mismatches 17; Indels 0; Gaps 0;

```

; PRIOR FILING DATE: 2000-03-21

Query Match	36.8%;	Score 23.2;	DB 15;	Length 834;
Best Local Similarity	65.4%;	Pred. No. 78;		
Matches	24;	Concentrative	0;	Mismatches
			18;	Indels

QY 2 TTAAGTCCCTAGCTGATACATAAAGCGCATTTGACCATTCACCATTTGG 53
Db 275 TTATAGCCTAGCTCTAAAGGATTAACCTGATTCAGTTTCACCACTCTGG 224

RESULT 51

US-10-027-632-165753/c
; Sequence 165753, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 168827.129
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 165753
; LENGTH: 834
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-165753

Query Match 36.8%; Score 23.2; DB 15; Length 834;
Best Local Similarity 65.4%; Pred. No. 78;
Matches 34; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 2 TTAAGTCCCTAGCTGATACATAAAGCGCATTTGACCATTCACCATTTGG 53
Db 275 TTATAGCCTAGCTCTAAAGGATTAACCTGATTCAGTTTCACCACTCTGG 224

RESULT 52

US-09-764-869-459/c
; Sequence 459, Application US/09764869
; Patent No. US20020061521A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007
; CURRENT APPLICATION NUMBER: US/09/764,869
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2442
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 459
; LENGTH: 644
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (3)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (30)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (523)

; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (526)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (596)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (630)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-869-459

Query Match 36.5%; Score 23; DB 9; Length 644;
Best Local Similarity 65.3%; Pred. No. 86;
Matches 32; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 14 CTCGATACATAAAGCGCATTTGACCATTCACCATTTGGTGTGCACCT 62
Db 553 CTCCTTAATAATACAGACCCCTGGTCCANTCNCACATGGGCTTGCACCT 505

RESULT 53

US-10-091-504-459/c
; Sequence 459, Application US/10091504
; Publication No. US20030039908A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007C1
; CURRENT APPLICATION NUMBER: US/10/091,504
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 2442
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 459
; LENGTH: 644
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (30)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (523)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (526)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (596)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (630)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-091-504-459

Query Match 36.5%; Score 23; DB 14; Length 644;
Best Local Similarity 65.3%; Pred. No. 86;
Matches 32; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 14 CTCGATACATAAAGCGCATTTGACCATTCACCATTTGGTGTGCACCT 62
Db 553 CTCCTTAATAATACAGACCCCTGGTCCANTCNCACATGGGCTTGCACCT 505

RESULT 54

US-10-227-577-459/c
; Sequence 459, Application US/10227577
; Publication No. US20040005575A1
; GENERAL INFORMATION:

```

; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007C2
; CURRENT APPLICATION NUMBER: US/10/227,577
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 10/091,504
; PRIOR FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: 03/764,869
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2442
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 459
; LENGTH: 644
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (3)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (30)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (523)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (526)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (596)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (630)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-227-577-459

Query Match          36.5%; Score 23; DB 15; Length 644;
Best Local Similarity 65.3%; Pred.No. 86;
Matches 32; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy      14  CTCGATACATAAAGCCATTGACCATTCACCATTCACCATTCGTTGCACT 62
          |||||
Db      553  CTCTTAATATACGAGCCCTGCTCCATCNCACATGCGCTTGCACT 505

RESULT 55
US-10-027-632-115884
; Sequence 115884, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.

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; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 115884
; LENGTH: 798
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-115884

Query Match          36.5%; Score 23; DB 15; Length 798;
Best Local Similarity 63.6%; Pred.No. 92;
Matches 35; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy      8  GCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTCACCATTCGTTGCACT 62
          |||||
Db      101  GACTGCTAGAGAGATTAAGGCTACTGTGCACTTTCCACATTTTGTTCGT 155

RESULT 56
US-09-738-626-1/c
; Sequence 1, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 1
; LENGTH: 3309400
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-1

Query Match          36.5%; Score 23; DB 9; Length 3309400;
Best Local Similarity 63.6%; Pred.No. 7.8e+02;
Matches 35; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

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```
Qy 2 TTAAGTCCTAGCTGATACATTAAGGCAATTCACCATTCACCACTGGTGT 56
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1882470 TTAAGTCCTGAGCGCATATAAAACACCGCTGTTGAAGTAATCAACAGCGTGT 1882416

RESULT 57
US-10-424-599-60097
; Sequence 60097, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 60097
; LENGTH: 347
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_2527C.1
US-10-424-599-60097

Query Match 36.2%; Score 22.8; DB 12; Length 347;
Best Local Similarity 66.0%; Pred. No. 84;
Matches 33; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 13 GCTCGATCAATAAAGCCATTTGACCAATTCACCAATTCGTTGTCACCT 62
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 82 GCTTGAATAAAACCTATTTGACCAATTCGTTGTCGAGTACTT 131

RESULT 58
US-10-027-632-24941
; Sequence 24941, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24941
; LENGTH: 605
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-24941

Query Match 36.2%; Score 22.8; DB 15; Length 605;
Best Local Similarity 79.4%; Pred. No. 1e+02;
Matches 27; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
```

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Qy 18 ATACAATAAAGCCATTTGACCAATTCACCAATTCACCACTT 51
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 114 ATCCAATAAAGTCCATTTGGCCATAGACACACTT 147

RESULT 59
US-10-027-632-106857/c
; Sequence 106857, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 106857
; LENGTH: 645
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-106857

Query Match 36.2%; Score 22.8; DB 15; Length 645;
Best Local Similarity 79.4%; Pred. No. 1e+02;
Matches 27; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 18 ATACAATAAAGCCATTTGACCAATTCACCAATTCACCACTT 51
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 530 ATCCAATAAAGTCCATTTGGCCATAGACACACTT 497

RESULT 60
US-10-027-632-136614/c
; Sequence 136614, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
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; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 136614
; LENGTH: 645
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-136614

Query Match      36.2%; Score 22.8; DB 15; Length 645;
Best Local Similarity 79.4%; Pred. No. 1.e+02;
Matches 27; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 18 ATCAATAAAGCCATTGACCAATTCACCAATT 51
Db 530 ATCCATAAAGTCCATTGGCCATAGACACATT 497

RESULT 61
US-10-424-599-1697/c
; Sequence 1697, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 1697
; LENGTH: 822
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_101531C.1
US-10-424-599-1697

Query Match      36.2%; Score 22.8; DB 12; Length 822;
Best Local Similarity 62.1%; Pred. No. 1.e+02;
Matches 36; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 3 TAAGTGCTAGCTCGATACATAAAGCCATTGACCAATTCACCAATTTGGTGTGCAC 60
Db 688 TAAGTAGCTTGACAAATATAGGAATGCCCATGATCAATTACCACCTTAGTGTCTC 631

RESULT 62
US-10-424-599-100590
; Sequence 100590, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 100590
; LENGTH: 388
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(388)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:

; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 136614
; LENGTH: 645
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-136614

; OTHER INFORMATION: Clone ID: PAT_MRT3847_61847C.1
US-10-424-599-100590

Query Match      35.9%; Score 22.6; DB 12; Length 388;
Best Local Similarity 60.7%; Pred. No. 1.e+02;
Matches 37; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 TTTAAGTGCTAGCTCGATACATAAAGCCATTGACCAATTCACCAATTTGGTGTGCAC 60
Db 160 TCTAAGGCCCGCTCGATACATAAAGCCATTGACCAATTCACCAATTTGGTGTGCAC 219

QY 61 C 61
Db 220 C 220

RESULT 63
US-10-311-455-1061/c
; Sequence 1061, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining Cytosine Methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 1061
; LENGTH: 6696
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1061

Query Match      35.9%; Score 22.6; DB 14; Length 6696;
Best Local Similarity 60.7%; Pred. No. 2.6e+02;
Matches 37; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 3 TAAGTGCTAGCTCGATACATAAAGCCATTGACCAATTCACCAATTTGGTGTGCACCT 62
Db 2816 TAATTTTATATTTTCAATAAATAAATAATTCACCAATTCACCAATTTCTTTACCT 2757

QY 63 C 63
Db 2756 C 2756

RESULT 64
US-10-240-485-87/c
; Sequence 87, Application US/10240485
; Publication No. US20030148327A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with
; FILE REFERENCE: 5013.1007
; CURRENT APPLICATION NUMBER: US/10/240,485
; CURRENT FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: PCT/EP01/03970
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8

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; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 202
; SEQ ID NO 87
; LENGTH: 6696
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-240-485-87

Query Match 35.9%; Score 22.6; DB 14; Length 6696;
Best Local Similarity 60.7%; Pred. No. 2.6e+02;
Matches 37; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 3 TAAGTGGCTAGCTCGATACATATAAGCCGCAATTTGACCATTCACCATTCACCATTCGTTGGTGACCT 62
Db 2816 TAAATTTTATATTTTCAATAAAAAACAAATTTTCCACCATTCACCATTCACCATTCGTTGGTGACCT 2757

QY 63 C 63
Db 2756 C 2756

RESULT 65
US-10-161-510-1
; Sequence 1, Application US/10161510
; Publication No. US20020192695A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: PIERS AS MODIFIERS OF THE P53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX02-074C
; CURRENT APPLICATION NUMBER: US/10/161,510
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/328,605
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/357,253
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 133893
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-161-510-1

Query Match 35.9%; Score 22.6; DB 13; Length 133893;
Best Local Similarity 60.7%; Pred. No. 6.8e+02;
Matches 37; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 3 TAAGTGGCTAGCTCGATACATATAAGCCGCAATTTGACCATTCACCATTCACCATTCGTTGGTGACCT 62
Db 16835 TATATACCTCCCTCGAAGGAGGACGAGCAATTCATCCATTCATCCATTCGTTGGTGACCT 16894

QY 63 C 63
Db 16895 C 16895

RESULT 66
US-09-908-975-5222/c
; Sequence 5222, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon

; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICING
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 5222
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-5222

Query Match 35.6%; Score 22.4; DB 10; Length 60;
Best Local Similarity 62.5%; Pred. No. 68;
Matches 35; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 7 TGCCTAGCTCGATACATATAAGCCGCAATTTGACCATTCACCATTCACCATTCGTTGGTGACCT 62
Db 56 TGTATTGGTGGCATCAACACCGCAATCTGACCATTCCTCCTCAGTGAGATAGCCCT 1

RESULT 67
US-10-027-632-67297
; Sequence 67297, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67297
; LENGTH: 433
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-67297

Query Match 35.6%; Score 22.4; DB 15; Length 433;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 32; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 4 AAGTGGCTAGCTCGATACATATAAGCCGCAATTTGACCATTCACCATTCACCATTCGTTGGTGACCT 51
Db 130 AAGTGGCTAGCTCGATACATATAAGCCGCAATTCATCCATTCCTCCTCAGTGAGATAGCCCT 177

RESULT 68
US-10-027-632-311371

```
; Sequence 311371, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108927.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 311371
; LENGTH: 433
; TYPE: DNA
; ORGANISM: Human
; US-10-027-632-311371

Query Match      35.6%; Score 22.4; DB 15; Length 433;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 32; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 4 AAGTGGCTAGCTCGATACATAAAGCCGATTTGACCATTCACACATT 51
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 130 AAGTGCATAGGCTAGAGAGACCAAGACCAAGACCTTACCAATT 177

RESULT 69
US-09-814-353-4354
; Sequence 4354, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4354
; LENGTH: 501
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-814-353-4354

Query Match      35.6%; Score 22.4; DB 15; Length 433;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 32; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 4 AAGTGGCTAGCTCGATACATAAAGCCGATTTGACCATTCACACATT 51
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 130 AAGTGCATAGGCTAGAGAGACCAAGACCAAGACCTTACCAATT 177
```

```
Query Match      35.6%; Score 22.4; DB 10; Length 501;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 32; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 14 CTCGATACATAAAGCCGATTTGACCATTCACCAATTGGTGTGCACC 61
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 393 CTTGAACAACAATAAACAATTGATCTCTCACACAATTTTGTGCATC 440

RESULT 70
US-09-814-353-10658
; Sequence 10658, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10658
; LENGTH: 501
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-814-353-10658

Query Match      35.6%; Score 22.4; DB 10; Length 501;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 32; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 14 CTCGATACATAAAGCCGATTTGACCATTCACCAATTGGTGTGCACC 61
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 393 CTTGAACAACAATAAACAATTGATCTCTCACACAATTTTGTGCATC 440

RESULT 71
US-10-138-701-54/c
; Sequence 54, Application US/10138701
; Publication No. US20030186364A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc. et al.
; TITLE OF INVENTION: Staphylococcus aureus genes and polypeptides
; FILE REFERENCE: PR484
; CURRENT APPLICATION NUMBER: US/10/138,701
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: US/09/512,255A
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/098,964
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: US 60/009,861
; PRIOR FILING DATE: 1996-01-05
; PRIOR APPLICATION NUMBER: PCT/ US99/19726
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: US 08/956,171
; PRIOR FILING DATE: 1997-10-20
```

; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 54
; LENGTH: 504
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-138-701-54

Query Match 35.6%; Score 22.4; DB 14; Length 504;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 32; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
QY 4 AAGTGGCTAGCTGATACATAAAGCCATTGACCATTCACCACTT 51
DB 276 ACCTTCGGGGCGTGGTCAATAAAGCACTTCCTCCCTTAACACACTT 229

RESULT 72

US-09-814-353-17042
; Sequence 17042, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17042
; LENGTH: 571
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-17042

Query Match 35.6%; Score 22.4; DB 10; Length 571;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 32; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
QY 14 CTCGATACATAAAGCCATTGACCATTCACCACTTGGTGTGCAC 61
DB 471 CTGAAACACATAAAGCACTTCCTCACACAACTTTTGTGCATC 518

RESULT 73

US-10-027-632-55098/c
; Sequence 55098, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12

; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55098
; LENGTH: 586
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-55098

Query Match 35.6%; Score 22.4; DB 15; Length 586;
Best Local Similarity 72.5%; Pred. No. 1.4e+02;
Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 12 AGCTCGATACATAAAGCCATTGACCATTCACCACTT 51
DB 585 AGCTTCTTTGATATGGGACATTGACCATTCATGACATT 546

RESULT 74

US-10-027-632-315554/c
; Sequence 315554, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 315554
; LENGTH: 586
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-315554

Query Match 35.6%; Score 22.4; DB 15; Length 586;
Best Local Similarity 72.5%; Pred. No. 1.4e+02;
Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 12 AGCTCGATACATAAAGCCATTGACCATTCACCACTT 51
DB 585 AGCTTCTTTGATATGGGACATTGACCATTCATGACATT 546

RESULT 75

US-10-027-632-202555

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; Sequence 202555, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 202555
; LENGTH: 611
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-202555

Query Match      35.6%; Score 22.4; DB 15; Length 611;
Best Local Similarity 62.5%; Pred. No. 1.4e+02;
Matches 35; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy      7  TGCTAGCTCGATACATAACGCCATTGACCATTCACCATTCGTGTGCACCT 62
Db     411  TTCACAGTCTCTTCCAGATAGACATTGACCTCCAGCTCTTTCAGGTGACCT 466
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Search completed: March 11, 2004, 11:20:29
Job time : 52.7306 secs